E value	1.0e-30
Match length	66
% identity	98
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	123210
Contig ID	10926_2.R1010
5'-most EST	LIB35-042-Q1-E1-C7
Method	BLASTN
NCBI GI	g2832667
BLAST score	129
E value	4.0e-66
Match length	324
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	123211
Contig ID	10932_1.R1010
5'-most EST	jC-atXLIB327410P1g06b1
Method	BLASTX
NCBI GI	g1653702
BLAST score	295
E value	2.0e-26
Match length	82
% identity	72
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	123212
Contig ID	10937_1.R1010
5'-most EST	jC-atXLIB327415P4a10b1

Seq. No.	123213
Contig ID	10938_1.R1010
5'-most EST	jC-atXLIB327415P4a11b1
Method	BLASTX
NCBI GI	g3413704
BLAST score	157
E value	2.0e-10
Match length	118
% identity	37
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123214
Contig ID	10941_1.R1010
5'-most EST	jC-atXLIB327415P4a05b1
Method	BLASTX
NCBI GI	g2129772
BLAST score	1354
E value	1.0e-150
Match length	284
% identity	86
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	123215
Contig ID	10950_1.R1010
5'-most EST	LIB22-087-Q1-E1-H6
Method	BLASTX
NCBI GI	g3152581
BLAST score	640
E value	8.0e-67
Match length	118
% identity	99
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	123216
Contig ID	10962_1.R1010
5'-most EST	jC-atXmonuni25Bd02b1

Seq. No.	123217
Contig ID	10968_1.R1010
5'-most EST	LIB3176-037-P1-K1-B10
Method	BLASTX
NCBI GI	g4538897
BLAST score	737
E value	3.0e-78
Match length	150
% identity	98
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	123218
Contig ID	10968_3.R1010
5'-most EST	jC-atXLIB327415P1a12b1
Method	BLASTX
NCBI GI	g4538897
BLAST score	77
E value	1.0e-41
Match length	112
% identity	94
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	123219
Contig ID	10969_1.R1010
5'-most EST	jC-atXLIB327426P3h04b1
Method	BLASTX
NCBI GI	g1256424
BLAST score	474
E value	4.0e-53
Match length	126
% identity	89
NCBI Description	(U51119) cysteine proteinase inhibitor [Brassica campestris]

Seq. No.	123220
Contig ID	10970_1.R1010
5'-most EST	LIB3176-007-P1-K1-C12
Method	BLASTN
NCBI GI	g3241917
BLAST score	185

E value	2.0e-99
Match length	715
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	123221
Contig ID	10977_1.R1010
5'-most EST	g937701
Method	BLASTX
NCBI GI	g731415
BLAST score	401
E value	5.0e-39
Match length	159
% identity	53
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 6 >gi_1077608_pir__S50428 hypothetical protein YEL031w - yeast (Saccharomyces cerevisiae) >gi_602398 (U18530) P-type ATPase; YEL031W [Saccharomyces cerevisiae]

Seq. No.	123222
Contig ID	10980_1.R1010
5'-most EST	jC-atXLIB327414P4h11b2
Method	BLASTN
NCBI GI	g3492855
BLAST score	205
E value	1.0e-111
Match length	513
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	123223
Contig ID	10982_1.R1010
5'-most EST	LIB3176-118-P2-K1-F11
Method	BLASTX
NCBI GI	g3150415
BLAST score	592
E value	2.0e-61
Match length	120
% identity	35
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	123224
Contig ID	10985_1.R1010
5'-most EST	g2749131
Method	BLASTN
NCBI GI	g3033373
BLAST score	375
E value	0.0e+00
Match length	446
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123225
Contig ID	10986_1.R1010
5'-most EST	jC-atXLIB327423P1f11b1
Method	BLASTX
NCBI GI	g3386618
BLAST score	486
E value	1.0e-48
Match length	168
% identity	62
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123226
Contig ID	10988_1.R1010
5'-most EST	jC-atXLIB327414P1h11b1
Method	BLASTX
NCBI GI	g4314386
BLAST score	682
E value	7.0e-72
Match length	148
% identity	85
NCBI Description	(AC006232) putative rac GTPase activating protein [Arabidopsis thaliana]

Seq. No.	123227
Contig ID	10988_2.R1010
5'-most EST	LIB3175-032-P1-K1-B11
Method	BLASTX
NCBI GI	g4314386
BLAST score	205
E value	2.0e-26
Match length	127
% identity	60
NCBI Description	(AC006232) putative rac GTPase activating protein [Arabidopsis thaliana]

Seq. No.	123228
Contig ID	10995_1.R1010
5'-most EST	LIB22-088-Q1-E1-E10
Method	BLASTX
NCBI GI	g4240303
BLAST score	145
E value	4.0e-09
Match length	65
% identity	43
NCBI Description	(AB020714) KIAA0907 protein [Homo sapiens]

Seq. No.	123229
Contig ID	10997_1.R1010
5'-most EST	g1158671
Method	BLASTX
NCBI GI	g3142294
BLAST score	642
E value	3.0e-67
Match length	127
% identity	98
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and

gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	123230
Contig ID	10999_1.R1010
5'-most EST	LIB24-077-Q1-E1-F10
Method	BLASTX
NCBI GI	g2894599
BLAST score	603
E value	9.0e-63
Match length	107
% identity	100
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	123231
Contig ID	11000_1.R1010
5'-most EST	g2762284
Method	BLASTX
NCBI GI	g1086586
BLAST score	349
E value	2.0e-32
Match length	232
% identity	32
NCBI Description	(U41007) similar to G beta repeats (PROSITE:PS00670) [Caenorhabditis elegans]

Seq. No.	123232
Contig ID	11000_3.R1010
5'-most EST	LIB22-088-Q1-E1-E4
Method	BLASTN
NCBI GI	g4159700
BLAST score	227
E value	1.0e-124
Match length	381
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	123233
Contig ID	11001_1.R1010
5'-most EST	LIB22-088-Q1-E1-E5

Seq. No.	123234
Contig ID	11003_1.R1010
5'-most EST	g493463
Method	BLASTX
NCBI GI	g2642157
BLAST score	608
E value	1.0e-102
Match length	176
% identity	97
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	123235
Contig ID	11010_1.R1010
5'-most EST	g936791
Method	BLASTN
NCBI GI	g2570223

BLAST score	305
E value	1.0e-171
Match length	1049
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123236
Contig ID	11025_1.R1010
5'-most EST	LIB22-088-Q1-E1-G7
Method	BLASTN
NCBI GI	g3449322
BLAST score	413
E value	0.0e+00
Match length	575
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	123237
Contig ID	11026_1.R1010
5'-most EST	LIB3175-068-P1-K1-G6
Method	BLASTX
NCBI GI	g3757520
BLAST score	227
E value	3.0e-18
Match length	165
% identity	35
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	123238
Contig ID	11030_1.R1010
5'-most EST	jC-atXLIB327422P1h11b1
Method	BLASTX
NCBI GI	g3157927
BLAST score	414
E value	3.0e-40
Match length	136
% identity	62
NCBI Description	(AC002131) Contains similarity to GDP-dissociation inhibitor gb_L07918 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	123239
Contig ID	11036_1.R1010
5'-most EST	ARABL1-025-Q1-B1-A5
Method	BLASTN
NCBI GI	g2264302
BLAST score	409
E value	0.0e+00
Match length	669
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	123240
Contig ID	11038_1.R1010

5'-most EST	LIB22-089-Q1-E1-A10
Method	BLASTX
NCBI GI	g3377764
BLAST score	815
E value	2.0e-87
Match length	169
% identity	88
NCBI Description	(AF079851) nodule-enhanced sucrose synthase [Pisum sativum]

Seq. No.	123241
Contig ID	11040_1.R1010
5'-most EST	jC-atXLIB327414P3f01b1
Method	BLASTX
NCBI GI	g1781226
BLAST score	316
E value	2.0e-28
Match length	336
% identity	29
NCBI Description	(Z83867) fadB4 [Mycobacterium tuberculosis]

Seq. No.	123242
Contig ID	11041_1.R1010
5'-most EST	jC-atXP82CG2B4T7d3
Method	BLASTX
NCBI GI	g3850821
BLAST score	321
E value	3.0e-29
Match length	104
% identity	66
NCBI Description	(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]

Seq. No.	123243
Contig ID	11041_2.R1010
5'-most EST	jC-atXP83CG3A11T7091a1
Method	BLASTN
NCBI GI	g4006885
BLAST score	218
E value	1.0e-119
Match length	483
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	123244
Contig ID	11042_1.R1010
5'-most EST	jC-alXLIB327434P2c12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	1.0e-20
Match length	61
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 123245

Contig ID	11044_1.R1010
5'-most EST	LIB23-017-Q1-E1-D3
Method	BLASTX
NCBI GI	g2137812
BLAST score	249
E value	3.0e-21
Match length	114
% identity	46
NCBI Description	tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) precursor - mouse >gi_1199594 (U32197) folylpolyglutamate synthetase [Mus musculus] >gi_1587164_prf__2206297A folylpoly-gamma-Glu synthetase [Mus musculus]

Seq. No.	123246
Contig ID	11046_1.R1010
5'-most EST	jC-atXLIB327408P2g09b1
Method	BLASTX
NCBI GI	g2252840
BLAST score	904
E value	2.0e-97
Match length	211
% identity	83
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	123247
Contig ID	11049_1.R1010
5'-most EST	jC-atXLIB327414P4f08b2

Seq. No.	123248
Contig ID	11050_1.R1010
5'-most EST	jC-atXP18C108P24T7d2
Method	BLASTX
NCBI GI	g2244818
BLAST score	196
E value	8.0e-15
Match length	145
% identity	41
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123249
Contig ID	11054_1.R1010
5'-most EST	jC-atXLIB327414P3f08b1

Seq. No.	123250
Contig ID	11058_1.R1010
5'-most EST	g905447
Method	BLASTX
NCBI GI	g3329475
BLAST score	71
E value	1.0e-36
Match length	257
% identity	37
NCBI Description	(AF069781) Bem46-like protein [Drosophila melanogaster]

Seq. No.	123251
Contig ID	11059_1.R1010

5'-most EST	jC-atXLIB327414P1g11b1
Method	BLASTX
NCBI GI	g3218410
BLAST score	313
E value	2.0e-28
Match length	144
% identity	47
NCBI Description	(AL023859) putative prolyl-trna synthetase [Schizosaccharomyces pombe]

Seq. No.	123252
Contig ID	11059_2.R1010
5'-most EST	LIB3176-036-P1-K1-A7
Method	BLASTX
NCBI GI	g459009
BLAST score	566
E value	4.0e-58
Match length	194
% identity	54
NCBI Description	(U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]

Seq. No.	123253
Contig ID	11060_2.R1010
5'-most EST	jC-atXP60C198F21T7038d1
Method	BLASTX
NCBI GI	g4006829
BLAST score	273
E value	1.0e-23
Match length	208
% identity	21
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	123254
Contig ID	11061_1.R1010
5'-most EST	LIB25-015-Q1-E1-F12
Method	BLASTX
NCBI GI	g2459420
BLAST score	688
E value	2.0e-72
Match length	131
% identity	100
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	123255
Contig ID	11061_3.R1010
5'-most EST	g3449824
Method	BLASTX
NCBI GI	g2341028
BLAST score	312
E value	1.0e-28
Match length	69
% identity	90
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene.

[Arabidopsis thaliana]

Seq. No.	123256
Contig ID	11062_1.R1010
5'-most EST	jC-atXLIB327414P2b01b1
Method	BLASTX
NCBI GI	g4455159
BLAST score	612
E value	2.0e-63
Match length	105
% identity	99
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	123257
Contig ID	11062_3.R1010
5'-most EST	LIB24-035-Q1-E1-G9
Method	BLASTN
NCBI GI	g2828278
BLAST score	372
E value	0.0e+00
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	123258
Contig ID	11064_1.R1010
5'-most EST	jC-atXLIB327414P3g01b1
Method	BLASTX
NCBI GI	g3413707
BLAST score	588
E value	7.0e-61
Match length	116
% identity	36
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123259
Contig ID	11066_1.R1010
5'-most EST	jC-atXLIB327414P2b05b1
Method	BLASTX
NCBI GI	g3878737
BLAST score	183
E value	4.0e-13
Match length	132
% identity	36
NCBI Description	(Z73428) predicted using Genefinder; cDNA EST EMBL:T01774 comes from this gene; cDNA EST yk470a9.3 comes from this gene; cDNA EST yk470a9.5 comes from this gene; cDNA EST yk476b6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	123260
Contig ID	11068_1.R1010
5'-most EST	jC-atXLIB327414P2b04b1
Method	BLASTX
NCBI GI	g4093155
BLAST score	202
E value	1.0e-15

Match length	112
% identity	49
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	123261
Contig ID	11078_1.R1010
5'-most EST	jC-atXLIB327414P3g09b1

Seq. No.	123262
Contig ID	11080_1.R1010
5'-most EST	jC-atXLIB327414P3g10b1
Method	BLASTX
NCBI GI	g3335372
BLAST score	197
E value	5.0e-15
Match length	96
% identity	41
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	123263
Contig ID	11084_1.R1010
5'-most EST	LIB3176-025-P1-K1-A9
Method	BLASTX
NCBI GI	g3935168
BLAST score	594
E value	2.0e-61
Match length	207
% identity	59
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	123264
Contig ID	11085_1.R1010
5'-most EST	jC-alXLIB327435P2c04a1
Method	BLASTX
NCBI GI	g4186184
BLAST score	275
E value	5.0e-24
Match length	126
% identity	44
NCBI Description	(AF111168) unknown [Homo sapiens]

Seq. No.	123265
Contig ID	11091_1.R1010
5'-most EST	jC-atXLIB327414P1h10b1
Method	BLASTN
NCBI GI	g2351062
BLAST score	348
E value	0.0e+00
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	123266
Contig ID	11093_1.R1010
5'-most EST	LIB22-089-Q1-E1-F10

Method	BLASTX
NCBI GI	g2828241
BLAST score	515
E value	4.0e-52
Match length	186
% identity	51
NCBI Description	(AJ000885) Expansin [Brassica napus]

Seq. No.	123267
Contig ID	11096_1.R1010
5'-most EST	jC-atX24056Q1E2G06b1
Method	BLASTX
NCBI GI	g4185140
BLAST score	332
E value	2.0e-38
Match length	88
% identity	91
NCBI Description	(AC005724) putative small nuclear ribonucleoprotein E (snRNP-E) [Arabidopsis thaliana]

Seq. No.	123268
Contig ID	11098_1.R1010
5'-most EST	jC-atXLIB327416P4f07b1
Method	BLASTX
NCBI GI	g2191141
BLAST score	944
E value	1.0e-102
Match length	182
% identity	100
NCBI Description	(AF007269) A_IG002N01.21 gene product [Arabidopsis thaliana]

Seq. No.	123269
Contig ID	11100_1.R1010
5'-most EST	LIB22-089-Q1-E1-F8
Method	BLASTN
NCBI GI	g1143510
BLAST score	33
E value	6.0e-09
Match length	69
% identity	87
NCBI Description	M.domestica Borkh mRNA for serine/threonine protein phosphatase (PPX)

Seq. No.	123270
Contig ID	11104_1.R1010
5'-most EST	jC-atXLIB327415P2a12b2

Seq. No.	123271
Contig ID	11107_1.R1010
5'-most EST	jC-atXLIB327415P4a03b1
Method	BLASTN
NCBI GI	g4757392
BLAST score	278
E value	1.0e-155
Match length	504
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	123272
Contig ID	11108_1.R1010
5'-most EST	jC-atXLIB327401P2c01a1
Method	BLASTX
NCBI GI	g1938424
BLAST score	261
E value	1.0e-32
Match length	187
% identity	46
NCBI Description	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No.	123273
Contig ID	11109_1.R1010
5'-most EST	LIB3176-025-P1-K1-C7
Method	BLASTX
NCBI GI	g3650034
BLAST score	561
E value	1.0e-57
Match length	181
% identity	65
NCBI Description	(AC005396) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	123274
Contig ID	11113_1.R1010
5'-most EST	jC-atXP64C205M1T7d1
Method	BLASTX
NCBI GI	g556409
BLAST score	371
E value	5.0e-35
Match length	143
% identity	56
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	123275
Contig ID	11118_1.R1010
5'-most EST	jC-atX25069Q1E1E11b1
Method	BLASTX
NCBI GI	g1653655
BLAST score	371
E value	7.0e-35
Match length	175
% identity	45
NCBI Description	(D90915) ATP-dependent Clp protease proteolytic subunit [Synechocystis sp.]

Seq. No.	123276
Contig ID	11121_2.R1010
5'-most EST	LIB22-089-Q1-E1-H8

Seq. No.	123277
Contig ID	11123_1.R1010
5'-most EST	LIB25-068-Q1-E1-E1

Method	BLASTX
NCBI GI	g4539327
BLAST score	423
E value	2.0e-50
Match length	106
% identity	89
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	123278
Contig ID	11128_1.R1010
5'-most EST	jC-atXLIB327427P4e10b2
Method	BLASTN
NCBI GI	g2244870
BLAST score	407
E value	0.0e+00
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	123279
Contig ID	11130_1.R1010
5'-most EST	LIB3175-037-P1-K1-E10
Method	BLASTX
NCBI GI	g3445209
BLAST score	634
E value	3.0e-66
Match length	153
% identity	72
NCBI Description	(AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	123280
Contig ID	11132_1.R1010
5'-most EST	jC-atXLIB327427P4e06b2
Method	BLASTN
NCBI GI	g4757662
BLAST score	498
E value	0.0e+00
Match length	498
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	123281
Contig ID	11133_1.R1010
5'-most EST	jC-atXLIB327427P3e06b2
Method	BLASTX
NCBI GI	g2435519
BLAST score	645
E value	3.0e-67
Match length	202
% identity	63
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	123282
Contig ID	11134_1.R1010
5'-most EST	jC-atXLIB327430P4g07b1
Method	BLASTN
NCBI GI	g4204173
BLAST score	373
E value	0.0e+00
Match length	847
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123283
Contig ID	11134_2.R1010
5'-most EST	jC-atXP102CE5F8T7064d1
Method	BLASTN
NCBI GI	g4204173
BLAST score	223
E value	1.0e-122
Match length	239
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123284
Contig ID	11136_1.R1010
5'-most EST	jC-atXLIB327427P3e12b2
Method	BLASTX
NCBI GI	g3540201
BLAST score	666
E value	7.0e-70
Match length	126
% identity	100
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No.	123285
Contig ID	11138_1.R1010
5'-most EST	g2048939
Method	BLASTX
NCBI GI	g4115387
BLAST score	357
E value	8.0e-34
Match length	95
% identity	77
NCBI Description	(AC005967) putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	123286
Contig ID	11138_2.R1010
5'-most EST	jC-atXLIB327414P2h11b1
Method	BLASTN
NCBI GI	g1871173
BLAST score	368
E value	0.0e+00
Match length	754
% identity	97

NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence
Seq. No.	123287
Contig ID	11139_1.R1010
5'-most EST	jC-atXP79C230N2T7b1
Method	BLASTN
NCBI GI	g3269280
BLAST score	315
E value	1.0e-177
Match length	635
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)
Seq. No.	123288
Contig ID	11139_2.R1010
5'-most EST	jC-atXLIB327408P1a05b1
Method	BLASTN
NCBI GI	g3269280
BLAST score	351
E value	0.0e+00
Match length	503
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)
Seq. No.	123289
Contig ID	11139_3.R1010
5'-most EST	LIB24-115-Q1-E1-G2
Method	BLASTX
NCBI GI	g3269293
BLAST score	349
E value	7.0e-33
Match length	97
% identity	71
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	123290
Contig ID	11140_1.R1010
5'-most EST	jC-atXLIB327427P2f03b1
Method	BLASTX
NCBI GI	g3953482
BLAST score	463
E value	3.0e-46
Match length	89
% identity	99
NCBI Description	(AC002328) F22O2.27 [Arabidopsis thaliana]
Seq. No.	123291
Contig ID	11141_1.R1010
5'-most EST	LIB3175-018-P1-K1-G9
Method	BLASTX
NCBI GI	g4115387
BLAST score	2000
E value	0.0e+00
Match length	418

% identity	93
NCBI Description	(AC005967) putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
Seq. No.	123292
Contig ID	11142_1.R1010
5'-most EST	jC-atXLIB327421P1f12b1
Seq. No.	123293
Contig ID	11143_1.R1010
5'-most EST	LIB3175-061-P1-K1-C4
Seq. No.	123294
Contig ID	11146_1.R1010
5'-most EST	jC-atXLIB327427P2f04b1
Method	BLASTX
NCBI GI	g1352683
BLAST score	996
E value	1.0e-108
Match length	233
% identity	90
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]
Seq. No.	123295
Contig ID	11147_1.R1010
5'-most EST	jC-atXLIB327427P1f06b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	24
E value	2.0e-03
Match length	47
% identity	56
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.	123296
Contig ID	11148_1.R1010
5'-most EST	jC-alX24093Q1E1C08b1
Method	BLASTX
NCBI GI	g4454032
BLAST score	572
E value	7.0e-59
Match length	202
% identity	57
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]
Seq. No.	123297
Contig ID	11158_1.R1010
5'-most EST	LIB25-007-Q1-E1-F10
Seq. No.	123298
Contig ID	11160_1.R1010
5'-most EST	jC-atXmonuni27Bf10b1
Method	BLASTX
NCBI GI	g3006088
BLAST score	183

E value	4.0e-13
Match length	82
% identity	45
NCBI Description	(AJ222724) SGT protein [Rattus norvegicus]

Seq. No.	123299
Contig ID	11163_1.R1010
5'-most EST	LIB23-001-Q1-E1-D4
Method	BLASTX
NCBI GI	g4567283
BLAST score	186
E value	1.0e-13
Match length	124
% identity	77
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	123300
Contig ID	11165_1.R1010
5'-most EST	jC-atXLIB327422P3b09b2

Seq. No.	123301
Contig ID	11166_1.R1010
5'-most EST	jC-atXLIB327427P2f09b1
Method	BLASTN
NCBI GI	g4757678
BLAST score	139
E value	5.0e-72
Match length	526
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	123302
Contig ID	11168_1.R1010
5'-most EST	jC-atXP91C247D6T7b1
Method	BLASTN
NCBI GI	g4335744
BLAST score	805
E value	0.0e+00
Match length	805
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123303
Contig ID	11168_2.R1010
5'-most EST	LIB35-041-Q1-E1-E10
Method	BLASTN
NCBI GI	g4335744
BLAST score	534
E value	0.0e+00
Match length	885
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 123304

Contig ID	11170_1.R1010
5'-most EST	jC-atXmonuni27Df02b1
Seq. No.	123305
Contig ID	11171_1.R1010
5'-most EST	jC-atXLIB327427P4f04b2
Method	BLASTX
NCBI GI	g4325343
BLAST score	699
E value	7.0e-74
Match length	154
% identity	90
NCBI Description	(AF128393) contains similarity to homeobox domains (Pfam: PF00046, Score,36.5, E=6.9e-08, N=1) [Arabidopsis thaliana]
Seq. No.	123306
Contig ID	11175_1.R1010
5'-most EST	jC-atX24049Q1E1D04b1
Method	BLASTX
NCBI GI	g99749
BLAST score	262
E value	2.0e-22
Match length	96
% identity	65
NCBI Description	probable serine/threonine-specific protein kinase ATPK64 (EC 2.7.1.-) - Arabidopsis thaliana >gi_217843_dbj_BAA01731_ (D10937) protein kinase [Arabidopsis thaliana]
Seq. No.	123307
Contig ID	11176_1.R1010
5'-most EST	jC-atXLIB327427P3f05b2
Method	BLASTX
NCBI GI	g4220512
BLAST score	190
E value	4.0e-14
Match length	93
% identity	42
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]
Seq. No.	123308
Contig ID	11177_1.R1010
5'-most EST	jC-atXLIB327427P2f12b1
Seq. No.	123309
Contig ID	11181_1.R1010
5'-most EST	jC-atXLIB327427P4f06b2
Method	BLASTX
NCBI GI	g2289005
BLAST score	555
E value	5.0e-57
Match length	109
% identity	96
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana] >gi_3763937 (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123310
Contig ID	11182_1.R1010
5'-most EST	jC-atXLIB327430P1g11b1
Method	BLASTN
NCBI GI	g4589428
BLAST score	487
E value	0.0e+00
Match length	718
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	123311
Contig ID	11182_2.R1010
5'-most EST	jC-alX25087Q1E1D08b1
Method	BLASTN
NCBI GI	g4589428
BLAST score	356
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	123312
Contig ID	11188_1.R1010
5'-most EST	g937086
Method	BLASTX
NCBI GI	g1799785
BLAST score	455
E value	4.0e-45
Match length	181
% identity	51
NCBI Description	(D90867) OXALYL-COA DECARBOXYLASE (EC 4.1.1.8). [Escherichia coli]

Seq. No.	123313
Contig ID	11190_1.R1010
5'-most EST	jC-atXLIB327427P4f07b2

Seq. No.	123314
Contig ID	11190_2.R1010
5'-most EST	jC-atXP64C207I6T7s1

Seq. No.	123315
Contig ID	11194_1.R1010
5'-most EST	LIB24-039-Q1-E1-E9
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123316
Contig ID	11196_1.R1010

5'-most EST	jC-atXLIB327427P1g02a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123317
Contig ID	11198_1.R1010
5'-most EST	jC-atXLIB327427P1g04b1

Seq. No.	123318
Contig ID	11200_1.R1010
5'-most EST	jC-atXLIB327417P3h06b1
Method	BLASTX
NCBI GI	g4539383
BLAST score	1001
E value	1.0e-109
Match length	229
% identity	90
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	123319
Contig ID	11200_2.R1010
5'-most EST	jC-atXLIB327427P4f11b2
Method	BLASTN
NCBI GI	g4539378
BLAST score	363
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	123320
Contig ID	11205_1.R1010
5'-most EST	jC-atXLIB327427P2g06b1
Method	BLASTX
NCBI GI	g3451074
BLAST score	181
E value	4.0e-13
Match length	58
% identity	66
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	123321
Contig ID	11207_1.R1010
5'-most EST	jC-atXLIB327427P2g07b1
Method	BLASTX
NCBI GI	g1076618
BLAST score	274
E value	5.0e-24
Match length	65
% identity	63

NCBI Description	alternative oxidase - common tobacco >gi_633600_emb_CAA56163_ (X79768) alternative oxidase [Nicotiana tabacum]
Seq. No.	123322
Contig ID	11209_1.R1010
5'-most EST	jC-atXLIB327427P2g09b1
Method	BLASTN
NCBI GI	g2262097
BLAST score	324
E value	0.0e+00
Match length	524
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence
Seq. No.	123323
Contig ID	11211_1.R1010
5'-most EST	LIB23-040-Q1-E1-F9
Method	BLASTX
NCBI GI	g3924611
BLAST score	205
E value	1.0e-15
Match length	106
% identity	43
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]
Seq. No.	123324
Contig ID	11211_2.R1010
5'-most EST	jC-atXP83CG3H1T7032a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	307
E value	1.0e-172
Match length	438
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence
Seq. No.	123325
Contig ID	11211_3.R1010
5'-most EST	jC-atX24056Q1E2A03b1
Method	BLASTN
NCBI GI	g4757662
BLAST score	278
E value	1.0e-155
Match length	411
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence
Seq. No.	123326
Contig ID	11213_1.R1010
5'-most EST	g2581705
Seq. No.	123327
Contig ID	11213_2.R1010

5'-most EST	jC-alXLIB327436P3g01b1
Method	BLASTX
NCBI GI	g2842477
BLAST score	204
E value	7.0e-16
Match length	107
% identity	39
NCBI Description	(AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No.	123328
Contig ID	11214_1.R1010
5'-most EST	g2763173
Method	BLASTN
NCBI GI	g2494106
BLAST score	650
E value	0.0e+00
Match length	686
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123329
Contig ID	11215_1.R1010
5'-most EST	jC-atXLIB327427P3e08b2
Method	BLASTX
NCBI GI	g4585900
BLAST score	513
E value	7.0e-52
Match length	103
% identity	100
NCBI Description	(AC007133) putative histone H2A [Arabidopsis thaliana]

Seq. No.	123330
Contig ID	11216_1.R1010
5'-most EST	LIB3176-114-P2-K1-E12
Method	BLASTX
NCBI GI	g4262236
BLAST score	171
E value	1.0e-57
Match length	235
% identity	54
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	123331
Contig ID	11216_2.R1010
5'-most EST	jC-atXLIB327427P3e09b2
Method	BLASTX
NCBI GI	g4262236
BLAST score	79
E value	2.0e-09
Match length	184
% identity	51
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	123332
Contig ID	11218_1.R1010
5'-most EST	LIB24-049-Q1-E2-C3
Method	BLASTX
NCBI GI	g4049350
BLAST score	695
E value	2.0e-73
Match length	132
% identity	100
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	123333
Contig ID	11218_2.R1010
5'-most EST	jC-alXLIB327435P2g02a1
Method	BLASTX
NCBI GI	g4049350
BLAST score	179
E value	1.0e-12
Match length	200
% identity	99
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	123334
Contig ID	11219_1.R1010
5'-most EST	jC-atXP117C141N20T7a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	252
E value	1.0e-139
Match length	609
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	123335
Contig ID	11219_2.R1010
5'-most EST	LIB3176-066-P1-K1-G10
Method	BLASTN
NCBI GI	g4589434
BLAST score	140
E value	1.0e-72
Match length	451
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	123336
Contig ID	11221_1.R1010
5'-most EST	jC-atXLIB327401P4c05b2

Seq. No.	123337
Contig ID	11223_1.R1010
5'-most EST	jC-alXLIB327434P3b01b1
Method	BLASTX
NCBI GI	g416681
BLAST score	617
E value	6.0e-64

Match length	233
% identity	58
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	123338
Contig ID	11223_2.R1010
5'-most EST	jC-atXLIB327408P1g08b1
Method	BLASTX
NCBI GI	g1480014
BLAST score	316
E value	5.0e-29
Match length	69
% identity	94
NCBI Description	(D78493) putative delta subunit of ATP synthase [Brassica rapa]

Seq. No.	123339
Contig ID	11226_1.R1010
5'-most EST	jC-atXLIB327427P2f01b1
Method	BLASTX
NCBI GI	g3080385
BLAST score	995
E value	1.0e-108
Match length	199
% identity	100
NCBI Description	(AL022603) serine/threonine protein kinase [Arabidopsis thaliana] >gi_3402760_emb_CAA20206.1_ (AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	123340
Contig ID	11228_2.R1010
5'-most EST	jC-atXmonuni27Af03b1
Method	BLASTN
NCBI GI	g4220635
BLAST score	746
E value	0.0e+00
Match length	746
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	123341
Contig ID	11231_1.R1010
5'-most EST	jC-atXLIB327427P4e11b2
Method	BLASTN
NCBI GI	g3241916
BLAST score	192
E value	1.0e-103
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	123342
Contig ID	11237_1.R1010
5'-most EST	jC-atXLIB327430P2g09b1
Method	BLASTX
NCBI GI	g2335102
BLAST score	342
E value	5.0e-32
Match length	68
% identity	100
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123343
Contig ID	11239_1.R1010
5'-most EST	jC-atXLIB327427P1f07b1

Seq. No.	123344
Contig ID	11242_1.R1010
5'-most EST	jC-atXP74C224K3T7050d1
Method	BLASTX
NCBI GI	g4531445
BLAST score	258
E value	6.0e-22
Match length	145
% identity	52
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	123345
Contig ID	11242_2.R1010
5'-most EST	jC-atXLIB327427P2f07b1
Method	BLASTX
NCBI GI	g4531445
BLAST score	200
E value	3.0e-15
Match length	69
% identity	61
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	123346
Contig ID	11243_2.R1010
5'-most EST	LIB23-002-Q1-E1-C5

Seq. No.	123347
Contig ID	11244_1.R1010
5'-most EST	g1159373
Method	BLASTX
NCBI GI	g4758520
BLAST score	188
E value	6.0e-14
Match length	103
% identity	3
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	123348
Contig ID	11245_1.R1010
5'-most EST	LIB25-109-Q1-E1-B8

Method	BLASTN
NCBI GI	g3236234
BLAST score	314
E value	1.0e-176
Match length	534
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123349
Contig ID	11245_2.R1010
5'-most EST	jC-atXLIB327425P3h11b1
Method	BLASTX
NCBI GI	g3236248
BLAST score	910
E value	2.0e-98
Match length	182
% identity	100
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	123350
Contig ID	11248_1.R1010
5'-most EST	jC-atXLIB327417P1c07b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	59
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123351
Contig ID	11249_1.R1010
5'-most EST	jC-alX25043Q1E1D05b1
Method	BLASTX
NCBI GI	g1172995
BLAST score	243
E value	3.0e-20
Match length	100
% identity	53
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	123352
Contig ID	11249_2.R1010
5'-most EST	LIB3176-123-P2-K1-A5
Method	BLASTX
NCBI GI	g1172995
BLAST score	241
E value	2.0e-20
Match length	101
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)

	ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]
Seq. No.	123353
Contig ID	11252_1.R1010
5'-most EST	jC-atXLIB327427P2f11b1
Method	BLASTX
NCBI GI	g1432056
BLAST score	206
E value	5.0e-16
Match length	76
% identity	59
NCBI Description	(U56834) WRKY3 [Petroselinum crispum]
Seq. No.	123354
Contig ID	11252_2.R1010
5'-most EST	jC-atXP66C210G1T7004a1
Method	BLASTX
NCBI GI	g1432056
BLAST score	161
E value	2.0e-10
Match length	63
% identity	59
NCBI Description	(U56834) WRKY3 [Petroselinum crispum]
Seq. No.	123355
Contig ID	11258_1.R1010
5'-most EST	jC-atXLIB327422P2b04b2
Method	BLASTX
NCBI GI	g3236238
BLAST score	595
E value	1.0e-61
Match length	122
% identity	91
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]
Seq. No.	123356
Contig ID	11266_1.R1010
5'-most EST	jC-atXLIB327427P4f01b2
Method	BLASTX
NCBI GI	g2088651
BLAST score	273
E value	6.0e-24
Match length	130
% identity	45
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]
Seq. No.	123357
Contig ID	11267_1.R1010
5'-most EST	jC-atXLIB327427P4f02b2
Method	BLASTX
NCBI GI	g4678364
BLAST score	313

E value	2.0e-28
Match length	111
% identity	57
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	123358
Contig ID	11267_2.R1010
5'-most EST	g2596842
Method	BLASTX
NCBI GI	g4678364
BLAST score	189
E value	4.0e-14
Match length	75
% identity	51
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	123359
Contig ID	11268_1.R1010
5'-most EST	jC-atXLIB327427P4f09b2
Method	BLASTN
NCBI GI	g2656032
BLAST score	57
E value	4.0e-23
Match length	262
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	123360
Contig ID	11269_1.R1010
5'-most EST	jC-atXP46C172H19T7005a1
Method	BLASTX
NCBI GI	g3860261
BLAST score	314
E value	2.0e-28
Match length	115
% identity	63
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	123361
Contig ID	11269_4.R1010
5'-most EST	jC-atXLIB327424P1b12b2
Method	BLASTX
NCBI GI	g3860261
BLAST score	176
E value	8.0e-18
Match length	55
% identity	95
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	123362
Contig ID	11269_7.R1010
5'-most EST	LIB24-079-Q1-E1-G7
Method	BLASTX
NCBI GI	g3860260

BLAST score	315
E value	1.0e-28
Match length	115
% identity	63
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	123363
Contig ID	11269_9.R1010
5'-most EST	LIB3176-012-P1-K1-A2
Method	BLASTX
NCBI GI	g3860261
BLAST score	217
E value	2.0e-17
Match length	46
% identity	100
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	123364
Contig ID	11269_11.R1010
5'-most EST	LIB3176-012-P1-K1-G2
Method	BLASTX
NCBI GI	g3860260
BLAST score	270
E value	2.0e-23
Match length	113
% identity	57
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	123365
Contig ID	11272_1.R1010
5'-most EST	LIB3168-059-P1-K1-H9
Method	BLASTX
NCBI GI	g2997591
BLAST score	170
E value	7.0e-12
Match length	84
% identity	52
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	123366
Contig ID	11273_1.R1010
5'-most EST	jC-atXLIB327429P1d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	72
E value	9.0e-32
Match length	76
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123367
Contig ID	11273_3.R1010

5'-most EST	LIB35-044-Q1-E1-C7
Seq. No.	123368
Contig ID	11273_4.R1010
5'-most EST	g2596637
Seq. No.	123369
Contig ID	11276_1.R1010
5'-most EST	jC-atXLIB327427P4f08b2
Method	BLASTN
NCBI GI	g3510345
BLAST score	280
E value	1.0e-156
Match length	482
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]
Seq. No.	123370
Contig ID	11278_1.R1010
5'-most EST	jC-alXLIB327434P1b07b1
Method	BLASTX
NCBI GI	g2739389
BLAST score	561
E value	3.0e-57
Match length	328
% identity	36
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
Seq. No.	123371
Contig ID	11278_2.R1010
5'-most EST	jC-atXLIB327408P3e07b1
Method	BLASTX
NCBI GI	g2739389
BLAST score	815
E value	3.0e-87
Match length	231
% identity	40
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
Seq. No.	123372
Contig ID	11280_1.R1010
5'-most EST	jC-atXLIB327430P2g11b1
Method	BLASTX
NCBI GI	g2209087
BLAST score	306
E value	1.0e-27
Match length	131
% identity	49
NCBI Description	(AF000309) putative serine/threonine kinase [Colletotrichum lindemuthianum]
Seq. No.	123373
Contig ID	11289_1.R1010
5'-most EST	LIB23-072-Q1-E1-C6
Method	BLASTX
NCBI GI	g3193320

BLAST score	915
E value	3.0e-99
Match length	178
% identity	100
NCBI Description	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No.	123374
Contig ID	11291_1.R1010
5'-most EST	g1327866
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123375
Contig ID	11291_2.R1010
5'-most EST	jC-atXLIB327427P1g08b1
Method	BLASTX
NCBI GI	g4585988
BLAST score	159
E value	1.0e-10
Match length	152
% identity	28
NCBI Description	(AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]

Seq. No.	123376
Contig ID	11293_1.R1010
5'-most EST	jC-atXLIB327408P3e06b1
Method	BLASTN
NCBI GI	g3860243
BLAST score	334
E value	0.0e+00
Match length	609
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123377
Contig ID	11293_2.R1010
5'-most EST	jC-atXmonuni27Ag09b1
Method	BLASTN
NCBI GI	g3860243
BLAST score	823
E value	0.0e+00
Match length	831
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 123378

Contig ID	11293_3.R1010
5'-most EST	jC-atXmonuni27Ag03a1
Method	BLASTN
NCBI GI	g3860243
BLAST score	404
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123379
Contig ID	11294_1.R1010
5'-most EST	jC-atXLIB327403P3g12b2
Method	BLASTX
NCBI GI	g3927827
BLAST score	1158
E value	1.0e-135
Match length	225
% identity	99
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No.	123380
Contig ID	11297_1.R1010
5'-most EST	jC-atXP85C241C4T7b1
Method	BLASTX
NCBI GI	g4263791
BLAST score	299
E value	6.0e-29
Match length	86
% identity	77
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	123381
Contig ID	11298_1.R1010
5'-most EST	jC-atXLIB327427P3g06b2
Method	BLASTN
NCBI GI	g3355463
BLAST score	525
E value	0.0e+00
Match length	587
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123382
Contig ID	11301_1.R1010
5'-most EST	jC-atXP92C247O8T7003d1
Method	BLASTX
NCBI GI	g4741960
BLAST score	890
E value	5.0e-96
Match length	165
% identity	100
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	123383
Contig ID	11301_2.R1010
5'-most EST	g957792
Method	BLASTX
NCBI GI	g4585935
BLAST score	1287
E value	1.0e-142
Match length	265
% identity	94
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	123384
Contig ID	11301_3.R1010
5'-most EST	jC-atXLIB327414P3e12a1
Method	BLASTX
NCBI GI	g4741960
BLAST score	1225
E value	1.0e-135
Match length	258
% identity	90
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	123385
Contig ID	11301_4.R1010
5'-most EST	jC-alXLIB327434P3f03b1
Method	BLASTX
NCBI GI	g4741950
BLAST score	1309
E value	1.0e-145
Match length	266
% identity	94
NCBI Description	(AF134125) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	123386
Contig ID	11301_5.R1010
5'-most EST	LIB3177-053-P1-K1-B9
Method	BLASTX
NCBI GI	g4741948
BLAST score	1288
E value	1.0e-142
Match length	265
% identity	94
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	123387
Contig ID	11301_6.R1010
5'-most EST	jC-atXLIB327426P3f10b1
Method	BLASTX
NCBI GI	g4741960
BLAST score	784
E value	1.0e-83
Match length	186
% identity	61
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	123388
Contig ID	11301_8.R1010
5'-most EST	LIB3177-081-P1-K1-H5
Method	BLASTN
NCBI GI	g4741959
BLAST score	230
E value	1.0e-126
Match length	288
% identity	96
NCBI Description	Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No.	123389
Contig ID	11301_9.R1010
5'-most EST	jC-atXLIB327427P4a03b2
Method	BLASTX
NCBI GI	g4741960
BLAST score	462
E value	4.0e-46
Match length	108
% identity	81
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	123390
Contig ID	11301_11.R1010
5'-most EST	LIB23-047-Q1-E1-E2
Method	BLASTX
NCBI GI	g1542941
BLAST score	520
E value	7.0e-53
Match length	125
% identity	88
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	123391
Contig ID	11301_12.R1010
5'-most EST	jC-atXLIB327437P2h02a2
Method	BLASTX
NCBI GI	g4741960
BLAST score	391
E value	9.0e-38
Match length	126
% identity	73
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	123392
Contig ID	11301_13.R1010
5'-most EST	LIB3177-006-P1-K2-D9
Method	BLASTX
NCBI GI	g4741948
BLAST score	125
E value	4.0e-43
Match length	127
% identity	77
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	123393
Contig ID	11301_14.R1010
5'-most EST	g2759153
Method	BLASTX
NCBI GI	g4585935
BLAST score	326
E value	3.0e-30
Match length	112
% identity	65
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	123394
Contig ID	11301_15.R1010
5'-most EST	LIB24-030-Q1-E1-E2
Method	BLASTX
NCBI GI	g4741960
BLAST score	103
E value	9.0e-25
Match length	61
% identity	98
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	123395
Contig ID	11301_16.R1010
5'-most EST	LIB25-029-Q1-E1-G6
Method	BLASTX
NCBI GI	g99600
BLAST score	157
E value	1.0e-28
Match length	125
% identity	63
NCBI Description	chlorophyll a/b-binding protein - upland cotton

Seq. No.	123396
Contig ID	11305_1.R1010
5'-most EST	jC-atXLIB327419P4f09b1
Method	BLASTX
NCBI GI	g2947060
BLAST score	697
E value	2.0e-84
Match length	177
% identity	84
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.	123397
Contig ID	11305_2.R1010
5'-most EST	jC-atXLIB327409P2c08b1
Method	BLASTX
NCBI GI	g2947060
BLAST score	337
E value	2.0e-31
Match length	103
% identity	62
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.	123398
Contig ID	11306_1.R1010
5'-most EST	LIB23-003-Q1-E1-A7
Method	BLASTX
NCBI GI	g2642443
BLAST score	894
E value	2.0e-96
Match length	177
% identity	95
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	123399
Contig ID	11308_1.R1010
5'-most EST	jC-atXLIB327427P4h04b2
Method	BLASTX
NCBI GI	g3702326
BLAST score	634
E value	1.0e-105
Match length	191
% identity	99
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123400
Contig ID	11310_1.R1010
5'-most EST	LIB24-129-Q1-E1-D6

Seq. No.	123401
Contig ID	11312_1.R1010
5'-most EST	LIB35-004-Q1-E1-B6
Method	BLASTX
NCBI GI	g2253426
BLAST score	148
E value	4.0e-09
Match length	112
% identity	30
NCBI Description	(AF007551) Bet1p homolog [Homo sapiens]

Seq. No.	123402
Contig ID	11314_1.R1010
5'-most EST	LIB23-003-Q1-E1-B8

Seq. No.	123403
Contig ID	11315_1.R1010
5'-most EST	jC-alXLIB327435P4d10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	4.0e-22
Match length	72
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123404
Contig ID	11315_2.R1010
5'-most EST	LIB23-003-Q1-E1-B9

Seq. No.	123405
Contig ID	11318_1.R1010
5'-most EST	LIB25-111-Q1-E1-E5
Method	BLASTX
NCBI GI	g1176658
BLAST score	277
E value	1.0e-24
Match length	128
% identity	47
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	123406
Contig ID	11319_1.R1010
5'-most EST	jC-alXLIB327435P2h05b1
Method	BLASTX
NCBI GI	g2497733
BLAST score	615
E value	8.0e-64
Match length	118
% identity	100
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	123407
Contig ID	11319_3.R1010
5'-most EST	jC-alXLIB327434P1c03b1
Method	BLASTX
NCBI GI	g2497733
BLAST score	615
E value	7.0e-64
Match length	118
% identity	100
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	123408
Contig ID	11319_4.R1010
5'-most EST	LIB25-033-Q1-E1-F10
Method	BLASTX
NCBI GI	g2497733
BLAST score	447
E value	6.0e-47
Match length	103
% identity	96
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	123409
Contig ID	11320_1.R1010

5'-most EST	jC-atXLIB327421P3e01b1
Method	BLASTN
NCBI GI	g4589437
BLAST score	344
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	123410
Contig ID	11322_1.R1010
5'-most EST	jC-atXP16C109H23T7d1
Method	BLASTX
NCBI GI	g2281649
BLAST score	467
E value	1.0e-46
Match length	106
% identity	88
NCBI Description	(AF003105) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana]

Seq. No.	123411
Contig ID	11324_1.R1010
5'-most EST	jC-atXP12C99I23T7013a1
Method	BLASTN
NCBI GI	g433664
BLAST score	468
E value	0.0e+00
Match length	488
% identity	99
NCBI Description	A.thaliana for Sec61 beta-subunit homolog

Seq. No.	123412
Contig ID	11328_1.R1010
5'-most EST	g453790
Method	BLASTX
NCBI GI	g1839188
BLAST score	520
E value	8.0e-53
Match length	102
% identity	97
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	123413
Contig ID	11332_1.R1010
5'-most EST	LIB35-044-Q1-E1-D6
Method	BLASTX
NCBI GI	g3747026
BLAST score	227
E value	2.0e-18
Match length	78
% identity	47
NCBI Description	(AF093244) import protein Tim9p [Saccharomyces cerevisiae]

Seq. No.	123414
Contig ID	11336_1.R1010

5'-most EST	LIB25-064-Q1-E1-E9
Method	BLASTX
NCBI GI	g2760327
BLAST score	589
E value	4.0e-61
Match length	121
% identity	75
NCBI Description	(AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No.	123415
Contig ID	11337_1.R1010
5'-most EST	jC-atXLIB327402P4b02b1
Method	BLASTN
NCBI GI	g2618599
BLAST score	736
E value	0.0e+00
Match length	810
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	123416
Contig ID	11339_1.R1010
5'-most EST	jC-atX23003Q1E1E08b1

Seq. No.	123417
Contig ID	11343_1.R1010
5'-most EST	jC-atXLIB327427P4h10b2
Method	BLASTN
NCBI GI	g2252848
BLAST score	445
E value	0.0e+00
Match length	480
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	123418
Contig ID	11356_1.R1010
5'-most EST	LIB3177-008-P1-K1-D4
Method	BLASTX
NCBI GI	g4539292
BLAST score	513
E value	7.0e-52
Match length	96
% identity	100
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	123419
Contig ID	11361_1.R1010
5'-most EST	jC-atXLIB327408P1d12b1
Method	BLASTX
NCBI GI	g3342552
BLAST score	242
E value	3.0e-20
Match length	141
% identity	43

NCBI Description	(AF076979) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	123420
Contig ID	11362_1.R1010
5'-most EST	LIB24-032-Q1-E1-D1
Method	BLASTX
NCBI GI	g2335096
BLAST score	578
E value	2.0e-59
Match length	199
% identity	56
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123421
Contig ID	11366_1.R1010
5'-most EST	LIB3177-019-P1-K2-C8
Method	BLASTX
NCBI GI	g1352881
BLAST score	153
E value	1.0e-09
Match length	90
% identity	33
NCBI Description	HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION >gi_1078266_pir__S57063 probable membrane protein YJR044c - yeast (Saccharomyces cerevisiae) >gi_1015699_emb_CAA89572_ (Z49544) ORF YJR044c [Saccharomyces cerevisiae] >gi_1197072 (L36344) ORF; putative [Saccharomyces cerevisiae]

Seq. No.	123422
Contig ID	11369_1.R1010
5'-most EST	LIB24-117-Q1-E1-C3

Seq. No.	123423
Contig ID	11372_1.R1010
5'-most EST	jC-atXP108C190F5T7040d1
Method	BLASTX
NCBI GI	g4531443
BLAST score	891
E value	4.0e-96
Match length	222
% identity	81
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	123424
Contig ID	11372_2.R1010
5'-most EST	LIB23-003-Q1-E1-H4
Method	BLASTX
NCBI GI	g4531443
BLAST score	542
E value	1.0e-127
Match length	272
% identity	88
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	123425
Contig ID	11372_3.R1010
5'-most EST	LIB24-023-Q1-E1-A12
Method	BLASTX
NCBI GI	g4531443
BLAST score	424
E value	1.0e-41
Match length	131
% identity	71
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	123426
Contig ID	11375_1.R1010
5'-most EST	jC-atXLIB327427P4g07b2
Method	BLASTX
NCBI GI	g4432860
BLAST score	1687
E value	0.0e+00
Match length	424
% identity	69
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	123427
Contig ID	11377_1.R1010
5'-most EST	g2749705
Method	BLASTN
NCBI GI	g1532162
BLAST score	394
E value	0.0e+00
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	123428
Contig ID	11377_2.R1010
5'-most EST	jC-atXLIB327416P3d08b1
Method	BLASTX
NCBI GI	g2498977
BLAST score	194
E value	1.0e-14
Match length	117
% identity	38
NCBI Description	SURFEIT LOCUS PROTEIN 5 >gi_1150512_emb_CAA59453_ (X85169) SURF-5 protein [Mus musculus]

Seq. No.	123429
Contig ID	11379_1.R1010
5'-most EST	jC-atXLIB327427P3g08b2
Method	BLASTN
NCBI GI	g4589443
BLAST score	473

E value	0.0e+00
Match length	566
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	123430
Contig ID	11382_1.R1010
5'-most EST	jC-atXLIB327415P3d03b1
Method	BLASTX
NCBI GI	g2864617
BLAST score	776
E value	1.0e-82
Match length	219
% identity	75
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	123431
Contig ID	11382_2.R1010
5'-most EST	g2758383
Method	BLASTN
NCBI GI	g2864607
BLAST score	334
E value	0.0e+00
Match length	489
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	123432
Contig ID	11382_3.R1010
5'-most EST	jC-atXLIB327414P4a03a2
Method	BLASTX
NCBI GI	g2864617
BLAST score	414
E value	3.0e-40
Match length	123
% identity	73
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	123433
Contig ID	11383_1.R1010
5'-most EST	LIB23-004-Q1-E1-A8
Method	BLASTX
NCBI GI	g2253583
BLAST score	366
E value	7.0e-35
Match length	124
% identity	64
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123434
Contig ID	11384_1.R1010
5'-most EST	LIB25-115-Q1-E1-E8
Method	BLASTX

NCBI GI	g1419090
BLAST score	1142
E value	1.0e-125
Match length	339
% identity	67
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	123435
Contig ID	11387_1.R1010
5'-most EST	jC-atXLIB327420P1g09b1
Method	BLASTX
NCBI GI	g2459417
BLAST score	1821
E value	0.0e+00
Match length	473
% identity	90
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	123436
Contig ID	11387_2.R1010
5'-most EST	jC-atXLIB327419P4e02b1
Method	BLASTX
NCBI GI	g2459417
BLAST score	946
E value	1.0e-102
Match length	202
% identity	92
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	123437
Contig ID	11387_4.R1010
5'-most EST	jC-atXLIB327417P1e03a1
Method	BLASTX
NCBI GI	g2459417
BLAST score	353
E value	3.0e-44
Match length	107
% identity	98
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	123438
Contig ID	11388_1.R1010
5'-most EST	jC-atXLIB327417P1a12b1

Seq. No.	123439
Contig ID	11399_1.R1010
5'-most EST	jC-atXP60C196O23T7035d1
Method	BLASTX
NCBI GI	g4582459
BLAST score	581
E value	6.0e-60
Match length	206
% identity	57

NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]
Seq. No.	123440
Contig ID	11401_1.R1010
5'-most EST	LIB23-004-Q1-E1-C3
Seq. No.	123441
Contig ID	11402_1.R1010
5'-most EST	LIB23-004-Q1-E1-C4
Method	BLASTX
NCBI GI	g1946367
BLAST score	165
E value	3.0e-11
Match length	94
% identity	37
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]
Seq. No.	123442
Contig ID	11403_1.R1010
5'-most EST	LIB24-007-Q1-E1-G1
Method	BLASTN
NCBI GI	g4454447
BLAST score	175
E value	1.0e-93
Match length	506
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	123443
Contig ID	11404_1.R1010
5'-most EST	ARABLI-023-Q1-B1-C9
Seq. No.	123444
Contig ID	11410_1.R1010
5'-most EST	jC-atXLIB327427P4h05b2
Method	BLASTX
NCBI GI	g4585993
BLAST score	884
E value	3.0e-95
Match length	190
% identity	87
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]
Seq. No.	123445
Contig ID	11417_1.R1010
5'-most EST	jC-atXP34C151H8T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	46
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123446
Contig ID	11417_2.R1010
5'-most EST	g2047810
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123447
Contig ID	11424_1.R1010
5'-most EST	jC-atXP11C98E5T7048d1
Method	BLASTX
NCBI GI	g4567207
BLAST score	971
E value	1.0e-105
Match length	183
% identity	100
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	123448
Contig ID	11426_1.R1010
5'-most EST	LIB23-004-Q1-E1-F11
Method	BLASTX
NCBI GI	g3135277
BLAST score	213
E value	8.0e-17
Match length	101
% identity	53
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana] >gi_4191776 (AC005917) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123449
Contig ID	11430_1.R1010
5'-most EST	jC-atXLIB327427P3a04b2
Method	BLASTX
NCBI GI	g2708750
BLAST score	616
E value	7.0e-64
Match length	166
% identity	80
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	123450
Contig ID	11430_2.R1010
5'-most EST	jC-atXLIB327427P4d08b2
Method	BLASTX
NCBI GI	g2708750
BLAST score	916
E value	6.0e-99
Match length	201
% identity	92
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis

thaliana]

Seq. No.	123451
Contig ID	11430_3.R1010
5'-most EST	LIB3176-071-P1-K1-C6
Method	BLASTX
NCBI GI	g2708750
BLAST score	1340
E value	1.0e-148
Match length	305
% identity	88
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	123452
Contig ID	11434_1.R1010
5'-most EST	LIB23-041-Q1-E1-C10
Method	BLASTX
NCBI GI	g2651314
BLAST score	384
E value	8.0e-37
Match length	110
% identity	70
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	123453
Contig ID	11435_1.R1010
5'-most EST	jC-atXLIB327431P1h08a1
Method	BLASTX
NCBI GI	g2505874
BLAST score	480
E value	3.0e-48
Match length	116
% identity	87
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	123454
Contig ID	11435_2.R1010
5'-most EST	LIB3234-008-P1-K1-G6
Method	BLASTX
NCBI GI	g2505874
BLAST score	194
E value	6.0e-15
Match length	57
% identity	74
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	123455
Contig ID	11436_1.R1010
5'-most EST	jC-atXLIB327428P4a01b2
Method	BLASTX
NCBI GI	g82652
BLAST score	330
E value	1.0e-30
Match length	137
% identity	47

NCBI Description	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - maize (fragment) >gi_217960_dbj_BAA01854_ (D11081) branching enzyme-I precursor [Zea mays]
Seq. No.	123456
Contig ID	11437_1.R1010
5'-most EST	LIB3176-015-P1-K1-F6
Method	BLASTX
NCBI GI	g1402878
BLAST score	610
E value	2.0e-63
Match length	206
% identity	56
NCBI Description	(X98130) unknown [Arabidopsis thaliana]
Seq. No.	123457
Contig ID	11439_1.R1010
5'-most EST	LIB23-004-Q1-E1-G5
Method	BLASTX
NCBI GI	g267421
BLAST score	225
E value	3.0e-18
Match length	90
% identity	48
NCBI Description	DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS HOMOLOG (XERODERMA PIGMENTOSUM GROUP G COMPLEMENTING PROTEIN HOMOLOG) >gi_422627_pir__S35994 DNA repair protein XPGC - African clawed frog >gi_312433_emb_CAA49597_ (X69977) XP-G related factor [Xenopus laevis]
Seq. No.	123458
Contig ID	11440_1.R1010
5'-most EST	LIB25-116-Q1-E1-D6
Method	BLASTN
NCBI GI	g4733952
BLAST score	76
E value	2.0e-34
Match length	549
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence
Seq. No.	123459
Contig ID	11441_1.R1010
5'-most EST	LIB23-004-Q1-E1-G7
Seq. No.	123460
Contig ID	11442_1.R1010
5'-most EST	jC-alXLIB327435P2e11a1
Method	BLASTX
NCBI GI	g3915847
BLAST score	675
E value	8.0e-71
Match length	171
% identity	69
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	123461
Contig ID	11442_2.R1010
5'-most EST	LIB24-128-Q1-E1-B11
Method	BLASTX
NCBI GI	g3915847
BLAST score	412
E value	2.0e-40
Match length	88
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	123462
Contig ID	11445_3.R1010
5'-most EST	jC-atXLIB327428P4a09b2

Seq. No.	123463
Contig ID	11453_1.R1010
5'-most EST	LIB3176-086-P1-K1-D1

Seq. No.	123464
Contig ID	11454_1.R1010
5'-most EST	jC-atXLIB327426P2e04b1
Method	BLASTX
NCBI GI	g1213460
BLAST score	386
E value	1.0e-36
Match length	200
% identity	41
NCBI Description	(U03374) C subunit of V-ATPase [Amblyomma americanum]

Seq. No.	123465
Contig ID	11454_3.R1010
5'-most EST	LIB25-062-Q1-E1-D5
Method	BLASTX
NCBI GI	g4502315
BLAST score	361
E value	4.0e-34
Match length	195
% identity	38
NCBI Description	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD >gi_401329_sp_P21283_VATC_HUMAN VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT) >gi_542836_pir__JN0907 H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - human >gi_37643_emb_CAA48903_ (X69151) vacuolar proton-ATPase [Homo sapiens]

Seq. No.	123466
Contig ID	11456_1.R1010
5'-most EST	jC-atXmonuni27Ag12b1
Method	BLASTX
NCBI GI	g4006926
BLAST score	561
E value	7.0e-58
Match length	116
% identity	95

NCBI Description (Z99708) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 123467
Contig ID 11459_1.R1010
5'-most EST jC-atXLIB327427P3g02b2
Method BLASTN
NCBI GI g2582640
BLAST score 62
E value 4.0e-26
Match length 73
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 123468
Contig ID 11460_1.R1010
5'-most EST jC-atXP95CG12E1T7051b1

Seq. No. 123469
Contig ID 11461_1.R1010
5'-most EST jC-atXLIB327427P3g03b2
Method BLASTX
NCBI GI g4104933
BLAST score 784
E value 2.0e-83
Match length 324
% identity 47
NCBI Description (AF042346) putative phenylalanyl-tRNA synthetase beta-subunit; PheHB [Homo sapiens]

Seq. No. 123470
Contig ID 11463_1.R1010
5'-most EST jC-atXmonuni27Ag10b1
Method BLASTX
NCBI GI g417328
BLAST score 326
E value 6.0e-30
Match length 226
% identity 35
NCBI Description UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2, 6-DIAMINOPIMELATE LIGASE (UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE) >gi_477729_pir__B47691 UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase (EC 6.3.2.13) - Bacillus subtilis >gi_40162_emb_CAA78767_ (Z15056) murE [Bacillus subtilis] >gi_2633889_emb_CAB13391_ (Z99111) UDP-N-acetylmuramoylananine-D-glutamate-2,6-diaminopimelate ligase [Bacillus subtilis]

Seq. No. 123471
Contig ID 11464_1.R1010
5'-most EST g634779

Seq. No. 123472
Contig ID 11464_2.R1010
5'-most EST g394819

Seq. No.	123473
Contig ID	11468_1.R1010
5'-most EST	jC-atXLIB327421P3e11b1
Method	BLASTX
NCBI GI	g2342685
BLAST score	632
E value	7.0e-66
Match length	147
% identity	85
NCBI Description	(AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No.	123474
Contig ID	11468_2.R1010
5'-most EST	jC-atXLIB327404P4f11b1
Method	BLASTN
NCBI GI	g2342673
BLAST score	153
E value	2.0e-80
Match length	533
% identity	97
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	123475
Contig ID	11470_1.R1010
5'-most EST	jC-alXLIB327435P2f12a1
Method	BLASTX
NCBI GI	g3822036
BLAST score	262
E value	1.0e-22
Match length	146
% identity	40
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	123476
Contig ID	11470_2.R1010
5'-most EST	g2763628
Method	BLASTX
NCBI GI	g3822036
BLAST score	318
E value	5.0e-29
Match length	174
% identity	41
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	123477
Contig ID	11477_1.R1010
5'-most EST	LIB23-005-Q1-E1-C1

Seq. No.	123478
Contig ID	11479_1.R1010
5'-most EST	jC-alXLIB327436P3a11b1
Method	BLASTX
NCBI GI	g730526
BLAST score	967

E value	1.0e-105
Match length	186
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	123479
Contig ID	11479_2.R1010
5'-most EST	LIB25-006-Q1-E2-G5
Method	BLASTX
NCBI GI	g730526
BLAST score	551
E value	2.0e-77
Match length	183
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	123480
Contig ID	11479_3.R1010
5'-most EST	jC-atXLIB327419P3f10b2
Method	BLASTX
NCBI GI	g730526
BLAST score	669
E value	2.0e-70
Match length	137
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	123481
Contig ID	11479_4.R1010
5'-most EST	jC-atXLIB327427P2h06b1
Method	BLASTX
NCBI GI	g730450
BLAST score	97
E value	4.0e-03
Match length	135
% identity	22
NCBI Description	60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B) >gi_480649_pir__S37134 cold-induced protein BnC24B - rape >gi_398922_emb_CAA80343_ (Z22620) cold induced protein (BnC24B) [Brassica napus]

Seq. No.	123482
Contig ID	11479_6.R1010
5'-most EST	g3450059
Method	BLASTN
NCBI GI	g2264316
BLAST score	316
E value	1.0e-178

Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	123483
Contig ID	11482_1.R1010
5'-most EST	jC-atXLIB327437P3b12a1
Method	BLASTX
NCBI GI	g1946367
BLAST score	742
E value	2.0e-78
Match length	164
% identity	96
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	123484
Contig ID	11483_1.R1010
5'-most EST	LIB24-135-Q1-E1-D12
Method	BLASTX
NCBI GI	g1055224
BLAST score	146
E value	3.0e-09
Match length	58
% identity	11
NCBI Description	(U20977) cellular nucleic acid binding protein [Xenopus laevis]

Seq. No.	123485
Contig ID	11484_1.R1010
5'-most EST	jC-atXmonuni27Ah05b1
Method	BLASTX
NCBI GI	g1084334
BLAST score	416
E value	1.0e-40
Match length	86
% identity	93
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) 1 - Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	123486
Contig ID	11488_1.R1010
5'-most EST	jC-atXLIB327427P4h01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	61
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123487
Contig ID	11491_1.R1010
5'-most EST	LIB23-005-Q1-E1-D12

Seq. No.	123488
Contig ID	11493_1.R1010
5'-most EST	LIB35-010-Q1-E1-E4
Method	BLASTX
NCBI GI	g3927837
BLAST score	752
E value	6.0e-80
Match length	148
% identity	100
NCBI Description	(AC005727) putative core protein [Arabidopsis thaliana]

Seq. No.	123489
Contig ID	11494_1.R1010
5'-most EST	jC-atXLIB327437P2f06b2
Method	BLASTX
NCBI GI	g1619300
BLAST score	888
E value	1.0e-95
Match length	194
% identity	85
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	123490
Contig ID	11494_2.R1010
5'-most EST	g2047570
Method	BLASTX
NCBI GI	g1619300
BLAST score	429
E value	4.0e-42
Match length	97
% identity	81
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	123491
Contig ID	11494_4.R1010
5'-most EST	jC-atXP6C90J7T7d2
Method	BLASTX
NCBI GI	g1619300
BLAST score	415
E value	1.0e-40
Match length	102
% identity	77
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	123492
Contig ID	11498_1.R1010
5'-most EST	g2748663
Method	BLASTX
NCBI GI	g2664210
BLAST score	367
E value	1.0e-34
Match length	234
% identity	46
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 123493

Contig ID	11499_1.R1010
5'-most EST	jC-atXLIB327427P2h12b1
Method	BLASTX
NCBI GI	g3559811
BLAST score	945
E value	1.0e-102
Match length	181
% identity	99
NCBI Description	(AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No.	123494
Contig ID	11500_1.R1010
5'-most EST	jC-atXLIB327427P4h08b2
Method	BLASTX
NCBI GI	g4678323
BLAST score	479
E value	8.0e-48
Match length	93
% identity	97
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	123495
Contig ID	11500_2.R1010
5'-most EST	g2393594
Method	BLASTX
NCBI GI	g4678322
BLAST score	110
E value	7.0e-05
Match length	112
% identity	65
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	123496
Contig ID	11501_1.R1010
5'-most EST	jC-atXLIB327421P3h03b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	149
E value	3.0e-09
Match length	114
% identity	37
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	123497
Contig ID	11501_2.R1010
5'-most EST	g507014
Method	BLASTX
NCBI GI	g3548810
BLAST score	97
E value	4.0e-03
Match length	191
% identity	39
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No. 123498

Contig ID	11504_1.R1010
5'-most EST	jC-atXmonuni27Dh08b1
Method	BLASTX
NCBI GI	g3047116
BLAST score	323
E value	6.0e-30
Match length	86
% identity	79
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	123499
Contig ID	11505_1.R1010
5'-most EST	LIB24-089-Q1-E1-H3
Method	BLASTX
NCBI GI	g4455180
BLAST score	1156
E value	1.0e-127
Match length	248
% identity	92
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	123500
Contig ID	11505_2.R1010
5'-most EST	LIB23-005-Q1-E1-E4
Method	BLASTX
NCBI GI	g4455180
BLAST score	1071
E value	1.0e-141
Match length	258
% identity	98
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	123501
Contig ID	11506_1.R1010
5'-most EST	jC-atXLIB327429P3f09b2
Method	BLASTX
NCBI GI	g4454051
BLAST score	952
E value	1.0e-103
Match length	243
% identity	74
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	123502
Contig ID	11509_1.R1010
5'-most EST	LIB23-005-Q1-E1-E8
Method	BLASTN
NCBI GI	g4454447
BLAST score	286
E value	1.0e-160
Match length	485
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 123503

Contig ID	11510_1.R1010
5'-most EST	jC-atXLIB327427P3h07b2
Method	BLASTX
NCBI GI	g4678925
BLAST score	669
E value	3.0e-70
Match length	133
% identity	98
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	123504
Contig ID	11513_1.R1010
5'-most EST	LIB23-005-Q1-E1-F11
Method	BLASTN
NCBI GI	g4538990
BLAST score	474
E value	0.0e+00
Match length	633
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	123505
Contig ID	11515_1.R1010
5'-most EST	LIB24-087-Q1-E1-H6
Method	BLASTX
NCBI GI	g3236258
BLAST score	686
E value	2.0e-72
Match length	131
% identity	100
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	123506
Contig ID	11517_1.R1010
5'-most EST	LIB3175-027-P1-K1-G10
Method	BLASTN
NCBI GI	g2828185
BLAST score	413
E value	0.0e+00
Match length	942
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	123507
Contig ID	11526_1.R1010
5'-most EST	jC-atXLIB327423P1d10b1
Method	BLASTX
NCBI GI	g3582335
BLAST score	1603
E value	1.0e-179
Match length	303
% identity	98
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	123508
Contig ID	11526_2.R1010
5'-most EST	jC-atXLIB327427P1d11b1
Method	BLASTX
NCBI GI	g3582335
BLAST score	1983
E value	0.0e+00
Match length	423
% identity	92
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	123509
Contig ID	11529_1.R1010
5'-most EST	jC-alXLIB327434P1b02b1
Method	BLASTX
NCBI GI	g4204270
BLAST score	863
E value	1.0e-169
Match length	356
% identity	82
NCBI Description	(AC005223) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	123510
Contig ID	11530_1.R1010
5'-most EST	LIB24-051-Q1-E1-D2
Method	BLASTX
NCBI GI	g3776581
BLAST score	556
E value	3.0e-57
Match length	126
% identity	90
NCBI Description	(AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	123511
Contig ID	11532_1.R1010
5'-most EST	jC-alX24082Q1E1C07b1
Method	BLASTX
NCBI GI	g4204263
BLAST score	211
E value	9.0e-17
Match length	77
% identity	56
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	123512
Contig ID	11539_1.R1010
5'-most EST	LIB23-005-Q1-E1-H3
Method	BLASTN
NCBI GI	g3402671
BLAST score	393
E value	0.0e+00
Match length	437
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123513
Contig ID	11543_1.R1010
5'-most EST	LIB23-005-Q1-E1-H8
Method	BLASTX
NCBI GI	g2119927
BLAST score	521
E value	7.0e-53
Match length	158
% identity	68
NCBI Description	translation elongation factor G, chloroplast - soybean

Seq. No.	123514
Contig ID	11544_1.R1010
5'-most EST	jC-atXLIB327428P4a04b2
Method	BLASTX
NCBI GI	g4100433
BLAST score	534
E value	4.0e-54
Match length	181
% identity	58
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	123515
Contig ID	11544_2.R1010
5'-most EST	jC-atXLIB327408P4h03b1
Method	BLASTX
NCBI GI	g2181180
BLAST score	555
E value	2.0e-56
Match length	406
% identity	36
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	123516
Contig ID	11544_3.R1010
5'-most EST	jC-atXLIB327420P4e05b1
Method	BLASTX
NCBI GI	g4235093
BLAST score	376
E value	1.0e-35
Match length	190
% identity	44
NCBI Description	(AF108944) beta-xylosidase [Aspergillus niger]

Seq. No.	123517
Contig ID	11544_4.R1010
5'-most EST	jC-atXP89CG6D7T7022d1
Method	BLASTX
NCBI GI	g2723496
BLAST score	288
E value	2.0e-25
Match length	133
% identity	44
NCBI Description	(AB009972) beta-1,4-xylosidase [Aspergillus oryzae]

Seq. No.	123518

Contig ID	11544_6.R1010
5'-most EST	jC-atXLIB327408P4h03a1
Method	BLASTN
NCBI GI	g2760172
BLAST score	451
E value	0.0e+00
Match length	463
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	123519
Contig ID	11549_1.R1010
5'-most EST	jC-atXLIB327427P4g02b2
Method	BLASTX
NCBI GI	g2131358
BLAST score	327
E value	3.0e-30
Match length	130
% identity	49
NCBI Description	hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae) >gi_1429356_emb_CAA67468_ (X99000) ORF D1075 [Saccharomyces cerevisiae] >gi_1431332_emb_CAA98779_ (Z74249) ORF YDL201w [Saccharomyces cerevisiae]

Seq. No.	123520
Contig ID	11551_1.R1010
5'-most EST	jC-atX23006Q1E1A05b1
Method	BLASTX
NCBI GI	g4539465
BLAST score	776
E value	1.0e-87
Match length	277
% identity	68
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	123521
Contig ID	11551_2.R1010
5'-most EST	jC-atXLIB327427P4g04a2
Method	BLASTX
NCBI GI	g3292830
BLAST score	342
E value	4.0e-32
Match length	79
% identity	82
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	123522
Contig ID	11552_1.R1010
5'-most EST	jC-atXLIB327430P4g02b1
Method	BLASTN
NCBI GI	g3228389
BLAST score	195
E value	1.0e-105
Match length	425
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No.	123523
Contig ID	11557_1.R1010
5'-most EST	jC-atXLIB327427P3g11b2
Method	BLASTX
NCBI GI	g3386612
BLAST score	412
E value	5.0e-40
Match length	172
% identity	51
NCBI Description	(AC004665) DNA-binding protein, dbp [Arabidopsis thaliana]

Seq. No.	123524
Contig ID	11557_3.R1010
5'-most EST	LIB24-033-Q1-E1-H6
Method	BLASTX
NCBI GI	g320558
BLAST score	168
E value	1.0e-11
Match length	91
% identity	45
NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi_601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123525
Contig ID	11560_1.R1010
5'-most EST	LIB23-006-Q1-E1-B2
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	5.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	123526
Contig ID	11565_1.R1010
5'-most EST	jC-atXLIB327427P4g11b1
Method	BLASTX
NCBI GI	g3287679
BLAST score	795
E value	4.0e-85

Match length 160
% identity 100
NCBI Description (AC003979) T22J18.6 [Arabidopsis thaliana]

Seq. No. 123527
Contig ID 11569_1.R1010
5'-most EST jC-atXLIB327422P2g06b2

Seq. No. 123528
Contig ID 11569_2.R1010
5'-most EST jC-atXmonuni27Ah07b1

Seq. No. 123529
Contig ID 11575_1.R1010
5'-most EST LIB23-006-Q1-E1-C7

Seq. No. 123530
Contig ID 11575_2.R1010
5'-most EST LIB25-098-Q1-E1-F8

Seq. No. 123531
Contig ID 11576_1.R1010
5'-most EST jC-atXLIB327416P4c01b1
Method BLASTX
NCBI GI g4539291
BLAST score 615
E value 5.0e-64
Match length 119
% identity 100
NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 123532
Contig ID 11577_1.R1010
5'-most EST g2757764
Method BLASTX
NCBI GI g3928099
BLAST score 548
E value 4.0e-56
Match length 130
% identity 39
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 123533
Contig ID 11581_1.R1010
5'-most EST LIB25-061-Q1-E1-F7
Method BLASTN
NCBI GI g3757512
BLAST score 253
E value 1.0e-140
Match length 369
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 123534
Contig ID 11582_1.R1010
5'-most EST LIB24-109-Q1-E1-G4

Method	BLASTX
NCBI GI	g4582434
BLAST score	498
E value	2.0e-50
Match length	99
% identity	100
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	123535
Contig ID	11585_1.R1010
5'-most EST	jC-atXmonuni27Ah11b1
Method	BLASTX
NCBI GI	g4544402
BLAST score	189
E value	3.0e-14
Match length	137
% identity	31
NCBI Description	(AC007047) putative leucine rich repeat protein [Arabidopsis thaliana]

Seq. No.	123536
Contig ID	11587_1.R1010
5'-most EST	LIB23-006-Q1-E1-D8
Method	BLASTX
NCBI GI	g418507
BLAST score	182
E value	4.0e-13
Match length	75
% identity	48
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	123537
Contig ID	11587_2.R1010
5'-most EST	g2581750
Method	BLASTX
NCBI GI	g418507
BLAST score	195
E value	9.0e-15
Match length	101
% identity	40
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	123538
Contig ID	11588_1.R1010
5'-most EST	jC-atXLIB327427P4h06b2

Method	BLASTX
NCBI GI	g1170781
BLAST score	429
E value	1.0e-68
Match length	212
% identity	57
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) >gi_629615_pir__S47177 lactoylglutathione lyase (EC 4.4.1.5) - soybean >gi_505585_emb_CAA48717_ (X68819) lactoylglutathione lyase [Glycine max]

Seq. No.	123539
Contig ID	11589_1.R1010
5'-most EST	g502031
Method	BLASTX
NCBI GI	g2062167
BLAST score	685
E value	6.0e-72
Match length	202
% identity	71
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	123540
Contig ID	11589_3.R1010
5'-most EST	jC-atXP89C242K11T7073d1
Method	BLASTX
NCBI GI	g2062167
BLAST score	541
E value	3.0e-55
Match length	115
% identity	90
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	123541
Contig ID	11590_1.R1010
5'-most EST	g1158996
Method	BLASTX
NCBI GI	g4586256
BLAST score	909
E value	4.0e-98
Match length	219
% identity	82
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	123542
Contig ID	11590_3.R1010
5'-most EST	g2581676
Method	BLASTX
NCBI GI	g4586256
BLAST score	415
E value	2.0e-40
Match length	107
% identity	79

NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	123543
Contig ID	11590_4.R1010
5'-most EST	g936166
Method	BLASTX
NCBI GI	g4586256
BLAST score	434
E value	8.0e-43
Match length	137
% identity	77
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	123544
Contig ID	11590_5.R1010
5'-most EST	g2758195
Method	BLASTX
NCBI GI	g4586256
BLAST score	470
E value	5.0e-47
Match length	142
% identity	70
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	123545
Contig ID	11590_6.R1010
5'-most EST	LIB3177-094-P1-K1-A5
Method	BLASTX
NCBI GI	g4586256
BLAST score	271
E value	7.0e-34
Match length	126
% identity	63
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	123546
Contig ID	11592_1.R1010
5'-most EST	jC-alX25021Q1E1B11b1

Seq. No.	123547
Contig ID	11592_2.R1010
5'-most EST	g2749721

Seq. No.	123548
Contig ID	11595_1.R1010
5'-most EST	LIB3234-039-P1-K1-H7
Method	BLASTX
NCBI GI	g2981475
BLAST score	716
E value	5.0e-82
Match length	217
% identity	72
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus

domestica]

Seq. No.	123549
Contig ID	11598_1.R1010
5'-most EST	jC-alXLIB327436P3g05b1
Method	BLASTX
NCBI GI	g498038
BLAST score	696
E value	5.0e-73
Match length	262
% identity	50
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	123550
Contig ID	11599_1.R1010
5'-most EST	LIB25-034-Q1-E1-E5
Method	BLASTN
NCBI GI	g4220510
BLAST score	283
E value	1.0e-158
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	123551
Contig ID	11605_1.R1010
5'-most EST	LIB23-006-Q1-E1-F9
Method	BLASTN
NCBI GI	g4589440
BLAST score	253
E value	1.0e-140
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	123552
Contig ID	11606_1.R1010
5'-most EST	jC-atXLIB327428P1a07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123553
Contig ID	11613_1.R1010
5'-most EST	jC-atXLIB327428P1a08b2
Method	BLASTN
NCBI GI	g2618600
BLAST score	221
E value	1.0e-121
Match length	443

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	123554
Contig ID	11614_1.R1010
5'-most EST	LIB23-006-Q1-E1-G8
Method	BLASTN
NCBI GI	g3047074
BLAST score	69
E value	5.0e-30
Match length	149
% identity	45
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	123555
Contig ID	11616_1.R1010
5'-most EST	LIB23-017-Q1-E1-A11
Method	BLASTX
NCBI GI	g4512651
BLAST score	657
E value	4.0e-69
Match length	126
% identity	99
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	123556
Contig ID	11617_1.R1010
5'-most EST	LIB23-006-Q1-E1-H11

Seq. No.	123557
Contig ID	11627_1.R1010
5'-most EST	LIB23-007-Q1-E1-A1
Method	BLASTX
NCBI GI	g3063471
BLAST score	373
E value	8.0e-36
Match length	71
% identity	100
NCBI Description	(AC003981) F22O13.33 [Arabidopsis thaliana]

Seq. No.	123558
Contig ID	11629_1.R1010
5'-most EST	jC-atXLIB327428P1b04b2
Method	BLASTX
NCBI GI	g2980795
BLAST score	199
E value	3.0e-15
Match length	73
% identity	52
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	123559
Contig ID	11630_1.R1010
5'-most EST	LIB23-007-Q1-E1-A12
Method	BLASTN

NCBI GI	g3449312
BLAST score	41
E value	1.0e-13
Match length	252
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No.	123560
Contig ID	11632_1.R1010
5'-most EST	LIB23-007-Q1-E1-A4
Method	BLASTX
NCBI GI	g4510377
BLAST score	557
E value	2.0e-57
Match length	109
% identity	99
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	123561
Contig ID	11633_1.R1010
5'-most EST	LIB23-030-Q1-E1-C9
Method	BLASTX
NCBI GI	g2506276
BLAST score	1670
E value	0.0e+00
Match length	360
% identity	95
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	123562
Contig ID	11636_1.R1010
5'-most EST	LIB3175-041-P1-K1-A5
Method	BLASTN
NCBI GI	g2618599
BLAST score	636
E value	0.0e+00
Match length	636
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	123563
Contig ID	11641_1.R1010
5'-most EST	LIB23-007-Q1-E1-B12

Seq. No.	123564
Contig ID	11645_1.R1010
5'-most EST	jC-atXLIB327431P2c06a1
Method	BLASTX
NCBI GI	g3250695

BLAST score	227
E value	2.0e-18
Match length	105
% identity	51
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	123565
Contig ID	11645_2.R1010
5'-most EST	jC-atXLIB327428P4b02b2
Method	BLASTX
NCBI GI	g3250695
BLAST score	73
E value	7.0e-20
Match length	118
% identity	51
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	123566
Contig ID	11657_1.R1010
5'-most EST	LIB35-039-Q1-E1-B2
Method	BLASTX
NCBI GI	g4587530
BLAST score	89
E value	5.0e-42
Match length	129
% identity	67
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	123567
Contig ID	11665_1.R1010
5'-most EST	LIB23-007-Q1-E1-D4
Method	BLASTX
NCBI GI	g4678311
BLAST score	470
E value	3.0e-47
Match length	90
% identity	99
NCBI Description	(AL049655) aquaporin/MIP-like protein [Arabidopsis thaliana]

Seq. No.	123568
Contig ID	11672_1.R1010
5'-most EST	jC-atX23007Q1E1E12b1
Method	BLASTX
NCBI GI	g2622629
BLAST score	181
E value	5.0e-13
Match length	109
% identity	40
NCBI Description	(AE000911) arsenical pump-driving ATPase [Methanobacterium thermoautotrophicum]

Seq. No.	123569
Contig ID	11673_1.R1010
5'-most EST	jC-atXLIB327428P1c09b2

Method	BLASTX
NCBI GI	g4544427
BLAST score	696
E value	2.0e-73
Match length	129
% identity	99
NCBI Description	(AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	123570
Contig ID	11675_1.R1010
5'-most EST	g2757836
Method	BLASTX
NCBI GI	g2497733
BLAST score	388
E value	3.0e-37
Match length	118
% identity	61
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	123571
Contig ID	11681_1.R1010
5'-most EST	LIB23-007-Q1-E1-F10
Method	BLASTN
NCBI GI	g3449326
BLAST score	613
E value	0.0e+00
Match length	699
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	123572
Contig ID	11682_1.R1010
5'-most EST	jC-atX24063Q1E1G04b1

Seq. No.	123573
Contig ID	11687_1.R1010
5'-most EST	LIB3234-060-P1-K1-H1
Method	BLASTX
NCBI GI	g2494113
BLAST score	983
E value	1.0e-107
Match length	209
% identity	87
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	123574
Contig ID	11688_1.R1010
5'-most EST	LIB3175-001-Q1-K1-F1
Method	BLASTX
NCBI GI	g3763919

BLAST score	512
E value	6.0e-52
Match length	140
% identity	74
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana] >gi_4531436_gb_AAD22121.1_AC006224_3 (AC006224) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	123575
Contig ID	11691_1.R1010
5'-most EST	LIB23-007-Q1-E1-G1
Method	BLASTN
NCBI GI	g3319365
BLAST score	91
E value	3.0e-43
Match length	172
% identity	96
NCBI Description	Arabidopsis thaliana BAC T24M8

Seq. No.	123576
Contig ID	11692_1.R1010
5'-most EST	LIB25-096-Q1-E1-H9
Method	BLASTX
NCBI GI	g2911148
BLAST score	589
E value	1.0e-60
Match length	132
% identity	81
NCBI Description	(AB005808) NADP-malic enzyme [Aloe arborescens]

Seq. No.	123577
Contig ID	11699_1.R1010
5'-most EST	g315877
Method	BLASTX
NCBI GI	g4467158
BLAST score	157
E value	2.0e-10
Match length	59
% identity	63
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	123578
Contig ID	11704_1.R1010
5'-most EST	g957799
Method	BLASTN
NCBI GI	g2656025
BLAST score	127
E value	7.0e-65
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	123579
Contig ID	11706_1.R1010
5'-most EST	jC-atXLIB327428P1d05b2

Method	BLASTX
NCBI GI	g4544473
BLAST score	473
E value	3.0e-47
Match length	104
% identity	89
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	123580
Contig ID	11707_1.R1010
5'-most EST	jC-atX23007Q1E1H05b1
Method	BLASTX
NCBI GI	g3264778
BLAST score	630
E value	1.0e-65
Match length	235
% identity	67
NCBI Description	(AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]

Seq. No.	123581
Contig ID	11709_1.R1010
5'-most EST	LIB25-074-Q1-E1-G9
Method	BLASTX
NCBI GI	g2673920
BLAST score	557
E value	2.0e-57
Match length	109
% identity	100
NCBI Description	(AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No.	123582
Contig ID	11710_1.R1010
5'-most EST	LIB23-007-Q1-E1-H9
Method	BLASTN
NCBI GI	g4689466
BLAST score	34
E value	1.0e-09
Match length	188
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	123583
Contig ID	11712_1.R1010
5'-most EST	jC-atXP115C251K15T7d1

Seq. No.	123584
Contig ID	11718_1.R1010
5'-most EST	jC-atXP115C122N6T7008d1
Method	BLASTX
NCBI GI	g2119848
BLAST score	1330
E value	1.0e-147
Match length	252
% identity	99

NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123585
Contig ID	11718_2.R1010
5'-most EST	jC-atXLIB327418P4b03b1
Method	BLASTX
NCBI GI	g2119846
BLAST score	737
E value	1.0e-133
Match length	263
% identity	84
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123586
Contig ID	11718_3.R1010
5'-most EST	g2747382
Method	BLASTX
NCBI GI	g2119846
BLAST score	227
E value	1.0e-135
Match length	246
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123587
Contig ID	11718_4.R1010
5'-most EST	jC-alXLIB327436P2e02b1
Method	BLASTX
NCBI GI	g115767
BLAST score	1394
E value	1.0e-155
Match length	267
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	123588
Contig ID	11718_5.R1010
5'-most EST	jC-atXP85C241F5T7b1
Method	BLASTX
NCBI GI	g2119848
BLAST score	605
E value	1.0e-112
Match length	251
% identity	86
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123589
Contig ID	11718_6.R1010
5'-most EST	LIB3177-006-P1-K2-F3
Method	BLASTX
NCBI GI	g115783
BLAST score	705
E value	3.0e-74
Match length	256
% identity	68
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123590
Contig ID	11718_7.R1010
5'-most EST	g937354
Method	BLASTX
NCBI GI	g115783
BLAST score	304
E value	2.0e-27
Match length	117
% identity	47
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123591
Contig ID	11718_8.R1010
5'-most EST	jC-atXLIB327417P3g10b1
Method	BLASTX
NCBI GI	g2119846
BLAST score	1114
E value	1.0e-122
Match length	268

% identity	83
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	123592
Contig ID	11718_9.R1010
5'-most EST	jC-alXLIB327435P2h06a1
Method	BLASTX
NCBI GI	g115783
BLAST score	790
E value	2.0e-84
Match length	179
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	123593
Contig ID	11718_10.R1010
5'-most EST	g1520807
Method	BLASTX
NCBI GI	g16374
BLAST score	244
E value	2.0e-20
Match length	119
% identity	50
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	123594
Contig ID	11718_11.R1010
5'-most EST	jC-atXLIB327414P4e08a2
Method	BLASTX
NCBI GI	g2119848
BLAST score	573
E value	1.0e-58
Match length	261
% identity	55
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	123595
Contig ID	11718_12.R1010
5'-most EST	LIB35-041-Q1-E1-E12
Method	BLASTX

NCBI GI	g115767
BLAST score	110
E value	9.0e-05
Match length	119
% identity	42
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	123596
Contig ID	11718_13.R1010
5'-most EST	g2758728
Method	BLASTX
NCBI GI	g115783
BLAST score	350
E value	2.0e-67
Match length	341
% identity	55
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123597
Contig ID	11718_14.R1010
5'-most EST	LIB3177-092-P1-K1-H5
Method	BLASTX
NCBI GI	g2119846
BLAST score	702
E value	1.0e-106
Match length	260
% identity	67
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123598
Contig ID	11718_15.R1010
5'-most EST	jC-atXLIB327438P1c11a1
Method	BLASTX
NCBI GI	g16374
BLAST score	147
E value	5.0e-09
Match length	127
% identity	25
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 123599

Contig ID	11718_16.R1010
5'-most EST	LIB3176-056-P1-K1-A4
Method	BLASTX
NCBI GI	g115783
BLAST score	509
E value	3.0e-51
Match length	264
% identity	52
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123600
Contig ID	11718_17.R1010
5'-most EST	jC-atXLIB327416P2b07b1
Method	BLASTX
NCBI GI	g115783
BLAST score	744
E value	9.0e-79
Match length	270
% identity	61
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123601
Contig ID	11718_18.R1010
5'-most EST	ARABLI-037-Q1-B1-H6
Method	BLASTX
NCBI GI	g16374
BLAST score	506
E value	5.0e-51
Match length	179
% identity	70
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	123602
Contig ID	11718_19.R1010
5'-most EST	jC-atXLIB327431P1b03a1
Method	BLASTX
NCBI GI	g2119846
BLAST score	694
E value	3.0e-73
Match length	176
% identity	72
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 123603

Contig ID	11718_20.R1010
5'-most EST	jC-atXLIB327421P4g03b1
Method	BLASTX
NCBI GI	g115783
BLAST score	146
E value	5.0e-09
Match length	124
% identity	26
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123604
Contig ID	11718_21.R1010
5'-most EST	LIB3175-043-P1-K1-D12
Method	BLASTX
NCBI GI	g115783
BLAST score	428
E value	2.0e-47
Match length	119
% identity	90
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	123605
Contig ID	11718_22.R1010
5'-most EST	jC-atXLIB327438P4b11a2
Method	BLASTX
NCBI GI	g115791
BLAST score	154
E value	7.0e-10
Match length	129
% identity	41
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-2) (LHCP) >gi_81770_pir__S01961 chlorophyll a/b-binding protein 2 precursor - soybean >gi_18548_emb_CAA31418_ (X12980) chlorophyll a/b binding preprotein (AA -33 to 223) [Glycine max]

Seq. No.	123606
Contig ID	11718_23.R1010
5'-most EST	g1159622
Method	BLASTX
NCBI GI	g115783
BLAST score	85
E value	9.0e-52
Match length	141
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No. 123607

Contig ID	11718_24.R1010
5'-most EST	jC-atXLIB327420P4f07b1
Method	BLASTX
NCBI GI	g2119846
BLAST score	657
E value	8.0e-69
Match length	129
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123608
Contig ID	11718_25.R1010
5'-most EST	ARABL1-022-Q1-B1-C9
Method	BLASTX
NCBI GI	g115767
BLAST score	582
E value	3.0e-62
Match length	161
% identity	68
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	123609
Contig ID	11718_26.R1010
5'-most EST	LIB3175-005-P1-K1-D1
Method	BLASTX
NCBI GI	g2119848
BLAST score	715
E value	1.0e-75
Match length	166
% identity	84
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123610
Contig ID	11718_28.R1010
5'-most EST	LIB25-045-Q1-E1-B12
Method	BLASTX
NCBI GI	g2119846
BLAST score	641

E value	6.0e-95
Match length	204
% identity	86
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123611
Contig ID	11718_29.R1010
5'-most EST	LIB3177-071-P1-K1-B10
Method	BLASTX
NCBI GI	g115778
BLAST score	238
E value	2.0e-32
Match length	116
% identity	71
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_282896_pir__S22511 chlorophyll a/b-binding protein (cab-1) - white mustard >gi_21138_emb_CAA34459_ (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi_21140_emb_CAA33903_ (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba]

Seq. No.	123612
Contig ID	11718_30.R1010
5'-most EST	jC-atXP53C185A4T7036a1
Method	BLASTX
NCBI GI	g2119848
BLAST score	358
E value	6.0e-34
Match length	129
% identity	67
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123613
Contig ID	11718_31.R1010
5'-most EST	g935586
Method	BLASTX
NCBI GI	g115783
BLAST score	442
E value	7.0e-44
Match length	91
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No.	123614
Contig ID	11718_33.R1010
5'-most EST	jC-atX25091Q1E1F09a1
Method	BLASTX
NCBI GI	g2119846
BLAST score	394
E value	2.0e-38
Match length	75
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	123615
Contig ID	11718_34.R1010
5'-most EST	LIB3175-046-P1-K1-A2
Method	BLASTX
NCBI GI	g16374
BLAST score	398
E value	1.0e-38
Match length	80
% identity	96
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	123616
Contig ID	11718_35.R1010
5'-most EST	LIB3168-087-P1-K1-G10
Method	BLASTX
NCBI GI	g115767
BLAST score	282
E value	6.0e-47
Match length	106
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	123617
Contig ID	11718_36.R1010
5'-most EST	jC-atXP53C183O15T7083a1
Method	BLASTX
NCBI GI	g115768
BLAST score	90
E value	1.0e-11
Match length	92
% identity	55

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_72743_pir__CDKV chlorophyll a/b-binding protein precursor - cucumber (fragment) >gi_167523 (M16057) chlorophyll a/b-binding protein [Cucumis sativus]
Seq. No.	123618
Contig ID	11718_37.R1010
5'-most EST	LIB3175-070-P1-K-E6
Method	BLASTX
NCBI GI	g115783
BLAST score	476
E value	7.0e-48
Match length	103
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	123619
Contig ID	11718_39.R1010
5'-most EST	ARABL1-019-Q1-B1-E1
Method	BLASTX
NCBI GI	g16374
BLAST score	580
E value	7.0e-60
Match length	151
% identity	94
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	123620
Contig ID	11718_42.R1010
5'-most EST	LIB23-069-Q1-E1-A7
Method	BLASTX
NCBI GI	g115767
BLAST score	573
E value	2.0e-59
Match length	109
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	123621
Contig ID	11718_49.R1010
5'-most EST	LIB23-066-Q1-E1-B4
Method	BLASTX
NCBI GI	g115783
BLAST score	215
E value	2.0e-17
Match length	82
% identity	61

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	123622
Contig ID	11718_53.R1010
5'-most EST	ARABL1-037-Q1-B1-E1
Method	BLASTX
NCBI GI	g115785
BLAST score	272
E value	3.0e-24
Match length	51
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-2) (LHCP) >gi_82380_pir__S04028 chlorophyll a/b-binding protein 2 precursor - barley >gi_18943_emb_CAA31232_ (X12735) LHC precursor protein (AA -34 to 230) [Hordeum vulgare]
Seq. No.	123623
Contig ID	11723_1.R1010
5'-most EST	jC-atXLIB327428P1b11b2
Method	BLASTX
NCBI GI	g1176505
BLAST score	213
E value	7.0e-17
Match length	89
% identity	40
NCBI Description	HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III >gi_500770 (U10438) B0280.9 gene product [Caenorhabditis elegans]
Seq. No.	123624
Contig ID	11725_1.R1010
5'-most EST	LIB23-008-Q1-E1-B2
Method	BLASTN
NCBI GI	g2827513
BLAST score	302
E value	1.0e-169
Match length	445
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)
Seq. No.	123625
Contig ID	11727_1.R1010
5'-most EST	LIB23-061-Q1-E1-H5
Seq. No.	123626
Contig ID	11732_1.R1010
5'-most EST	LIB23-008-Q1-E1-C1
Method	BLASTN
NCBI GI	g4589430
BLAST score	338
E value	0.0e+00
Match length	446

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	123627
Contig ID	11733_1.R1010
5'-most EST	jC-atXLIB327407P1a03b2
Method	BLASTN
NCBI GI	g2351069
BLAST score	448
E value	0.0e+00
Match length	460
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	123628
Contig ID	11734_1.R1010
5'-most EST	jC-atXLIB327431P2e11a1
Method	BLASTX
NCBI GI	g4588003
BLAST score	765
E value	2.0e-81
Match length	175
% identity	87
NCBI Description	(AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No.	123629
Contig ID	11739_1.R1010
5'-most EST	jC-atXLIB327428P4b07b2
Method	BLASTN
NCBI GI	g2980787
BLAST score	359
E value	0.0e+00
Match length	468
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	123630
Contig ID	11742_1.R1010
5'-most EST	jC-alXLIB327434P3h11b1
Method	BLASTX
NCBI GI	g2245125
BLAST score	151
E value	2.0e-09
Match length	70
% identity	46
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123631
Contig ID	11745_1.R1010
5'-most EST	jC-alXLIB327436P1e02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12

Match length	55
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123632
Contig ID	11750_1.R1010
5'-most EST	LIB23-008-Q1-E1-D4
Method	BLASTX
NCBI GI	g4559346
BLAST score	301
E value	5.0e-27
Match length	118
% identity	46
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	123633
Contig ID	11752_1.R1010
5'-most EST	LIB23-008-Q1-E1-D6
Method	BLASTN
NCBI GI	g4490734
BLAST score	399
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	123634
Contig ID	11754_1.R1010
5'-most EST	jC-atXP115C115I3T7055d1
Method	BLASTX
NCBI GI	g4455223
BLAST score	931
E value	1.0e-100
Match length	354
% identity	56
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	123635
Contig ID	11754_2.R1010
5'-most EST	g1269258
Method	BLASTX
NCBI GI	g4455223
BLAST score	610
E value	4.0e-63
Match length	206
% identity	30
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	123636
Contig ID	11754_3.R1010
5'-most EST	jC-atXLIB327408P1f05b1
Method	BLASTX
NCBI GI	g2708532

BLAST score	180
E value	7.0e-13
Match length	61
% identity	54
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No.	123637
Contig ID	11755_1.R1010
5'-most EST	LIB25-021-Q1-E1-B4
Method	BLASTN
NCBI GI	g4510360
BLAST score	300
E value	1.0e-168
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	123638
Contig ID	11758_1.R1010
5'-most EST	LIB25-095-Q1-E1-C7
Method	BLASTX
NCBI GI	g3341688
BLAST score	286
E value	1.0e-25
Match length	73
% identity	81
NCBI Description	(AC003672) putative casein kinase II beta subunit [Arabidopsis thaliana]

Seq. No.	123639
Contig ID	11767_1.R1010
5'-most EST	jC-alXLIB327434P3d07b1
Method	BLASTX
NCBI GI	g1363488
BLAST score	755
E value	4.0e-80
Match length	186
% identity	80
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	123640
Contig ID	11770_1.R1010
5'-most EST	jC-atXLIB327416P2h01b1
Method	BLASTN
NCBI GI	g2656024
BLAST score	462
E value	0.0e+00
Match length	462
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	123641

Contig ID	11775_1.R1010
5'-most EST	jC-atXLIB327428P4c05b2
Method	BLASTN
NCBI GI	g2264321
BLAST score	250
E value	1.0e-138
Match length	407
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	123642
Contig ID	11782_1.R1010
5'-most EST	jC-atXLIB327421P3e04b1
Method	BLASTX
NCBI GI	g3540183
BLAST score	554
E value	1.0e-56
Match length	176
% identity	57
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	123643
Contig ID	11785_1.R1010
5'-most EST	LIB3177-076-P1-K1-F4
Method	BLASTX
NCBI GI	g3850579
BLAST score	687
E value	0.0e+00
Match length	429
% identity	95
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	123644
Contig ID	11785_4.R1010
5'-most EST	g3449810
Method	BLASTX
NCBI GI	g3850580
BLAST score	155
E value	2.0e-50
Match length	107
% identity	93
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_84105 and gb_AI100071 come from this gene. [Arabidopsis thaliana]

Seq. No.	123645
Contig ID	11796_1.R1010
5'-most EST	jC-atXP109C208I9T7d1
Method	BLASTN
NCBI GI	g2264309

BLAST score	95
E value	7.0e-46
Match length	187
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	123646
Contig ID	11797_2.R1010
5'-most EST	g905641
Method	BLASTX
NCBI GI	g4101591
BLAST score	315
E value	2.0e-29
Match length	161
% identity	47
NCBI Description	(AF005051) aspartyl aminopeptidase [Mus musculus]

Seq. No.	123647
Contig ID	11803_1.R1010
5'-most EST	jC-atX23009Q1E1B02b1
Method	BLASTX
NCBI GI	g4827060
BLAST score	578
E value	2.0e-59
Match length	228
% identity	50
NCBI Description	xylulokinase (H. influenzae) homolog >gi_3298502_dbj_BAA31527_ (AB015046) xylulokinase [Homo sapiens]

Seq. No.	123648
Contig ID	11805_1.R1010
5'-most EST	LIB23-009-Q1-E1-B4
Method	BLASTN
NCBI GI	g2281081
BLAST score	41
E value	1.0e-13
Match length	199
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123649
Contig ID	11806_1.R1010
5'-most EST	LIB24-033-Q1-E1-G5
Method	BLASTX
NCBI GI	g4539459
BLAST score	565
E value	4.0e-58
Match length	190
% identity	60
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	123650
Contig ID	11816_1.R1010
5'-most EST	LIB23-009-Q1-E1-D2

Method	BLASTN
NCBI GI	g3128143
BLAST score	177
E value	7.0e-95
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	123651
Contig ID	11817_1.R1010
5'-most EST	jC-atXLIB327405P3c09b1
Method	BLASTN
NCBI GI	g2191126
BLAST score	276
E value	1.0e-154
Match length	500
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	123652
Contig ID	11821_1.R1010
5'-most EST	LIB24-026-Q1-E1-C3
Method	BLASTX
NCBI GI	g2583118
BLAST score	161
E value	6.0e-11
Match length	120
% identity	33
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123653
Contig ID	11823_1.R1010
5'-most EST	g2047696

Seq. No.	123654
Contig ID	11823_2.R1010
5'-most EST	g949302

Seq. No.	123655
Contig ID	11826_1.R1010
5'-most EST	g2733143
Method	BLASTX
NCBI GI	g2506788
BLAST score	633
E value	8.0e-66
Match length	189
% identity	35
NCBI Description	GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi_1332508_emb_CAA66638_ (X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No.	123656
Contig ID	11827_1.R1010
5'-most EST	LIB3168-037-P1-K1-A6

Method	BLASTN
NCBI GI	g3510347
BLAST score	171
E value	3.0e-91
Match length	427
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	123657
Contig ID	11828_1.R1010
5'-most EST	jC-atXLIB327409P2c11b1
Method	BLASTX
NCBI GI	g1170851
BLAST score	185
E value	2.0e-13
Match length	107
% identity	37
NCBI Description	MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A) >gi_1083410_pir__A54408 mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - mouse >gi_474280 (U04299) mannosyl-oligosaccharide alpha-1,2-mannosidase [Mus musculus]

Seq. No.	123658
Contig ID	11830_1.R1010
5'-most EST	jC-atXLIB327428P1b05b2
Method	BLASTX
NCBI GI	g4678301
BLAST score	276
E value	5.0e-24
Match length	87
% identity	62
NCBI Description	(AL049655) pectate lyase-like protein [Arabidopsis thaliana]

Seq. No.	123659
Contig ID	11834_1.R1010
5'-most EST	LIB23-009-Q1-E1-F6
Method	BLASTX
NCBI GI	g2244963
BLAST score	247
E value	4.0e-21
Match length	116
% identity	47
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123660
Contig ID	11838_1.R1010
5'-most EST	LIB23-009-Q1-E1-G2

Seq. No.	123661
Contig ID	11841_1.R1010
5'-most EST	LIB3176-024-P1-K1-E11
Method	BLASTX
NCBI GI	g4263646

BLAST score 1289
E value 1.0e-143
Match length 245
% identity 98
NCBI Description (AC006136) putative TA1-like reverse transcriptase [Arabidopsis thaliana]

Seq. No. 123662
Contig ID 11846_1.R1010
5'-most EST jC-atXP65C208B3T7037d1
Method BLASTX
NCBI GI g3953473
BLAST score 796
E value 4.0e-85
Match length 160
% identity 99
NCBI Description (AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No. 123663
Contig ID 11846_2.R1010
5'-most EST LIB317-065-P1-K1-F5
Method BLASTX
NCBI GI g3953473
BLAST score 624
E value 5.0e-65
Match length 125
% identity 98
NCBI Description (AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No. 123664
Contig ID 11846_3.R1010
5'-most EST jC-atXLI11Q1B1H05a1
Method BLASTX
NCBI GI g3953473
BLAST score 803
E value 8.0e-86
Match length 160
% identity 99
NCBI Description (AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No. 123665
Contig ID 11848_1.R1010
5'-most EST LIB23-009-Q1-E1-H5

Seq. No. 123666
Contig ID 11852_1.R1010
5'-most EST g1103355
Method BLASTN
NCBI GI g3643588
BLAST score 764
E value 0.0e+00
Match length 806
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 123667

Contig ID	11855_1.R1010
5'-most EST	LIB25-098-Q1-E1-B9
Method	BLASTX
NCBI GI	g4586029
BLAST score	310
E value	2.0e-28
Match length	119
% identity	57
NCBI Description	(AC007109) putative protein kinase [Arabidopsis thaliana]

Seq. No.	123668
Contig ID	11870_1.R1010
5'-most EST	jC-atXLIB327425P1f12b1
Method	BLASTX
NCBI GI	g416758
BLAST score	423
E value	2.0e-41
Match length	148
% identity	57
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	123669
Contig ID	11871_1.R1010
5'-most EST	LIB25-043-Q1-E1-B8
Method	BLASTX
NCBI GI	g3250697
BLAST score	479
E value	5.0e-48
Match length	113
% identity	79
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	123670
Contig ID	11883_1.R1010
5'-most EST	jC-alXLIB327434P2d04b1
Method	BLASTN
NCBI GI	g3241939
BLAST score	133
E value	2.0e-68
Match length	322
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T26J13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123671
Contig ID	11893_1.R1010
5'-most EST	LIB23-009-Q1-E2-F9
Method	BLASTX
NCBI GI	g4586041
BLAST score	382
E value	8.0e-37
Match length	129
% identity	60
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

>gi_4587998_gb_AAD25939.1_AF085279_12 (AF085279)
hypothetical protein [Arabidopsis thaliana]

Seq. No.	123672
Contig ID	11895_1.R1010
5'-most EST	LIB23-015-Q1-E1-B11
Method	BLASTX
NCBI GI	g4678332
BLAST score	705
E value	2.0e-74
Match length	219
% identity	64
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	123673
Contig ID	11901_1.R1010
5'-most EST	jC-alXLIB327435P3g08b1
Method	BLASTX
NCBI GI	g2497753
BLAST score	263
E value	1.0e-22
Match length	95
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	123674
Contig ID	11901_2.R1010
5'-most EST	g2749440
Method	BLASTX
NCBI GI	g2497753
BLAST score	71
E value	1.0e-13
Match length	92
% identity	39
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	123675
Contig ID	11901_3.R1010
5'-most EST	LIB25-019-Q1-E1-H10
Method	BLASTX
NCBI GI	g2497753
BLAST score	255
E value	6.0e-22
Match length	91
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	123676
Contig ID	11907_1.R1010
5'-most EST	LIB3175-055-P1-K1-A5

Method	BLASTN
NCBI GI	g3985958
BLAST score	238
E value	1.0e-131
Match length	465
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	123677
Contig ID	11911_1.R1010
5'-most EST	LIB23-010-Q1-E1-A7
Method	BLASTN
NCBI GI	g3241917
BLAST score	189
E value	1.0e-102
Match length	672
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	123678
Contig ID	11912_1.R1010
5'-most EST	jC-atXLIB327428P4a12b2
Method	BLASTX
NCBI GI	g4104058
BLAST score	252
E value	3.0e-21
Match length	116
% identity	46
NCBI Description	(AF031195) blue copper-binding protein homolog [Triticum aestivum]

Seq. No.	123679
Contig ID	11914_1.R1010
5'-most EST	jC-atXLIB327416P3g05b1
Method	BLASTX
NCBI GI	g2281093
BLAST score	699
E value	1.0e-73
Match length	137
% identity	97
NCBI Description	(AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No.	123680
Contig ID	11916_1.R1010
5'-most EST	jC-atXLIB327428P1b09b2

Seq. No.	123681
Contig ID	11916_2.R1010
5'-most EST	jC-atXP33C151K13T7d2

Seq. No.	123682
Contig ID	11918_1.R1010
5'-most EST	jC-atXLIB327416P4g12b1
Method	BLASTX
NCBI GI	g2213590

BLAST score	196
E value	8.0e-15
Match length	97
% identity	39
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	123683
Contig ID	11922_1.R1010
5'-most EST	LIB23-010-Q1-E1-C3
Method	BLASTX
NCBI GI	g3928150
BLAST score	223
E value	3.0e-18
Match length	48
% identity	92
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	123684
Contig ID	11923_1.R1010
5'-most EST	jC-atXLIB327428P4b06b2
Method	BLASTX
NCBI GI	g4679028
BLAST score	321
E value	2.0e-29
Match length	138
% identity	46
NCBI Description	(AF077207) HSPC021 [Homo sapiens]

Seq. No.	123685
Contig ID	11924_1.R1010
5'-most EST	LIB23-010-Q1-E2-C5
Method	BLASTN
NCBI GI	g3869066
BLAST score	188
E value	1.0e-101
Match length	393
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	123686
Contig ID	11926_1.R1010
5'-most EST	jC-atX35002Q1E1G12b1
Method	BLASTX
NCBI GI	g4309741
BLAST score	811
E value	9.0e-87
Match length	176
% identity	93
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123687
Contig ID	11928_1.R1010
5'-most EST	jC-alXLIB327436P2h03b1
Method	BLASTX
NCBI GI	g4097547
BLAST score	113

E value	3.0e-05
Match length	65
% identity	24
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	123688
Contig ID	11936_1.R1010
5'-most EST	LIB3176-012-P1-K1-D4
Method	BLASTX
NCBI GI	g4006848
BLAST score	1167
E value	1.0e-128
Match length	317
% identity	70
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	123689
Contig ID	11940_1.R1010
5'-most EST	jC-atXLIB327419P4d10b1
Method	BLASTN
NCBI GI	g2760166
BLAST score	37
E value	4.0e-11
Match length	158
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK20, complete sequence [Arabidopsis thaliana]

Seq. No.	123690
Contig ID	11941_1.R1010
5'-most EST	LIB23-010-Q1-E2-E7
Method	BLASTX
NCBI GI	g2330797
BLAST score	261
E value	2.0e-22
Match length	125
% identity	44
NCBI Description	(Z98601) zinc finger protein [Schizosaccharomyces pombe]

Seq. No.	123691
Contig ID	11945_1.R1010
5'-most EST	LIB23-010-Q1-E1-F4
Method	BLASTX
NCBI GI	g3193323
BLAST score	345
E value	1.0e-32
Match length	89
% identity	76
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

Seq. No.	123692
Contig ID	11947_1.R1010
5'-most EST	jC-atXLIB327428P4c07b2

Seq. No.	123693
Contig ID	11950_1.R1010
5'-most EST	g2757011
Method	BLASTX
NCBI GI	g2194129
BLAST score	541
E value	5.0e-55
Match length	126
% identity	91
NCBI Description	(AC002062) EST gb_T21469 comes from this gene. [Arabidopsis thaliana]

Seq. No.	123694
Contig ID	11951_1.R1010
5'-most EST	jC-atXLIB327414P2d08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	33
E value	9.0e-09
Match length	45
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	123695
Contig ID	11953_1.R1010
5'-most EST	jC-atXLIB327417P2b08b1
Method	BLASTN
NCBI GI	g3985952
BLAST score	490
E value	0.0e+00
Match length	602
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	123696
Contig ID	11958_1.R1010
5'-most EST	jC-atXP65C208F1T7054d1

Seq. No.	123697
Contig ID	11974_1.R1010
5'-most EST	LIB23-010-Q1-E2-B5
Method	BLASTX
NCBI GI	g4755200
BLAST score	609
E value	2.0e-63
Match length	125
% identity	90
NCBI Description	(AC007018) unknown protein [Arabidopsis thaliana]

Seq. No.	123698
Contig ID	11974_2.R1010
5'-most EST	ARABL1-02-Q1-B1-E3
Method	BLASTX
NCBI GI	g4755200

BLAST score	102
E value	1.0e-03
Match length	80
% identity	85
NCBI Description	(AC007018) unknown protein [Arabidopsis thaliana]

Seq. No.	123699
Contig ID	11978_1.R1010
5'-most EST	LIB3168-046-P1-K1-F12

Seq. No.	123700
Contig ID	11980_1.R1010
5'-most EST	LIB25-115-Q1-E1-B5
Method	BLASTX
NCBI GI	g2323344
BLAST score	380
E value	9.0e-37
Match length	113
% identity	71
NCBI Description	(AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]

Seq. No.	123701
Contig ID	11990_1.R1010
5'-most EST	LIB23-057-Q1-E1-D2
Method	BLASTN
NCBI GI	g4159700
BLAST score	478
E value	0.0e+00
Match length	513
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	123702
Contig ID	12001_1.R1010
5'-most EST	LIB3175-031-P1-K1-B2
Method	BLASTN
NCBI GI	g3426033
BLAST score	182
E value	9.0e-98
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123703
Contig ID	12001_2.R1010
5'-most EST	LIB23-010-Q1-E2-D9
Method	BLASTN
NCBI GI	g3426033
BLAST score	231
E value	1.0e-127
Match length	429
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123704
Contig ID	12011_1.R1010
5'-most EST	jC-atXP110CG7D4T7013a1
Method	BLASTX
NCBI GI	g2352492
BLAST score	482
E value	4.0e-48
Match length	127
% identity	67
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	123705
Contig ID	12014_1.R1010
5'-most EST	jC-atXP112C129P12T7d2
Method	BLASTX
NCBI GI	g2245066
BLAST score	875
E value	3.0e-94
Match length	170
% identity	96
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	123706
Contig ID	12014_3.R1010
5'-most EST	jC-atXLIB327419P4e07b1
Method	BLASTX
NCBI GI	g2245066
BLAST score	903
E value	2.0e-97
Match length	297
% identity	84
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	123707
Contig ID	12014_4.R1010
5'-most EST	jC-atXLIB327428P4c02b2
Method	BLASTX
NCBI GI	g2245066
BLAST score	1021
E value	1.0e-135
Match length	233
% identity	100
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	123708
Contig ID	12014_6.R1010
5'-most EST	LIB23-055-Q1-E1-A6
Method	BLASTX
NCBI GI	g2245066
BLAST score	789
E value	1.0e-84
Match length	146
% identity	100
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	123709
Contig ID	12021_1.R1010
5'-most EST	jC-atXLIB327422P4f08a1
Method	BLASTN
NCBI GI	g2351064
BLAST score	392
E value	0.0e+00
Match length	522
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	123710
Contig ID	12024_1.R1010
5'-most EST	g932742
Method	BLASTN
NCBI GI	g3510340
BLAST score	345
E value	0.0e+00
Match length	469
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	123711
Contig ID	12028_1.R1010
5'-most EST	LIB23-010-Q1-E2-G12
Method	BLASTN
NCBI GI	g3420042
BLAST score	136
E value	2.0e-70
Match length	447
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123712
Contig ID	12056_1.R1010
5'-most EST	jC-atXLIB327417P1g07b1
Method	BLASTN
NCBI GI	g3702724
BLAST score	303
E value	1.0e-170
Match length	523
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	123713
Contig ID	12056_2.R1010
5'-most EST	LIB23-068-Q1-E1-H7
Method	BLASTX
NCBI GI	g3037045
BLAST score	150
E value	3.0e-09
Match length	117
% identity	34

NCBI Description	(AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No.	123714
Contig ID	12056_3.R1010
5'-most EST	jC-atXLIB327416P2d03b1
Method	BLASTN
NCBI GI	g3108025
BLAST score	302
E value	1.0e-169
Match length	533
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	123715
Contig ID	12056_5.R1010
5'-most EST	jC-atXmonuni26Cd06b1
Method	BLASTN
NCBI GI	g3702724
BLAST score	346
E value	0.0e+00
Match length	658
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	123716
Contig ID	12056_6.R1010
5'-most EST	g2733696
Method	BLASTN
NCBI GI	g3702724
BLAST score	271
E value	1.0e-151
Match length	407
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	123717
Contig ID	12063_1.R1010
5'-most EST	jC-atXLIB327407P1f10b2
Method	BLASTX
NCBI GI	g2982299
BLAST score	396
E value	5.0e-38
Match length	103
% identity	77
NCBI Description	(AF051234) transcription factor BTF3 homolog [Picea mariana]

Seq. No.	123718
Contig ID	12064_1.R1010
5'-most EST	LIB23-045-Q1-E1-H8
Method	BLASTX
NCBI GI	g1498315
BLAST score	129
E value	2.0e-15

Match length	114
% identity	43
NCBI Description	(U56419) IAP100 [Pisum sativum]

Seq. No.	123719
Contig ID	12067_1.R1010
5'-most EST	LIB23-011-Q1-E1-C7

Seq. No.	123720
Contig ID	12072_1.R1010
5'-most EST	LIB3176-009-P1-K2-C11
Method	BLASTX
NCBI GI	g3386621
BLAST score	697
E value	2.0e-73
Match length	150
% identity	89
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	123721
Contig ID	12084_1.R1010
5'-most EST	g2748855

Seq. No.	123722
Contig ID	12085_1.R1010
5'-most EST	LIB23-011-Q1-E1-F6

Seq. No.	123723
Contig ID	12086_1.R1010
5'-most EST	LIB25-023-Q1-E1-H8
Method	BLASTX
NCBI GI	g2642443
BLAST score	477
E value	6.0e-48
Match length	149
% identity	67
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	123724
Contig ID	12087_1.R1010
5'-most EST	jC-atXLIB327413P1g03b1
Method	BLASTX
NCBI GI	g3599491
BLAST score	338
E value	2.0e-31
Match length	80
% identity	80
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	123725
Contig ID	12093_1.R1010
5'-most EST	jC-atXLIB327423P4h04b1
Method	BLASTN
NCBI GI	g1617273
BLAST score	175
E value	1.0e-93
Match length	279

% identity	91
NCBI Description	B.napus mRNA for AMP-binding protein (2287 bp)

Seq. No.	123726
Contig ID	12093_2.R1010
5'-most EST	LIB23-066-Q1-E1-F9
Method	BLASTX
NCBI GI	g1617274
BLAST score	1034
E value	1.0e-113
Match length	250
% identity	81
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	123727
Contig ID	12101_1.R1010
5'-most EST	jC-atXP95CG11H12T7095b1
Method	BLASTN
NCBI GI	g3892595
BLAST score	54
E value	2.0e-21
Match length	73
% identity	95
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	123728
Contig ID	12105_1.R1010
5'-most EST	LIB23-012-Q1-E1-A12

Seq. No.	123729
Contig ID	12106_1.R1010
5'-most EST	LIB23-012-Q1-E1-A2

Seq. No.	123730
Contig ID	12108_1.R1010
5'-most EST	LIB25-111-Q1-E1-E12
Method	BLASTX
NCBI GI	g4008441
BLAST score	480
E value	8.0e-48
Match length	215
% identity	47
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	123731
Contig ID	12112_1.R1010
5'-most EST	g931166
Method	BLASTN
NCBI GI	g3510339
BLAST score	328
E value	0.0e+00
Match length	328
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	123732
Contig ID	12113_1.R1010
5'-most EST	LIB23-017-Q1-E1-D5
Method	BLASTX
NCBI GI	g3695385
BLAST score	390
E value	8.0e-38
Match length	104
% identity	80
NCBI Description	(AF096370) similar to Medicago truncatula MtN21 (GB:Y15293) [Arabidopsis thaliana]

Seq. No.	123733
Contig ID	12116_1.R1010
5'-most EST	jC-atXLIB327428P4d06b2
Method	BLASTX
NCBI GI	g3915186
BLAST score	325
E value	9.0e-30
Match length	143
% identity	45
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]

Seq. No.	123734
Contig ID	12119_1.R1010
5'-most EST	LIB23-012-Q1-E1-B9
Method	BLASTN
NCBI GI	g4688595
BLAST score	38
E value	1.0e-11
Match length	50
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for inositol 1,4,5-trisphosphate 5-phosphatase

Seq. No.	123735
Contig ID	12123_1.R1010
5'-most EST	jC-alXLIB327434P4g08b1
Method	BLASTX
NCBI GI	g3881976
BLAST score	990
E value	1.0e-107
Match length	260
% identity	71
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]

Seq. No.	123736
Contig ID	12132_1.R1010
5'-most EST	LIB23-056-Q1-E1-B6
Method	BLASTX
NCBI GI	g303742
BLAST score	582

E value	3.0e-60
Match length	121
% identity	93
NCBI Description	(D12544) GTP-binding protein [Pisum sativum] >gi_738936_prf__2001457D GTP-binding protein [Pisum sativum]

Seq. No.	123737
Contig ID	12134_1.R1010
5'-most EST	LIB23-012-Q1-E1-D5
Method	BLASTX
NCBI GI	g3355469
BLAST score	211
E value	9.0e-46
Match length	101
% identity	92
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	123738
Contig ID	12138_1.R1010
5'-most EST	LIB3176-121-P2-K1-A8

Seq. No.	123739
Contig ID	12139_1.R1010
5'-most EST	jC-atXmonuni26Af11b1
Method	BLASTN
NCBI GI	g3510347
BLAST score	109
E value	4.0e-54
Match length	507
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	123740
Contig ID	12140_2.R1010
5'-most EST	jC-atXLIB327430P1h02b1

Seq. No.	123741
Contig ID	12141_1.R1010
5'-most EST	jC-atXLIB327423P4d07b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	43
E value	1.0e-14
Match length	165
% identity	41
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	123742
Contig ID	12143_1.R1010
5'-most EST	g2758466
Method	BLASTX
NCBI GI	g1143427
BLAST score	1124
E value	1.0e-123

Match length	263
% identity	85
NCBI Description	(X73961) heat shock protein 70 [Cucumis sativus]

Seq. No.	123743
Contig ID	12143_2.R1010
5'-most EST	jC-atXP100CE3F12T7b1
Method	BLASTX
NCBI GI	g1709379
BLAST score	514
E value	5.0e-52
Match length	108
% identity	91
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST >gi_881441 (U27653) NADH-plastoquinone oxidoreductase [Lupinus luteus]

Seq. No.	123744
Contig ID	12143_3.R1010
5'-most EST	LIB3177-053-P1-K1-F12
Method	BLASTX
NCBI GI	g1709379
BLAST score	54
E value	1.0e-20
Match length	60
% identity	88
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST >gi_881441 (U27653) NADH-plastoquinone oxidoreductase [Lupinus luteus]

Seq. No.	123745
Contig ID	12147_1.R1010
5'-most EST	LIB3176-111-P1-K1-H2

Seq. No.	123746
Contig ID	12149_1.R1010
5'-most EST	jC-atXLIB327428P4e05b2
Method	BLASTX
NCBI GI	g3540183
BLAST score	881
E value	7.0e-95
Match length	189
% identity	93
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	123747
Contig ID	12149_2.R1010
5'-most EST	jC-atXLIB327413P1f10b1
Method	BLASTN
NCBI GI	g3176693
BLAST score	197
E value	1.0e-106
Match length	391
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123748
Contig ID	12152_1.R1010
5'-most EST	jC-atXP117C141M14T7a1
Method	BLASTX
NCBI GI	g4588906
BLAST score	501
E value	2.0e-50
Match length	125
% identity	73
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	123749
Contig ID	12152_2.R1010
5'-most EST	jC-atXLIB327414P2e08a1
Method	BLASTX
NCBI GI	g3851636
BLAST score	690
E value	2.0e-72
Match length	190
% identity	69
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	123750
Contig ID	12153_1.R1010
5'-most EST	LIB23-012-Q1-E1-F9
Method	BLASTX
NCBI GI	g3128218
BLAST score	983
E value	1.0e-107
Match length	199
% identity	96
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	123751
Contig ID	12157_1.R1010
5'-most EST	jC-atXLIB327428P4e08b2
Method	BLASTX
NCBI GI	g4835227
BLAST score	758
E value	2.0e-80
Match length	149
% identity	93
NCBI Description	(AL049862) glycosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	123752
Contig ID	12158_1.R1010
5'-most EST	g587048

Seq. No.	123753
Contig ID	12163_1.R1010
5'-most EST	LIB23-012-Q1-E1-H2

Seq. No.	123754
Contig ID	12164_1.R1010

5'-most EST	LIB23-012-Q1-E1-H3
Method	BLASTX
NCBI GI	g125568
BLAST score	202
E value	2.0e-36
Match length	200
% identity	49
NCBI Description	PROTEIN KINASE PVPK-1 >gi_100013_pir__A30311 protein kinase C (EC 2.7.1.-) homolog - kidney bean >gi_169361 (J04555) PVPK-1 protein [Phaseolus vulgaris]

Seq. No.	123755
Contig ID	12169_1.R1010
5'-most EST	jC-atXLIB327410P1g12a1
Method	BLASTN
NCBI GI	g4585952
BLAST score	783
E value	0.0e+00
Match length	799
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	123756
Contig ID	12172_1.R1010
5'-most EST	LIB23-013-Q1-E1-A2
Method	BLASTX
NCBI GI	g3928099
BLAST score	1140
E value	1.0e-125
Match length	219
% identity	56
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	123757
Contig ID	12177_1.R1010
5'-most EST	LIB3176-044-P1-K1-C2
Method	BLASTX
NCBI GI	g1621268
BLAST score	519
E value	9.0e-53
Match length	136
% identity	68
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	123758
Contig ID	12182_1.R1010
5'-most EST	ARABLI-10-Q1-B1-D6
Method	BLASTN
NCBI GI	g3241921
BLAST score	239
E value	1.0e-132
Match length	461
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCM23, complete sequence [Arabidopsis thaliana]

Seq. No.	123759
Contig ID	12191_1.R1010
5'-most EST	jC-atXLIB327428P4d10b2
Method	BLASTN
NCBI GI	g4006885
BLAST score	341
E value	0.0e+00
Match length	494
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	123760
Contig ID	12192_1.R1010
5'-most EST	LIB23-013-Q1-E1-C2
Method	BLASTX
NCBI GI	g3367569
BLAST score	431
E value	3.0e-42
Match length	152
% identity	57
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	123761
Contig ID	12193_1.R1010
5'-most EST	jC-atXP96C248H5T7b1
Method	BLASTX
NCBI GI	g4741954
BLAST score	946
E value	1.0e-102
Match length	245
% identity	81
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	123762
Contig ID	12193_2.R1010
5'-most EST	jC-atXLIB327431P4b03a1
Method	BLASTX
NCBI GI	g4741954
BLAST score	801
E value	1.0e-85
Match length	153
% identity	100
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	123763
Contig ID	12193_3.R1010
5'-most EST	g2756939
Method	BLASTX
NCBI GI	g4741954
BLAST score	289
E value	2.0e-40
Match length	114
% identity	74
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No. 123764

Contig ID	12193_4.R1010
5'-most EST	g949234
Method	BLASTX
NCBI GI	g4741954
BLAST score	474
E value	2.0e-56
Match length	130
% identity	88
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	123765
Contig ID	12193_5.R1010
5'-most EST	g1269305
Method	BLASTX
NCBI GI	g4741954
BLAST score	498
E value	2.0e-50
Match length	92
% identity	100
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	123766
Contig ID	12194_1.R1010
5'-most EST	LIB25-071-Q1-E1-F9
Method	BLASTN
NCBI GI	g3046852
BLAST score	386
E value	0.0e+00
Match length	567
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	123767
Contig ID	12196_1.R1010
5'-most EST	LIB25-020-Q1-E1-B11
Method	BLASTX
NCBI GI	g3894171
BLAST score	608
E value	4.0e-65
Match length	143
% identity	90
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	123768
Contig ID	12196_3.R1010
5'-most EST	LIB3168-071-P1-K1-G2
Method	BLASTX
NCBI GI	g3894171
BLAST score	520
E value	1.0e-56
Match length	126
% identity	93
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	123769
Contig ID	12197_1.R1010
5'-most EST	jC-atXLIB327413P4e04b1
Method	BLASTN
NCBI GI	g2618599
BLAST score	66
E value	2.0e-28
Match length	185
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	123770
Contig ID	12197_2.R1010
5'-most EST	LIB3176-069-P1-K1-H1
Method	BLASTN
NCBI GI	g2618599
BLAST score	66
E value	2.0e-28
Match length	288
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	123771
Contig ID	12198_1.R1010
5'-most EST	jC-atXLIB327423P1g09b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	237
E value	1.0e-130
Match length	617
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	123772
Contig ID	12204_1.R1010
5'-most EST	jC-atXLIB327428P1e04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123773
Contig ID	12205_1.R1010
5'-most EST	LIB3175-043-P1-K1-G6
Method	BLASTX
NCBI GI	g3738339
BLAST score	506
E value	2.0e-51
Match length	154
% identity	73

NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	123774
Contig ID	12209_1.R1010
5'-most EST	jC-atXLIB327430P4g09b1
Method	BLASTN
NCBI GI	g2244991
BLAST score	212
E value	1.0e-115
Match length	522
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	123775
Contig ID	12209_2.R1010
5'-most EST	LIB23-040-Q1-E1-F3
Method	BLASTN
NCBI GI	g2244991
BLAST score	231
E value	1.0e-127
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	123776
Contig ID	12210_1.R1010
5'-most EST	LIB23-013-Q1-E1-E10
Method	BLASTX
NCBI GI	g3928862
BLAST score	177
E value	1.0e-12
Match length	70
% identity	53
NCBI Description	(AF089710) disease resistance protein RPP8 [Arabidopsis thaliana]

Seq. No.	123777
Contig ID	12212_1.R1010
5'-most EST	jC-atXLIB327428P1e09b2
Method	BLASTX
NCBI GI	g2129753
BLAST score	676
E value	3.0e-71
Match length	141
% identity	94
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	123778
Contig ID	12214_1.R1010
5'-most EST	LIB23-013-Q1-E1-E3
Method	BLASTN
NCBI GI	g4757409
BLAST score	39

E value	3.0e-12
Match length	453
% identity	43
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	123779
Contig ID	12227_1.R1010
5'-most EST	jC-atXLIB327428P1e12b2
Method	BLASTX
NCBI GI	g2982285
BLAST score	350
E value	9.0e-33
Match length	69
% identity	80
NCBI Description	(AF051227) GASA5-like protein [Picea mariana]

Seq. No.	123780
Contig ID	12231_1.R1010
5'-most EST	jC-atXLIB327428P4e01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	80
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123781
Contig ID	12235_1.R1010
5'-most EST	g2757623
Method	BLASTX
NCBI GI	g1825727
BLAST score	84
E value	6.0e-32
Match length	148
% identity	50
NCBI Description	(U88308) C32E8.5 gene product [Caenorhabditis elegans]

Seq. No.	123782
Contig ID	12238_1.R1010
5'-most EST	jC-alXLIB327434P1c05b1
Method	BLASTN
NCBI GI	g4335711
BLAST score	278
E value	1.0e-155
Match length	857
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123783
Contig ID	12240_1.R1010
5'-most EST	g2759627
Method	BLASTX
NCBI GI	g1351271

BLAST score	842
E value	2.0e-90
Match length	177
% identity	91
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	123784
Contig ID	12240_3.R1010
5'-most EST	LIB3177-056-P1-K1-C4
Method	BLASTX
NCBI GI	g1351271
BLAST score	339
E value	2.0e-31
Match length	126
% identity	60
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	123785
Contig ID	12240_5.R1010
5'-most EST	g2758721
Method	BLASTN
NCBI GI	g806311
BLAST score	34
E value	2.0e-09
Match length	66
% identity	88
NCBI Description	Spinacia oleracea nuclear encoded triosephosphate isomerase, chloroplast isozyme mRNA, complete cds

Seq. No.	123786
Contig ID	12242_1.R1010
5'-most EST	LIB23-013-Q1-E1-G9
Method	BLASTN
NCBI GI	g4753195
BLAST score	379
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	123787
Contig ID	12243_1.R1010
5'-most EST	g2747548
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	2.0e-19
Match length	66

% identity	97
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	123788
Contig ID	12243_3.R1010
5'-most EST	LIB24-099-Q1-E1-C4
Seq. No.	123789
Contig ID	12243_4.R1010
5'-most EST	jC-atXLIB327428P4e12b2
Method	BLASTN
NCBI GI	g4678371
BLAST score	38
E value	1.0e-11
Match length	86
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)
Seq. No.	123790
Contig ID	12244_1.R1010
5'-most EST	LIB23-013-Q1-E1-H10
Method	BLASTX
NCBI GI	g4105269
BLAST score	222
E value	6.0e-18
Match length	123
% identity	41
NCBI Description	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]
Seq. No.	123791
Contig ID	12246_1.R1010
5'-most EST	LIB3168-030-P1-K1-H6
Method	BLASTX
NCBI GI	g3935150
BLAST score	279
E value	9.0e-25
Match length	102
% identity	64
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]
Seq. No.	123792
Contig ID	12250_1.R1010
5'-most EST	jC-atXLIB327428P4e10b2
Method	BLASTX
NCBI GI	g4468813
BLAST score	298
E value	2.0e-26
Match length	102
% identity	53
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]
Seq. No.	123793
Contig ID	12250_2.R1010
5'-most EST	jC-atX35022Q1E1D12b1
Method	BLASTX

NCBI GI	g4468813
BLAST score	498
E value	1.0e-50
Match length	176
% identity	55
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	123794
Contig ID	12253_1.R1010
5'-most EST	jC-atXLIB327430P4g10b1
Method	BLASTX
NCBI GI	g3281855
BLAST score	389
E value	2.0e-37
Match length	155
% identity	55
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123795
Contig ID	12254_1.R1010
5'-most EST	jC-atXLIB327428P1g09b2
Method	BLASTN
NCBI GI	g4092471
BLAST score	64
E value	3.0e-27
Match length	157
% identity	92
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	123796
Contig ID	12256_1.R1010
5'-most EST	jC-atXLIB327428P1d07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123797
Contig ID	12259_1.R1010
5'-most EST	jC-atXLIB327428P1d08b2
Method	BLASTX
NCBI GI	g4585991
BLAST score	616
E value	4.0e-64
Match length	146
% identity	71
NCBI Description	(AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]

Seq. No.	123798
Contig ID	12266_1.R1010
5'-most EST	LIB3175-022-P1-K1-C6

Method	BLASTN
NCBI GI	g3335356
BLAST score	328
E value	0.0e+00
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123799
Contig ID	12267_1.R1010
5'-most EST	jC-atXLIB327417P2e12b1
Method	BLASTX
NCBI GI	g4678368
BLAST score	696
E value	2.0e-73
Match length	133
% identity	99
NCBI Description	(AJ132436) GA 2-oxidase [Arabidopsis thaliana]

Seq. No.	123800
Contig ID	12268_1.R1010
5'-most EST	LIB24-103-Q1-E1-A2
Method	BLASTX
NCBI GI	g2230757
BLAST score	987
E value	1.0e-107
Match length	236
% identity	84
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	123801
Contig ID	12269_1.R1010
5'-most EST	LIB23-014-Q1-E1-B4

Seq. No.	123802
Contig ID	12271_1.R1010
5'-most EST	LIB24-093-Q1-E1-E12

Seq. No.	123803
Contig ID	12272_1.R1010
5'-most EST	LIB23-014-Q1-E1-B8
Method	BLASTX
NCBI GI	g2443886
BLAST score	335
E value	7.0e-59
Match length	138
% identity	89
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	123804
Contig ID	12281_1.R1010
5'-most EST	LIB3177-088-P1-K1-G2
Method	BLASTX
NCBI GI	g114339
BLAST score	1039
E value	1.0e-113

Match length	228
% identity	91
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625 (J04737) ATPase [Arabidopsis thaliana]

Seq. No.	123805
Contig ID	12282_1.R1010
5'-most EST	LIB25-008-Q1-E1-H12
Method	BLASTN
NCBI GI	g2477521
BLAST score	253
E value	1.0e-140
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123806
Contig ID	12291_1.R1010
5'-most EST	LIB23-014-Q1-E1-D5
Method	BLASTN
NCBI GI	g3582315
BLAST score	317
E value	1.0e-178
Match length	1073
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123807
Contig ID	12306_1.R1010
5'-most EST	ARABL1-044-Q1-B1-F10
Method	BLASTX
NCBI GI	g4115933
BLAST score	238
E value	4.0e-20
Match length	81
% identity	64
NCBI Description	(AF118223) contains similarity to human RNA polymerase II complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No.	123808
Contig ID	12307_1.R1010
5'-most EST	LIB24-013-Q1-E1-A5
Method	BLASTX
NCBI GI	g3868853
BLAST score	466
E value	3.0e-46
Match length	115
% identity	74
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	123809
Contig ID	12310_1.R1010
5'-most EST	jC-atXLIB327415P2f04b2

Seq. No.	123810
Contig ID	12312_1.R1010
5'-most EST	jC-alXLIB327434P4b12b1
Method	BLASTX
NCBI GI	g4510363
BLAST score	198
E value	4.0e-15
Match length	47
% identity	79
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123811
Contig ID	12312_2.R1010
5'-most EST	LIB3175-078-P1-K1-C11
Method	BLASTX
NCBI GI	g4510363
BLAST score	524
E value	4.0e-53
Match length	134
% identity	71
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123812
Contig ID	12312_3.R1010
5'-most EST	jC-atXP7C91L8T7d1
Method	BLASTX
NCBI GI	g4510363
BLAST score	552
E value	2.0e-56
Match length	134
% identity	75
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123813
Contig ID	12318_1.R1010
5'-most EST	LIB25-074-Q1-E1-E7
Method	BLASTN
NCBI GI	g2815519
BLAST score	211
E value	1.0e-115
Match length	301
% identity	100
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	123814
Contig ID	12320_1.R1010
5'-most EST	jC-atXLIB327416P1d04b1
Method	BLASTX
NCBI GI	g3928103
BLAST score	697
E value	2.0e-73
Match length	151

% identity	91
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	123815
Contig ID	12320_2.R1010
5'-most EST	g2763364
Method	BLASTX
NCBI GI	g3928103
BLAST score	1046
E value	1.0e-114
Match length	201
% identity	100
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	123816
Contig ID	12320_4.R1010
5'-most EST	jC-atXP109C209O14T7s1
Method	BLASTX
NCBI GI	g3928103
BLAST score	382
E value	1.0e-36
Match length	71
% identity	100
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	123817
Contig ID	12321_1.R1010
5'-most EST	jC-atXLIB327416P4c04b1
Method	BLASTX
NCBI GI	g3170230
BLAST score	611
E value	3.0e-63
Match length	195
% identity	61
NCBI Description	(AF041848) fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No.	123818
Contig ID	12323_1.R1010
5'-most EST	LIB3177-088-P1-K1-B10
Method	BLASTX
NCBI GI	g4539400
BLAST score	181
E value	6.0e-13
Match length	221
% identity	33
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	123819
Contig ID	12325_1.R1010
5'-most EST	LIB23-029-Q1-E1-D6
Method	BLASTX
NCBI GI	g629646
BLAST score	145

E value	4.0e-09
Match length	111
% identity	42
NCBI Description	phosphorylase (EC 2.4.1.1) alpha-1,4 glucan, L isoform precursor - fava bean

Seq. No.	123820
Contig ID	12326_1.R1010
5'-most EST	LIB23-014-Q1-E1-H12

Seq. No.	123821
Contig ID	12328_1.R1010
5'-most EST	jC-atXLIB327428P1f02b2
Method	BLASTX
NCBI GI	g4544404
BLAST score	56
E value	6.0e-86
Match length	163
% identity	98
NCBI Description	(AC007047) unknown protein [Arabidopsis thaliana]

Seq. No.	123822
Contig ID	12329_1.R1010
5'-most EST	jC-atXLIB327421P1c04b1
Method	BLASTX
NCBI GI	g2832625
BLAST score	1308
E value	1.0e-145
Match length	369
% identity	66
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	123823
Contig ID	12329_2.R1010
5'-most EST	jC-atXLIB327428P1f03b2
Method	BLASTX
NCBI GI	g2832625
BLAST score	301
E value	3.0e-27
Match length	75
% identity	71
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	123824
Contig ID	12329_3.R1010
5'-most EST	g906644
Method	BLASTX
NCBI GI	g2832625
BLAST score	247
E value	1.0e-21
Match length	114
% identity	52
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	123825
Contig ID	12334_1.R1010
5'-most EST	jC-atXLIB327428P4e11b2

Method	BLASTN
NCBI GI	g4455290
BLAST score	372
E value	0.0e+00
Match length	459
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	123826
Contig ID	12340_1.R1010
5'-most EST	jC-atXLIB327415P3c09a1
Method	BLASTX
NCBI GI	g2384956
BLAST score	386
E value	8.0e-37
Match length	201
% identity	37
NCBI Description	(AF022985) No definition line found [Caenorhabditis elegans]

Seq. No.	123827
Contig ID	12341_1.R1010
5'-most EST	jC-atXP22C114O19T7011a1
Method	BLASTX
NCBI GI	g3914449
BLAST score	653
E value	2.0e-68
Match length	135
% identity	95
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	123828
Contig ID	12344_1.R1010
5'-most EST	LIB25-078-Q1-E1-C11
Method	BLASTN
NCBI GI	g4191771
BLAST score	157
E value	1.0e-82
Match length	628
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123829
Contig ID	12356_1.R1010
5'-most EST	jC-atXLIB327428P1g05b2
Method	BLASTX
NCBI GI	g3033391
BLAST score	369
E value	3.0e-35
Match length	119
% identity	62
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	123830
Contig ID	12357_1.R1010
5'-most EST	jC-atXLIB327423P4f05b1
Method	BLASTX
NCBI GI	g3461820
BLAST score	321
E value	2.0e-29
Match length	71
% identity	76
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	123831
Contig ID	12360_1.R1010
5'-most EST	g947859
Method	BLASTX
NCBI GI	g2829899
BLAST score	518
E value	2.0e-52
Match length	160
% identity	80
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	123832
Contig ID	12360_2.R1010
5'-most EST	g2722195
Method	BLASTN
NCBI GI	g2645198
BLAST score	209
E value	1.0e-114
Match length	346
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123833
Contig ID	12361_1.R1010
5'-most EST	LIB23-015-Q1-E1-C5
Method	BLASTN
NCBI GI	g2191126
BLAST score	253
E value	1.0e-140
Match length	338
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	123834
Contig ID	12362_1.R1010
5'-most EST	jC-atXLIB327423P1g08b1
Method	BLASTX
NCBI GI	g3004551
BLAST score	197
E value	1.0e-14
Match length	184
% identity	48

NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123835
Contig ID	12363_1.R1010
5'-most EST	LIB25-037-Q1-E1-F3
Method	BLASTX
NCBI GI	g4220527
BLAST score	152
E value	8.0e-10
Match length	44
% identity	64
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	123836
Contig ID	12365_1.R1010
5'-most EST	jC-atXLIB327428P1g11b2
Method	BLASTX
NCBI GI	g3695378
BLAST score	317
E value	6.0e-35
Match length	106
% identity	74
NCBI Description	(AF096370) contains similarity to NAM (no apical meristem) -like proteins [Arabidopsis thaliana]

Seq. No.	123837
Contig ID	12369_1.R1010
5'-most EST	LIB23-015-Q1-E1-D2
Method	BLASTX
NCBI GI	g4115927
BLAST score	700
E value	4.0e-74
Match length	140
% identity	96
NCBI Description	(AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, Score=49.7, E=9.2e-13, n=3) [Arabidopsis thaliana]

Seq. No.	123838
Contig ID	12375_1.R1010
5'-most EST	jC-atXP74C223M20T7051d1
Method	BLASTX
NCBI GI	g1173345
BLAST score	1841
E value	0.0e+00
Match length	393
% identity	92
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]

Seq. No.	123839
Contig ID	12375_2.R1010

5'-most EST	jC-atXP63C204K13T7d2
Method	BLASTN
NCBI GI	g786465
BLAST score	285
E value	1.0e-159
Match length	387
% identity	97
NCBI Description	sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana, C24, Genomic, 2747 nt]

Seq. No.	123840
Contig ID	12375_4.R1010
5'-most EST	jC-atXP114C235H7T7s1
Method	BLASTX
NCBI GI	g1173345
BLAST score	553
E value	8.0e-57
Match length	110
% identity	100
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]

Seq. No.	123841
Contig ID	12375_8.R1010
5'-most EST	g1158706
Method	BLASTN
NCBI GI	g786465
BLAST score	129
E value	4.0e-66
Match length	313
% identity	97
NCBI Description	sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana, C24, Genomic, 2747 nt]

Seq. No.	123842
Contig ID	12376_1.R1010
5'-most EST	jC-atXmonuni27Ab06b1

Seq. No.	123843
Contig ID	12378_1.R1010
5'-most EST	jC-atXP79C231F19T7b1
Method	BLASTN
NCBI GI	g3702724
BLAST score	200
E value	1.0e-108
Match length	694
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	123844
Contig ID	12378_2.R1010

5'-most EST	g2749339
Method	BLASTN
NCBI GI	g3702724
BLAST score	216
E value	1.0e-118
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	123845
Contig ID	12379_1.R1010
5'-most EST	LIB23-015-Q1-E1-E3
Method	BLASTN
NCBI GI	g2244788
BLAST score	334
E value	0.0e+00
Match length	362
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	123846
Contig ID	12381_1.R1010
5'-most EST	jC-alXLIB327435P3c06b1
Method	BLASTN
NCBI GI	g3849811
BLAST score	596
E value	0.0e+00
Match length	621
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123847
Contig ID	12384_1.R1010
5'-most EST	jC-atXLIB327427P2e09b1
Method	BLASTX
NCBI GI	g3169182
BLAST score	394
E value	6.0e-38
Match length	75
% identity	100
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	123848
Contig ID	12385_1.R1010
5'-most EST	jC-atX23015Q1E1F01b1
Method	BLASTX
NCBI GI	g4099090
BLAST score	355
E value	8.0e-51
Match length	155
% identity	74
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No. 123849

Contig ID	12386_1.R1010
5'-most EST	jC-atXLIB327404P4b09b1
Method	BLASTX
NCBI GI	g4262156
BLAST score	792
E value	1.0e-108
Match length	222
% identity	89
NCBI Description	(AC005275) putative component of cytochrome B6-F complex [Arabidopsis thaliana]

Seq. No.	123850
Contig ID	12388_1.R1010
5'-most EST	jC-atXLIB327428P1h09b2
Method	BLASTN
NCBI GI	g3449312
BLAST score	225
E value	1.0e-123
Match length	432
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No.	123851
Contig ID	12390_1.R1010
5'-most EST	LIB23-026-Q1-E1-C11
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	63
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	123852
Contig ID	12391_1.R1010
5'-most EST	LIB23-015-Q1-E1-F7
Method	BLASTX
NCBI GI	g3249096
BLAST score	710
E value	5.0e-75
Match length	170
% identity	59
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	123853
Contig ID	12393_1.R1010
5'-most EST	g2749279

Seq. No.	123854
Contig ID	12396_1.R1010
5'-most EST	LIB23-015-Q1-E1-G11
Method	BLASTX
NCBI GI	g2245136

BLAST score	848
E value	4.0e-91
Match length	261
% identity	61
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	123855
Contig ID	12397_1.R1010
5'-most EST	g2763064
Method	BLASTX
NCBI GI	g2252844
BLAST score	1231
E value	1.0e-136
Match length	237
% identity	96
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	123856
Contig ID	12398_1.R1010
5'-most EST	LIB23-015-Q1-E1-G2
Method	BLASTN
NCBI GI	g4753195
BLAST score	730
E value	0.0e+00
Match length	750
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	123857
Contig ID	12405_1.R1010
5'-most EST	LIB24-006-Q1-E1-C1

Seq. No.	123858
Contig ID	12411_1.R1010
5'-most EST	jC-atXLIB327419P4f12b1
Method	BLASTN
NCBI GI	g3420042
BLAST score	259
E value	1.0e-143
Match length	476
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123859
Contig ID	12413_1.R1010
5'-most EST	jC-atXLIB327416P4h05b1
Method	BLASTX
NCBI GI	g4371298
BLAST score	545
E value	9.0e-56
Match length	127
% identity	64
NCBI Description	(AC006260) putative RNA-binding protein [Arabidopsis

thaliana]

Seq. No.	123860
Contig ID	12413_3.R1010
5'-most EST	g2748912
Method	BLASTX
NCBI GI	g4371298
BLAST score	509
E value	1.0e-51
Match length	163
% identity	69
NCBI Description	(AC006260) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	123861
Contig ID	12414_1.R1010
5'-most EST	LIB23-015-Q1-E1-H9
Method	BLASTX
NCBI GI	g2829902
BLAST score	718
E value	7.0e-76
Match length	193
% identity	79
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	123862
Contig ID	12415_1.R1010
5'-most EST	jC-atXLIB327430P3g11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123863
Contig ID	12415_2.R1010
5'-most EST	g937440
Method	BLASTN
NCBI GI	g2645198
BLAST score	71
E value	2.0e-31
Match length	287
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123864
Contig ID	12417_1.R1010
5'-most EST	LIB3234-012-P1-K1-G10

Seq. No.	123865
Contig ID	12419_1.R1010
5'-most EST	g2413771

Method	BLASTN
NCBI GI	g2618602
BLAST score	293
E value	1.0e-164
Match length	469
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	123866
Contig ID	12419_2.R1010
5'-most EST	jC-atXLIB327413P1g04b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	171
E value	4.0e-91
Match length	448
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	123867
Contig ID	12419_3.R1010
5'-most EST	LIB3176-093-P1-K1-H2
Method	BLASTN
NCBI GI	g2618602
BLAST score	87
E value	4.0e-41
Match length	352
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	123868
Contig ID	12420_1.R1010
5'-most EST	jC-atXLIB327428P4f02b1
Method	BLASTN
NCBI GI	g3789706
BLAST score	285
E value	1.0e-159
Match length	675
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123869
Contig ID	12422_1.R1010
5'-most EST	LIB23-016-Q1-E1-A6
Method	BLASTX
NCBI GI	g4455319
BLAST score	220
E value	8.0e-18
Match length	115
% identity	6
NCBI Description	(AL035528) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	123870
Contig ID	12423_1.R1010
5'-most EST	jC-atXLIB327428P1f11b2
Method	BLASTX
NCBI GI	g2739355
BLAST score	561
E value	1.0e-57
Match length	166
% identity	67
NCBI Description	(AC003972) pNORF1 [Homo sapiens] >gi_3328175 (AF074016) nonsense-mediated mRNA decay trans-acting factor [Homo sapiens]

Seq. No.	123871
Contig ID	12427_1.R1010
5'-most EST	LIB23-016-Q1-E1-B10
Method	BLASTX
NCBI GI	g4204303
BLAST score	298
E value	6.0e-27
Match length	92
% identity	72
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	123872
Contig ID	12430_1.R1010
5'-most EST	jC-atXLIB327407P4g10b1
Method	BLASTN
NCBI GI	g4581084
BLAST score	295
E value	1.0e-165
Match length	327
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	123873
Contig ID	12430_2.R1010
5'-most EST	jC-atXLIB327407P4g10a1
Method	BLASTN
NCBI GI	g4581084
BLAST score	247
E value	1.0e-136
Match length	283
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	123874
Contig ID	12430_4.R1010
5'-most EST	LIB3175-001-Q1-K1-H5
Method	BLASTN
NCBI GI	g4581084
BLAST score	374
E value	0.0e+00
Match length	657

% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	123875
Contig ID	12431_1.R1010
5'-most EST	jC-atXLIB327428P4f10b2
Method	BLASTN
NCBI GI	g3869069
BLAST score	316
E value	1.0e-177
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	123876
Contig ID	12441_1.R1010
5'-most EST	g2756747
Method	BLASTX
NCBI GI	g2583134
BLAST score	445
E value	6.0e-44
Match length	83
% identity	100
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	123877
Contig ID	12441_2.R1010
5'-most EST	jC-atXLIB327431P1f02a1
Method	BLASTN
NCBI GI	g2583106
BLAST score	94
E value	3.0e-45
Match length	175
% identity	59
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123878
Contig ID	12441_3.R1010
5'-most EST	jC-atX25067Q1E1B06a1
Method	BLASTN
NCBI GI	g1946354
BLAST score	406
E value	0.0e+00
Match length	457
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	123879
Contig ID	12441_4.R1010
5'-most EST	jC-atXP98CH8B4T7b1
Method	BLASTN
NCBI GI	g1946354

BLAST score	255
E value	1.0e-141
Match length	557
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	123880
Contig ID	12441_5.R1010
5'-most EST	jC-atX25060Q1E1B10a1
Method	BLASTN
NCBI GI	g2583106
BLAST score	50
E value	3.0e-19
Match length	294
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123881
Contig ID	12442_1.R1010
5'-most EST	LIB23-016-Q1-E1-C3
Method	BLASTN
NCBI GI	g2696018
BLAST score	559
E value	0.0e+00
Match length	729
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	123882
Contig ID	12443_1.R1010
5'-most EST	jC-atX23016Q1E1C04b1
Method	BLASTX
NCBI GI	g4164473
BLAST score	176
E value	2.0e-12
Match length	104
% identity	43
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	123883
Contig ID	12448_1.R1010
5'-most EST	LIB23-016-Q1-E1-D1

Seq. No.	123884
Contig ID	12450_1.R1010
5'-most EST	jC-atXP41C164H10T7d1
Method	BLASTX
NCBI GI	g1841355
BLAST score	253
E value	2.0e-21
Match length	60
% identity	70
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza

sativa]

Seq. No.	123885
Contig ID	12456_1.R1010
5'-most EST	jC-atXLIB327430P1h05b1

Seq. No.	123886
Contig ID	12457_1.R1010
5'-most EST	jC-atXLIB327405P3c03b1
Method	BLASTN
NCBI GI	g1245938
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	123887
Contig ID	12463_1.R1010
5'-most EST	LIB25-003-Q1-E1-D1
Method	BLASTX
NCBI GI	g4757796
BLAST score	317
E value	5.0e-29
Match length	134
% identity	48
NCBI Description	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1 >gi_1616741 (U60276) hASNA-I [Homo sapiens]

Seq. No.	123888
Contig ID	12464_1.R1010
5'-most EST	LIB24-102-Q1-E1-E11
Method	BLASTX
NCBI GI	g2506276
BLAST score	143
E value	4.0e-86
Match length	193
% identity	91
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	123889
Contig ID	12464_2.R1010
5'-most EST	jC-atXLIB327428P4g11b2
Method	BLASTX
NCBI GI	g2506276
BLAST score	266
E value	4.0e-23
Match length	75
% identity	72
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	123890
Contig ID	12474_1.R1010
5'-most EST	jC-atXLIB327428P4h08b2
Method	BLASTX
NCBI GI	g1707412
BLAST score	828
E value	1.0e-88
Match length	232
% identity	63
NCBI Description	(X95906) Cleavage and Polyadenylation Specifity Factor protein [Bos taurus]

Seq. No.	123891
Contig ID	12475_1.R1010
5'-most EST	LIB23-016-Q1-E1-F12
Method	BLASTX
NCBI GI	g2723393
BLAST score	286
E value	3.0e-25
Match length	196
% identity	36
NCBI Description	(AB009284) EXTR2 [Homo sapiens] >gi_2895062 (AF000416) EXT-like protein 2 [Homo sapiens]

Seq. No.	123892
Contig ID	12481_1.R1010
5'-most EST	LIB23-016-Q1-E1-F7
Method	BLASTN
NCBI GI	g4454022
BLAST score	222
E value	1.0e-121
Match length	513
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	123893
Contig ID	12482_1.R1010
5'-most EST	LIB23-016-Q1-E1-F8

Seq. No.	123894
Contig ID	12483_1.R1010
5'-most EST	jC-atXLIB327430P1h09b1

Seq. No.	123895
Contig ID	12485_1.R1010
5'-most EST	LIB25-092-Q1-E1-F3
Method	BLASTX
NCBI GI	g461899
BLAST score	120

E value	1.0e-05
Match length	192
% identity	62
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	123896
Contig ID	12485_2.R1010
5'-most EST	g2047961
Method	BLASTX
NCBI GI	g849081
BLAST score	94
E value	4.0e-12
Match length	74
% identity	62
NCBI Description	(U17900) cyclophilin B precursor [Orpinomyces sp. PC-2]

Seq. No.	123897
Contig ID	12492_1.R1010
5'-most EST	g2747435
Method	BLASTX
NCBI GI	g1173045
BLAST score	472
E value	4.0e-47
Match length	92
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L37A >gi_421866_pir__S34661 ribosomal protein L37a - turnip >gi_347062 (L21897) ribosomal protein [Brassica rapa] >gi_395077_emb_CAA80864_ (Z24739) ribosomal protein L37a [Brassica rapa]

Seq. No.	123898
Contig ID	12502_1.R1010
5'-most EST	jC-atXLIB327428P4h09b2
Method	BLASTN
NCBI GI	g3176701
BLAST score	227
E value	1.0e-124
Match length	825
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123899
Contig ID	12503_1.R1010
5'-most EST	jC-atXLIB327440P1g09a1
Method	BLASTX
NCBI GI	g485514
BLAST score	403
E value	1.0e-38
Match length	86
% identity	84
NCBI Description	ADR11-2 protein - soybean (fragment)

>gi_296443_emb_CAA49341_ (X69640) auxin down regulated [Glycine max]

Seq. No.	123900
Contig ID	12503_2.R1010
5'-most EST	g930545
Method	BLASTX
NCBI GI	g4662641
BLAST score	213
E value	6.0e-17
Match length	96
% identity	53
NCBI Description	(AC006429) putative auxin down-regulated protein [Arabidopsis thaliana]

Seq. No.	123901
Contig ID	12503_3.R1010
5'-most EST	g4210223
Method	BLASTN
NCBI GI	g4662640
BLAST score	107
E value	6.0e-53
Match length	350
% identity	23
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	123902
Contig ID	12503_4.R1010
5'-most EST	g2597205

Seq. No.	123903
Contig ID	12504_1.R1010
5'-most EST	LIB23-016-Q1-E1-H8
Method	BLASTN
NCBI GI	g2618677
BLAST score	632
E value	0.0e+00
Match length	632
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	123904
Contig ID	12519_1.R1010
5'-most EST	LIB24-118-Q1-E1-G3
Method	BLASTX
NCBI GI	g1707074
BLAST score	165
E value	2.0e-11
Match length	96
% identity	40
NCBI Description	(U80450) M01E11.2 [Caenorhabditis elegans]

Seq. No.	123905
Contig ID	12521_1.R1010
5'-most EST	jC-atXLIB327430P3g12b1

Method	BLASTX
NCBI GI	g4204300
BLAST score	312
E value	8.0e-34
Match length	126
% identity	62
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	123906
Contig ID	12522_1.R1010
5'-most EST	jC-atXLIB327403P3d11b2
Method	BLASTX
NCBI GI	g3242723
BLAST score	475
E value	3.0e-47
Match length	248
% identity	40
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	123907
Contig ID	12525_1.R1010
5'-most EST	LIB23-017-Q1-E1-C10
Method	BLASTN
NCBI GI	g4263774
BLAST score	222
E value	1.0e-121
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123908
Contig ID	12528_1.R1010
5'-most EST	jC-atXLIB327428P1g01b2
Method	BLASTX
NCBI GI	g2213882
BLAST score	738
E value	1.0e-105
Match length	322
% identity	57
NCBI Description	(AF004165) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	123909
Contig ID	12535_1.R1010
5'-most EST	jC-atXLIB327405P3g09b1
Method	BLASTX
NCBI GI	g484656
BLAST score	766
E value	2.0e-81
Match length	183
% identity	78
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	123910
Contig ID	12535_2.R1010
5'-most EST	jC-alXLIB327436P3f03a1
Method	BLASTX
NCBI GI	g4666287
BLAST score	255
E value	8.0e-22
Match length	71
% identity	61
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	123911
Contig ID	12539_1.R1010
5'-most EST	g936834
Method	BLASTX
NCBI GI	g480618
BLAST score	559
E value	3.0e-57
Match length	163
% identity	75
NCBI Description	ATAF1 protein - Arabidopsis thaliana (fragment) >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No.	123912
Contig ID	12540_1.R1010
5'-most EST	LIB23-056-Q1-E1-D7
Method	BLASTX
NCBI GI	g4220462
BLAST score	1019
E value	1.0e-111
Match length	196
% identity	99
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	123913
Contig ID	12541_1.R1010
5'-most EST	LIB23-017-Q1-E1-D9
Method	BLASTX
NCBI GI	g3360289
BLAST score	157
E value	2.0e-10
Match length	43
% identity	63
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	123914
Contig ID	12542_1.R1010
5'-most EST	LIB23-017-Q1-E1-E1
Method	BLASTX
NCBI GI	g1914683
BLAST score	742
E value	1.0e-78

Match length	223
% identity	68
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	123915
Contig ID	12544_1.R1010
5'-most EST	LIB24-018-Q1-E1-F2
Method	BLASTN
NCBI GI	g4519193
BLAST score	464
E value	0.0e+00
Match length	620
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	123916
Contig ID	12548_1.R1010
5'-most EST	g2749443
Method	BLASTN
NCBI GI	g1946354
BLAST score	423
E value	0.0e+00
Match length	456
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	123917
Contig ID	12548_2.R1010
5'-most EST	g498570
Method	BLASTX
NCBI GI	g1946368
BLAST score	449
E value	4.0e-44
Match length	322
% identity	80
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	123918
Contig ID	12549_1.R1010
5'-most EST	LIB23-017-Q1-E1-E9
Method	BLASTX
NCBI GI	g4506221
BLAST score	191
E value	2.0e-14
Match length	103
% identity	36
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No.	123919
Contig ID	12553_1.R1010
5'-most EST	jC-atXLIB327418P4g11b1
Method	BLASTX
NCBI GI	g3204108

BLAST score	745
E value	7.0e-79
Match length	180
% identity	77
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	123920
Contig ID	12554_1.R1010
5'-most EST	jC-atXLIB327428P1h02b2
Method	BLASTX
NCBI GI	g4580399
BLAST score	411
E value	4.0e-40
Match length	77
% identity	100
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123921
Contig ID	12562_1.R1010
5'-most EST	g397301
Method	BLASTN
NCBI GI	g4539331
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	123922
Contig ID	12565_1.R1010
5'-most EST	LIB25-080-Q1-E1-C7
Method	BLASTX
NCBI GI	g3451075
BLAST score	481
E value	3.0e-48
Match length	149
% identity	58
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	123923
Contig ID	12568_1.R1010
5'-most EST	jC-atX23017Q1E1G05b1
Method	BLASTN
NCBI GI	g3046855
BLAST score	254
E value	1.0e-141
Match length	462
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	123924
Contig ID	12570_1.R1010
5'-most EST	LIB3176-073-P1-K1-H2
Method	BLASTX

NCBI GI	g4510363
BLAST score	548
E value	4.0e-56
Match length	112
% identity	90
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123925
Contig ID	12570_2.R1010
5'-most EST	g1158885
Method	BLASTX
NCBI GI	g4510363
BLAST score	504
E value	6.0e-60
Match length	141
% identity	81
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123926
Contig ID	12570_3.R1010
5'-most EST	jC-atXP37C157O10T7d2
Method	BLASTX
NCBI GI	g4510363
BLAST score	489
E value	5.0e-49
Match length	101
% identity	86
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123927
Contig ID	12570_4.R1010
5'-most EST	jC-alX24101Q1E1A01a1
Method	BLASTX
NCBI GI	g4510363
BLAST score	54
E value	6.0e-18
Match length	67
% identity	81
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	123928
Contig ID	12571_1.R1010
5'-most EST	jC-atXP11C97N3T7015d1
Method	BLASTX
NCBI GI	g4455153
BLAST score	492
E value	2.0e-53
Match length	144
% identity	81
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	123929
Contig ID	12571_2.R1010

5'-most EST	jC-atXP13C103P8T7d2
Method	BLASTX
NCBI GI	g4337192
BLAST score	579
E value	1.0e-59
Match length	225
% identity	55
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123930
Contig ID	12571_3.R1010
5'-most EST	jC-atXLIB327419P2h12b2
Method	BLASTN
NCBI GI	g2980757
BLAST score	234
E value	1.0e-129
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	123931
Contig ID	12583_1.R1010
5'-most EST	jC-atXLIB327420P3f09b1
Method	BLASTX
NCBI GI	g133709
BLAST score	97
E value	9.0e-29
Match length	99
% identity	67
NCBI Description	CYANELLE 30S RIBOSOMAL PROTEIN S10 >gi_70927_pir__R3KT10 ribosomal protein S10 - Cyanophora paradoxa cyanelle >gi_11391_emb_CAA36388_ (X52143) ribosomal protein S10 (AA 1-105) [Cyanophora paradoxa] >gi_336632 (M35206) ribosomal protein S10 (rps10; rpsJ) [Cyanophora paradoxa] >gi_1016150 (U30821) ribosomal protein S10 [Cyanophora paradoxa]

Seq. No.	123932
Contig ID	12583_2.R1010
5'-most EST	g1520504
Method	BLASTX
NCBI GI	g1350919
BLAST score	228
E value	2.0e-18
Match length	58
% identity	71
NCBI Description	30S RIBOSOMAL PROTEIN S10 >gi_480901_pir__S37489 ribosomal protein S10 - Spirulina platensis >gi_406274_emb_CAA79773_ (Z21676) ribosomal protein S10 [Spirulina platensis]

Seq. No.	123933
Contig ID	12583_3.R1010
5'-most EST	LIB3175-061-P1-K1-C5

Seq. No.	123934
Contig ID	12586_1.R1010
5'-most EST	g2393589

Method	BLASTX
NCBI GI	g464720
BLAST score	256
E value	7.0e-22
Match length	52
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S28 >gi_409184 (L09755) ribosomal protein S28 [Arabidopsis thaliana]

Seq. No.	123935
Contig ID	12587_2.R1010
5'-most EST	LIB23-018-Q1-E1-A3
Method	BLASTX
NCBI GI	g4263775
BLAST score	507
E value	3.0e-51
Match length	112
% identity	88
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123936
Contig ID	12593_1.R1010
5'-most EST	jC-atXLIB327430P1f09b1
Method	BLASTN
NCBI GI	g2645198
BLAST score	101
E value	5.0e-49
Match length	579
% identity	84
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123937
Contig ID	12600_1.R1010
5'-most EST	jC-atXLIB327433P1b06b1
Method	BLASTX
NCBI GI	g4678226
BLAST score	613
E value	1.0e-63
Match length	139
% identity	90
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	123938
Contig ID	12600_2.R1010
5'-most EST	jC-atXLIB327431P2e04b1
Method	BLASTX
NCBI GI	g4678226
BLAST score	164
E value	4.0e-11
Match length	58
% identity	64
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No. 123939

Contig ID	12600_3.R1010
5'-most EST	jC-atXLIB327433P1b06a1
Method	BLASTX
NCBI GI	g4678226
BLAST score	91
E value	7.0e-10
Match length	51
% identity	63
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	123940
Contig ID	12602_1.R1010
5'-most EST	jC-atXLIB327419P4a09b1
Method	BLASTX
NCBI GI	g133872
BLAST score	1484
E value	1.0e-165
Match length	374
% identity	79
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	123941
Contig ID	12603_1.R1010
5'-most EST	LIB23-018-Q1-E1-B9
Method	BLASTN
NCBI GI	g4454587
BLAST score	136
E value	3.0e-70
Match length	503
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	123942
Contig ID	12614_1.R1010
5'-most EST	jC-atX23018Q1E1D02b1
Method	BLASTX
NCBI GI	g3236261
BLAST score	590
E value	2.0e-64
Match length	146
% identity	90
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	123943
Contig ID	12615_1.R1010
5'-most EST	ARABL1-023-Q1-B1-B4

Seq. No. 123944

Contig ID	12620_1.R1010
5'-most EST	LIB23-018-Q1-E1-E2
Method	BLASTX
NCBI GI	g4508078
BLAST score	496
E value	5.0e-50
Match length	89
% identity	100
NCBI Description	(AC005882) 64134 [Arabidopsis thaliana]

Seq. No.	123945
Contig ID	12633_1.R1010
5'-most EST	jC-atXLIB327418P3b08b1
Method	BLASTN
NCBI GI	g2760167
BLAST score	96
E value	3.0e-46
Match length	180
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	123946
Contig ID	12633_2.R1010
5'-most EST	LIB24-133-Q1-E1-C6
Method	BLASTX
NCBI GI	g4455199
BLAST score	436
E value	2.0e-67
Match length	186
% identity	77
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	123947
Contig ID	12633_3.R1010
5'-most EST	LIB3175-035-P1-K1-E5
Method	BLASTX
NCBI GI	g4455199
BLAST score	367
E value	5.0e-35
Match length	90
% identity	80
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	123948
Contig ID	12638_1.R1010
5'-most EST	g936424
Method	BLASTN
NCBI GI	g3046854
BLAST score	345
E value	0.0e+00
Match length	385
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No. 123949

Contig ID	12645_1.R1010
5'-most EST	jC-atXP1C64E6T7d1
Method	BLASTX
NCBI GI	g4033349
BLAST score	826
E value	9.0e-89
Match length	182
% identity	90
NCBI Description	(AJ223496) phosphoenolpyrovate carboxylase [Brassica juncea]

Seq. No.	123950
Contig ID	12650_1.R1010
5'-most EST	jC-atXLIB327430P4f04b1
Method	BLASTX
NCBI GI	g4585977
BLAST score	488
E value	8.0e-49
Match length	149
% identity	62
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	123951
Contig ID	12650_2.R1010
5'-most EST	g1158959

Seq. No.	123952
Contig ID	12650_4.R1010
5'-most EST	g671785
Method	BLASTX
NCBI GI	g4585977
BLAST score	227
E value	1.0e-18
Match length	66
% identity	65
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	123953
Contig ID	12653_1.R1010
5'-most EST	jC-atXmonuni25Af10b1

Seq. No.	123954
Contig ID	12657_1.R1010
5'-most EST	g958251

Seq. No.	123955
Contig ID	12657_2.R1010
5'-most EST	jC-atXP33C148K2T7d2

Seq. No.	123956
Contig ID	12658_1.R1010
5'-most EST	jC-atX22076Q1E1D03b1
Method	BLASTN
NCBI GI	g3510339
BLAST score	285
E value	1.0e-159
Match length	776

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	123957
Contig ID	12663_1.R1010
5'-most EST	LIB23-019-Q1-E1-B10
Method	BLASTN
NCBI GI	g4558586
BLAST score	390
E value	0.0e+00
Match length	705
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	123958
Contig ID	12663_2.R1010
5'-most EST	jC-atXLIB327429P2a11b1
Method	BLASTN
NCBI GI	g4558586
BLAST score	264
E value	1.0e-146
Match length	589
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	123959
Contig ID	12663_3.R1010
5'-most EST	LIB3177-087-P1-K1-E7
Method	BLASTN
NCBI GI	g4558586
BLAST score	379
E value	0.0e+00
Match length	455
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	123960
Contig ID	12664_1.R1010
5'-most EST	LIB23-019-Q1-E1-B2
Method	BLASTX
NCBI GI	g3176687
BLAST score	841
E value	2.0e-90
Match length	200
% identity	81
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	123961
Contig ID	12674_1.R1010
5'-most EST	LIB24-009-Q1-E1-E6

Seq. No.	123962
Contig ID	12679_1.R1010
5'-most EST	jC-atXP112C129H2T7d2
Method	BLASTN
NCBI GI	g4159707
BLAST score	273
E value	1.0e-152
Match length	526
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	123963
Contig ID	12679_2.R1010
5'-most EST	jC-atXLIB327429P3a06b2
Method	BLASTN
NCBI GI	g4159707
BLAST score	170
E value	2.0e-90
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	123964
Contig ID	12692_1.R1010
5'-most EST	LIB23-019-Q1-E1-D9
Method	BLASTN
NCBI GI	g2264309
BLAST score	505
E value	0.0e+00
Match length	513
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	123965
Contig ID	12699_1.R1010
5'-most EST	jC-atXLIB327430P4h04b1
Method	BLASTN
NCBI GI	g3309276
BLAST score	360
E value	0.0e+00
Match length	634
% identity	56
NCBI Description	Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3 cM, complete sequence

Seq. No.	123966
Contig ID	12701_1.R1010
5'-most EST	jC-atXLIB327429P4b08b2
Method	BLASTX
NCBI GI	g1699024
BLAST score	385
E value	5.0e-37
Match length	122

% identity	61
NCBI Description	(U78866) gene1000 [Arabidopsis thaliana] >gi_1699057 (U78870) unknown [Arabidopsis thaliana]

Seq. No.	123967
Contig ID	12703_1.R1010
5'-most EST	jC-atXP79C230N22T7b1
Method	BLASTX
NCBI GI	g3738320
BLAST score	57
E value	3.0e-69
Match length	165
% identity	81
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	123968
Contig ID	12703_2.R1010
5'-most EST	g2748028
Method	BLASTX
NCBI GI	g3738320
BLAST score	313
E value	2.0e-28
Match length	132
% identity	60
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	123969
Contig ID	12703_3.R1010
5'-most EST	LIB25-010-Q1-E1-H12
Method	BLASTX
NCBI GI	g3738320
BLAST score	1040
E value	1.0e-113
Match length	311
% identity	69
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	123970
Contig ID	12703_5.R1010
5'-most EST	jC-atXLIB327429P4b10b2
Method	BLASTX
NCBI GI	g3738320
BLAST score	218
E value	2.0e-17
Match length	77
% identity	88
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	123971
Contig ID	12706_1.R1010
5'-most EST	LIB3234-092-P1-K1-H9

Seq. No.	123972

Contig ID	12708_1.R1010
5'-most EST	jC-atXLIB327407P2b05b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	8.0e-10
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	123973
Contig ID	12708_3.R1010
5'-most EST	LIB23-019-Q1-E1-F6

Seq. No.	123974
Contig ID	12713_1.R1010
5'-most EST	g2757176
Method	BLASTN
NCBI GI	g4063730
BLAST score	377
E value	0.0e+00
Match length	437
% identity	97
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	123975
Contig ID	12715_1.R1010
5'-most EST	jC-atXP81C240M18T7d1
Method	BLASTN
NCBI GI	g3985958
BLAST score	308
E value	1.0e-173
Match length	510
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	123976
Contig ID	12719_1.R1010
5'-most EST	jC-atXLIB327438P4e04a2
Method	BLASTX
NCBI GI	g3549669
BLAST score	1018
E value	1.0e-111
Match length	198
% identity	100
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	123977
Contig ID	12720_1.R1010
5'-most EST	jC-atXLIB327403P3f10b1
Method	BLASTX
NCBI GI	g544242
BLAST score	501
E value	1.0e-50

Match length	145
% identity	74
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No.	123978
Contig ID	12726_1.R1010
5'-most EST	LIB35-028-Q1-E1-G5
Method	BLASTX
NCBI GI	g3873551
BLAST score	188
E value	6.0e-14
Match length	149
% identity	32
NCBI Description	(AL033534) putative vacuolar protein sorting protein subunit [Schizosaccharomyces pombe]

Seq. No.	123979
Contig ID	12729_1.R1010
5'-most EST	jC-atXLIB327418P3b06b1
Method	BLASTX
NCBI GI	g4469009
BLAST score	641
E value	6.0e-67
Match length	202
% identity	56
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	123980
Contig ID	12732_1.R1010
5'-most EST	g493329
Method	BLASTN
NCBI GI	g4757405
BLAST score	268
E value	1.0e-149
Match length	330
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	123981
Contig ID	12736_1.R1010
5'-most EST	LIB23-020-Q1-E1-A12
Method	BLASTX
NCBI GI	g3153205
BLAST score	262
E value	4.0e-42
Match length	112
% identity	85
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	123982
Contig ID	12748_1.R1010
5'-most EST	LIB3175-029-P1-K1-B4

Method	BLASTN
NCBI GI	g4469002
BLAST score	351
E value	0.0e+00
Match length	413
% identity	54
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	123983
Contig ID	12751_1.R1010
5'-most EST	jC-atXLIB327415P4b02b1
Method	BLASTN
NCBI GI	g2673901
BLAST score	353
E value	0.0e+00
Match length	462
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123984
Contig ID	12751_2.R1010
5'-most EST	LIB23-020-Q1-E1-B7
Method	BLASTN
NCBI GI	g2673901
BLAST score	378
E value	0.0e+00
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123985
Contig ID	12751_3.R1010
5'-most EST	g2757969
Method	BLASTN
NCBI GI	g2673901
BLAST score	293
E value	1.0e-164
Match length	604
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123986
Contig ID	12752_1.R1010
5'-most EST	jC-alXLIB327434P2d03b1
Method	BLASTX
NCBI GI	g3395756
BLAST score	689
E value	2.0e-72
Match length	129
% identity	100
NCBI Description	(U76297) plantacyanin [Arabidopsis thaliana] >gi_3461812 (AC004138) putative basic blue protein [Arabidopsis thaliana]

Seq. No.	123987
Contig ID	12755_1.R1010
5'-most EST	jC-atXLIB327429P3a07b2
Method	BLASTN
NCBI GI	g2980787
BLAST score	273
E value	1.0e-152
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	123988
Contig ID	12762_1.R1010
5'-most EST	LIB25-097-Q1-E1-A11
Method	BLASTX
NCBI GI	g3779021
BLAST score	1045
E value	1.0e-114
Match length	203
% identity	100
NCBI Description	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	123989
Contig ID	12766_1.R1010
5'-most EST	LIB23-020-Q1-E1-D10
Method	BLASTN
NCBI GI	g2924734
BLAST score	370
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	123990
Contig ID	12770_1.R1010
5'-most EST	LIB35-043-Q1-E1-F10

Seq. No.	123991
Contig ID	12771_1.R1010
5'-most EST	LIB24-035-Q1-E1-G1
Method	BLASTX
NCBI GI	g4454043
BLAST score	543
E value	2.0e-55
Match length	135
% identity	80
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	123992
Contig ID	12772_1.R1010
5'-most EST	jC-atXLIB327419P2a11b2
Method	BLASTX
NCBI GI	g1086757

BLAST score	446
E value	7.0e-44
Match length	199
% identity	47
NCBI Description	(U41037) coded for by C. elegans cDNA yk41a1.3; coded for by C. elegans cDNA yk128e3.3; coded for by C. elegans cDNA yk37c8.3; coded for by C. elegans cDNA CEESB01F; coded for by C. elegans cDNA CEESG45F; coded for by C. elegans cDNA CEESG45

Seq. No.	123993
Contig ID	12772_2.R1010
5'-most EST	jC-atX23020Q1E1D05b1
Method	BLASTX
NCBI GI	g465602
BLAST score	323
E value	2.0e-35
Match length	151
% identity	52
NCBI Description	HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490 (AE000306) orf, hypothetical protein [Escherichia coli] >gi_744200_prf__2014253BL yeiN gene [Escherichia coli]

Seq. No.	123994
Contig ID	12773_1.R1010
5'-most EST	jC-alXLIB327434P3c02b1
Method	BLASTX
NCBI GI	g1518540
BLAST score	151
E value	1.0e-42
Match length	103
% identity	88
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	123995
Contig ID	12776_1.R1010
5'-most EST	jC-atXLIB327437P4d11a2
Method	BLASTX
NCBI GI	g2500426
BLAST score	301
E value	8.0e-27
Match length	124
% identity	52
NCBI Description	30S RIBOSOMAL PROTEIN S9 >gi_1652399_dbj_BAA17321_ (D90905) 30S ribosomal protein S9 [Synechocystis sp.]

Seq. No.	123996
Contig ID	12797_1.R1010
5'-most EST	LIB35-048-Q1-E1-C9
Method	BLASTN
NCBI GI	g4510338
BLAST score	765
E value	0.0e+00
Match length	800
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No.	123997
Contig ID	12798_1.R1010
5'-most EST	LIB23-020-Q1-E1-F9

Seq. No.	123998
Contig ID	12804_1.R1010
5'-most EST	jC-atXLIB327429P1c05b2
Method	BLASTN
NCBI GI	g3985958
BLAST score	198
E value	1.0e-107
Match length	679
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	123999
Contig ID	12805_1.R1010
5'-most EST	jC-atXLIB327421P1d09b1
Method	BLASTX
NCBI GI	g4584346
BLAST score	699
E value	1.0e-73
Match length	173
% identity	84
NCBI Description	(AC007127) unknown protein [Arabidopsis thaliana]

Seq. No.	124000
Contig ID	12807_1.R1010
5'-most EST	g2048821
Method	BLASTX
NCBI GI	g4678328
BLAST score	444
E value	7.0e-44
Match length	98
% identity	91
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	124001
Contig ID	12807_2.R1010
5'-most EST	jC-atX25007Q1E1A12b1
Method	BLASTX
NCBI GI	g4678328
BLAST score	1940
E value	0.0e+00
Match length	473
% identity	98
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	124002
Contig ID	12808_1.R1010
5'-most EST	g3868973
Method	BLASTX

NCBI GI	g3913425
BLAST score	416
E value	8.0e-41
Match length	105
% identity	77
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	124003
Contig ID	12809_1.R1010
5'-most EST	jC-atXLIB327417P2b03b1
Method	BLASTN
NCBI GI	g2618600
BLAST score	219
E value	1.0e-119
Match length	522
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	124004
Contig ID	12822_1.R1010
5'-most EST	jC-atXLIB327429P2a01b1
Method	BLASTX
NCBI GI	g3142289
BLAST score	1265
E value	1.0e-140
Match length	276
% identity	89
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	124005
Contig ID	12825_1.R1010
5'-most EST	jC-atXLIB327409P3d09b1
Method	BLASTX
NCBI GI	g3687243
BLAST score	260
E value	2.0e-22
Match length	63
% identity	81
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	124006
Contig ID	12825_2.R1010
5'-most EST	jC-atXLIB327427P2d01b1
Method	BLASTX
NCBI GI	g2443755
BLAST score	641
E value	8.0e-67
Match length	160
% identity	76
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No. 124007

Contig ID	12825_3.R1010
5'-most EST	g3450152
Method	BLASTN
NCBI GI	g3985958
BLAST score	318
E value	1.0e-179
Match length	370
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	124008
Contig ID	12826_1.R1010
5'-most EST	LIB23-035-Q1-E112-G4

Seq. No.	124009
Contig ID	12829_1.R1010
5'-most EST	jC-atXLIB327420P3b11b1
Method	BLASTN
NCBI GI	g4510360
BLAST score	33
E value	1.0e-08
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	124010
Contig ID	12833_1.R1010
5'-most EST	LIB3176-039-P1-K1-B3
Method	BLASTX
NCBI GI	g4567319
BLAST score	700
E value	3.0e-74
Match length	129
% identity	98
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]

Seq. No.	124011
Contig ID	12838_1.R1010
5'-most EST	jC-atXLIB327431P4h02a1
Method	BLASTX
NCBI GI	g1749546
BLAST score	260
E value	3.0e-22
Match length	136
% identity	47
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	124012
Contig ID	12845_1.R1010
5'-most EST	LIB3176-021-P1-K1-D3
Method	BLASTX
NCBI GI	g4539408

BLAST score	392
E value	6.0e-38
Match length	133
% identity	65
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	124013
Contig ID	12850_1.R1010
5'-most EST	g398297
Method	BLASTN
NCBI GI	g3510331
BLAST score	750
E value	0.0e+00
Match length	761
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K13P22, complete sequence [Arabidopsis thaliana]

Seq. No.	124014
Contig ID	12855_1.R1010
5'-most EST	LIB23-021-Q2-E1-E3
Method	BLASTN
NCBI GI	g2880038
BLAST score	207
E value	1.0e-112
Match length	464
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124015
Contig ID	12858_1.R1010
5'-most EST	jC-atXLIB327429P1b10b1
Method	BLASTN
NCBI GI	g2335089
BLAST score	125
E value	1.0e-63
Match length	313
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124016
Contig ID	12863_1.R1010
5'-most EST	jC-atXP32C144M9T7d2
Method	BLASTN
NCBI GI	g4539309
BLAST score	213
E value	1.0e-116
Match length	406
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	124017
Contig ID	12863_2.R1010
5'-most EST	g3449720

Method	BLASTN
NCBI GI	g4539309
BLAST score	408
E value	0.0e+00
Match length	483
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	124018
Contig ID	12865_1.R1010
5'-most EST	LIB23-021-Q2-E1-F3
Method	BLASTN
NCBI GI	g2323343
BLAST score	87
E value	6.0e-41
Match length	144
% identity	89
NCBI Description	Arabidopsis thaliana alpha-glucosidase 1 (Aglu1) gene, complete cds

Seq. No.	124019
Contig ID	12866_1.R1010
5'-most EST	LIB23-021-Q2-E1-F4
Method	BLASTX
NCBI GI	g4191777
BLAST score	867
E value	2.0e-93
Match length	167
% identity	99
NCBI Description	(AC005917) putative casein kinase I [Arabidopsis thaliana]

Seq. No.	124020
Contig ID	12874_1.R1010
5'-most EST	jC-atX23020Q1E1F10b1
Method	BLASTN
NCBI GI	g4757401
BLAST score	241
E value	1.0e-133
Match length	387
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	124021
Contig ID	12877_1.R1010
5'-most EST	g1053596

Seq. No.	124022
Contig ID	12882_1.R1010
5'-most EST	LIB3176-073-P1-K1-F10
Method	BLASTX
NCBI GI	g2708532
BLAST score	848
E value	5.0e-91
Match length	258
% identity	38

NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]
Seq. No.	124023
Contig ID	12888_1.R1010
5'-most EST	LIB23-022-Q2-E1-A11
Method	BLASTX
NCBI GI	g4589123
BLAST score	774
E value	1.0e-82
Match length	151
% identity	100
NCBI Description	(AF126374) At14a protein [Arabidopsis thaliana]
Seq. No.	124024
Contig ID	12889_1.R1010
5'-most EST	LIB24-045-Q1-E1-F10
Method	BLASTN
NCBI GI	g4589427
BLAST score	224
E value	1.0e-123
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence
Seq. No.	124025
Contig ID	12890_1.R1010
5'-most EST	jC-atXLIB327429P1a03b2
Method	BLASTX
NCBI GI	g4586054
BLAST score	402
E value	9.0e-39
Match length	156
% identity	51
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.	124026
Contig ID	12892_1.R1010
5'-most EST	jC-atXLIB327408P3b12b1
Seq. No.	124027
Contig ID	12897_1.R1010
5'-most EST	LIB3176-036-P1-K1-D9
Method	BLASTX
NCBI GI	g3608135
BLAST score	334
E value	3.0e-31
Match length	89
% identity	69
NCBI Description	(AC005314) putative DNA binding factor [Arabidopsis thaliana]
Seq. No.	124028
Contig ID	12901_1.R1010
5'-most EST	jC-atXLIB327419P3e08b2
Method	BLASTN
NCBI GI	g4335744

BLAST score	73
E value	2.0e-32
Match length	243
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124029
Contig ID	12901_2.R1010
5'-most EST	jC-atXLIB327421P2e11b1
Method	BLASTN
NCBI GI	g4335744
BLAST score	73
E value	1.0e-32
Match length	197
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124030
Contig ID	12901_4.R1010
5'-most EST	LIB35-026-Q1-E1-F9
Method	BLASTX
NCBI GI	g4335755
BLAST score	199
E value	2.0e-15
Match length	99
% identity	57
NCBI Description	(AC006284) putative hydroxyproline-rich glycoprotein [Arabidopsis thaliana]

Seq. No.	124031
Contig ID	12906_1.R1010
5'-most EST	jC-atXP100C251L9T7b1
Method	BLASTN
NCBI GI	g3063690
BLAST score	99
E value	5.0e-48
Match length	406
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	124032
Contig ID	12906_2.R1010
5'-most EST	LIB23-056-Q1-E1-D5
Method	BLASTN
NCBI GI	g3063690
BLAST score	69
E value	3.0e-30
Match length	269
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	124033
Contig ID	12910_1.R1010

5'-most EST	jC-atXLIB327430P2h11b1
Method	BLASTX
NCBI GI	g3319354
BLAST score	810
E value	1.0e-86
Match length	211
% identity	81
NCBI Description	(AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No.	124034
Contig ID	12911_1.R1010
5'-most EST	jC-atXLIB327429P3a04a2
Method	BLASTX
NCBI GI	g3283996
BLAST score	485
E value	1.0e-48
Match length	123
% identity	76
NCBI Description	(AF072908) calcium-dependent protein kinase [Nicotiana tabacum]

Seq. No.	124035
Contig ID	12911_2.R1010
5'-most EST	LIB23-042-Q1-E1-F3
Method	BLASTX
NCBI GI	g2501766
BLAST score	993
E value	1.0e-108
Match length	246
% identity	63
NCBI Description	(U69174) calmodulin-like domain protein kinase isoenzyme gamma [Glycine max]

Seq. No.	124036
Contig ID	12917_1.R1010
5'-most EST	LIB23-022-Q2-E1-C9
Method	BLASTN
NCBI GI	g2252848
BLAST score	177
E value	7.0e-95
Match length	400
% identity	87
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	124037
Contig ID	12923_1.R1010
5'-most EST	LIB3175-061-P1-K1-E1
Method	BLASTX
NCBI GI	g3297813
BLAST score	401
E value	5.0e-39
Match length	80
% identity	99
NCBI Description	(AL031032) hypothetical protein [Arabidopsis thaliana]

Seq. No. 124038

Contig ID 12924_1.R1010
5'-most EST jC-atXLIB327429P1b03b2
Method BLASTN
NCBI GI g4220643
BLAST score 401
E value 0.0e+00
Match length 575
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 124039
Contig ID 12927_1.R1010
5'-most EST LIB35-030-Q1-E1-F5

Seq. No. 124040
Contig ID 12929_1.R1010
5'-most EST ARABLI-14-Q1-B1-D3

Seq. No. 124041
Contig ID 12934_1.R1010
5'-most EST LIB25-099-Q1-E1-G12
Method BLASTN
NCBI GI g2760169
BLAST score 338
E value 0.0e+00
Match length 383
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No. 124042
Contig ID 12935_1.R1010
5'-most EST LIB23-022-Q2-E1-E5
Method BLASTN
NCBI GI g3985931
BLAST score 386
E value 0.0e+00
Match length 398
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No. 124043
Contig ID 12936_1.R1010
5'-most EST jC-atXLIB327429P1b09b1
Method BLASTN
NCBI GI g3449312
BLAST score 467
E value 0.0e+00
Match length 608
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No. 124044
Contig ID 12940_1.R1010

5'-most EST	LIB23-022-Q2-E1-F1
Method	BLASTN
NCBI GI	g4406752
BLAST score	196
E value	1.0e-106
Match length	409
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124045
Contig ID	12942_1.R1010
5'-most EST	LIB23-063-Q1-E1-B1
Method	BLASTN
NCBI GI	g2264312
BLAST score	42
E value	6.0e-14
Match length	206
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	124046
Contig ID	12948_1.R1010
5'-most EST	LIB3175-040-P1-K1-H10
Method	BLASTN
NCBI GI	g4468103
BLAST score	181
E value	4.0e-97
Match length	359
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	124047
Contig ID	12951_1.R1010
5'-most EST	jC-atXLIB327417P2g05b1
Method	BLASTN
NCBI GI	g4309683
BLAST score	119
E value	7.0e-60
Match length	235
% identity	79
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124048
Contig ID	12951_2.R1010
5'-most EST	jC-alXLIB327435P2b02a1
Method	BLASTX
NCBI GI	g4337175
BLAST score	725
E value	1.0e-76
Match length	177
% identity	84
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,

gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	124049
Contig ID	12951_3.R1010
5'-most EST	jC-atXP25C125F6T7030a1
Method	BLASTN
NCBI GI	g4309683
BLAST score	451
E value	0.0e+00
Match length	459
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124050
Contig ID	12951_4.R1010
5'-most EST	g1517233
Method	BLASTN
NCBI GI	g4309683
BLAST score	446
E value	0.0e+00
Match length	519
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124051
Contig ID	12951_6.R1010
5'-most EST	jC-atX25100Q1E1G09b1
Method	BLASTN
NCBI GI	g4309683
BLAST score	123
E value	1.0e-62
Match length	178
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124052
Contig ID	12952_1.R1010
5'-most EST	LIB23-022-Q2-E1-G1
Method	BLASTN
NCBI GI	g4580744
BLAST score	183
E value	1.0e-98
Match length	326
% identity	99
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	124053
Contig ID	12974_1.R1010
5'-most EST	jC-atXLIB327422P2c05b2
Method	BLASTX
NCBI GI	g4539333
BLAST score	489

E value 2.0e-53
Match length 137
% identity 83
NCBI Description (AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No. 124054
Contig ID 12978_1.R1010
5'-most EST jC-atXLIB327429P3c09b2

Seq. No. 124055
Contig ID 12979_1.R1010
5'-most EST jC-atXLIB327429P4c10b2
Method BLASTN
NCBI GI g3293582
BLAST score 38
E value 2.0e-11
Match length 46
% identity 96
NCBI Description Arabidopsis thaliana BAC T15F16

Seq. No. 124056
Contig ID 12982_1.R1010
5'-most EST g2749038
Method BLASTX
NCBI GI g4455220
BLAST score 587
E value 7.0e-61
Match length 134
% identity 87
NCBI Description (AL035440) putative aconitase [Arabidopsis thaliana]

Seq. No. 124057
Contig ID 12984_1.R1010
5'-most EST jC-atXP112C128G24T7d2
Method BLASTX
NCBI GI g4457221
BLAST score 288
E value 2.0e-25
Match length 104
% identity 56
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No. 124058
Contig ID 12984_2.R1010
5'-most EST jC-atXP36C155C22T7d1
Method BLASTX
NCBI GI g4457221
BLAST score 195
E value 1.0e-14
Match length 62
% identity 61
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No. 124059

Contig ID	12984_4.R1010
5'-most EST	LIB3176-118-P2-K1-F4
Seq. No.	124060
Contig ID	12986_1.R1010
5'-most EST	jC-atXLIB327404P2d12b1
Method	BLASTN
NCBI GI	g4469002
BLAST score	407
E value	0.0e+00
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)
Seq. No.	124061
Contig ID	12987_1.R1010
5'-most EST	jC-atXP52C181K4T7d2
Method	BLASTX
NCBI GI	g3047090
BLAST score	800
E value	1.0e-85
Match length	150
% identity	99
NCBI Description	(AF058826) T26D22.18 gene product [Arabidopsis thaliana]
Seq. No.	124062
Contig ID	12987_2.R1010
5'-most EST	LIB3176-110-P1-K1-A3
Method	BLASTN
NCBI GI	g4589442
BLAST score	99
E value	1.0e-48
Match length	209
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP2, complete sequence
Seq. No.	124063
Contig ID	12989_1.R1010
5'-most EST	jC-atXLIB327431P2c02a1
Method	BLASTX
NCBI GI	g2464901
BLAST score	329
E value	2.0e-30
Match length	138
% identity	50
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	124064
Contig ID	12992_1.R1010
5'-most EST	jC-atXLIB327430P4h12b1
Method	BLASTX
NCBI GI	g2244902
BLAST score	752
E value	5.0e-80
Match length	148

% identity	99
NCBI Description	(Z97339) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	124065
Contig ID	12994_1.R1010
5'-most EST	jC-atXLIB327423P1d08b1
Method	BLASTX
NCBI GI	g462679
BLAST score	193
E value	4.0e-14
Match length	162
% identity	30
NCBI Description	MYOSIN IB HEAVY CHAIN >gi_102252_pir__A33284 myosin heavy chain IB - slime mold (Dictyostelium discoideum) >gi_167839 (M26037) myosin I heavy chain [Dictyostelium discoideum]

Seq. No.	124066
Contig ID	12994_2.R1010
5'-most EST	jC-atX23023Q1E1B09b1
Method	BLASTN
NCBI GI	g3128135
BLAST score	296
E value	1.0e-166
Match length	383
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	124067
Contig ID	12996_1.R1010
5'-most EST	jC-atXLIB327404P1f11b1
Method	BLASTX
NCBI GI	g3355311
BLAST score	526
E value	2.0e-53
Match length	116
% identity	88
NCBI Description	(AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No.	124068
Contig ID	13001_1.R1010
5'-most EST	jC-atXLIB327431P1a02b1
Method	BLASTX
NCBI GI	g3183454
BLAST score	333
E value	6.0e-31
Match length	133
% identity	48
NCBI Description	HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No.	124069
Contig ID	13006_1.R1010
5'-most EST	jC-atX24082Q1E1H03b1

Method	BLASTX
NCBI GI	g730463
BLAST score	322
E value	2.0e-29
Match length	105
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	124070
Contig ID	13006_2.R1010
5'-most EST	jC-atXLIB327427P1a05a2
Method	BLASTX
NCBI GI	g730463
BLAST score	272
E value	8.0e-24
Match length	100
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	124071
Contig ID	13007_1.R1010
5'-most EST	LIB25-098-Q1-E1-B1
Method	BLASTX
NCBI GI	g4455237
BLAST score	590
E value	4.0e-61
Match length	135
% identity	84
NCBI Description	(AL035523) ubiquitin activating enzyme-like protein [Arabidopsis thaliana]

Seq. No.	124072
Contig ID	13009_1.R1010
5'-most EST	jC-atXLIB327429P3d08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	5.0e-20
Match length	64
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124073
Contig ID	13014_1.R1010
5'-most EST	LIB23-023-Q1-E1-D7
Method	BLASTX

NCBI GI	g1679733
BLAST score	930
E value	1.0e-100
Match length	308
% identity	59
NCBI Description	(U77041) polygalacturonase-inhibiting protein [Malus domestica]

Seq. No.	124074
Contig ID	13016_1.R1010
5'-most EST	LIB23-023-Q1-E1-D9
Method	BLASTN
NCBI GI	g3046854
BLAST score	282
E value	1.0e-157
Match length	354
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	124075
Contig ID	13021_1.R1010
5'-most EST	jC-alX25045Q1E1B04b1
Method	BLASTX
NCBI GI	g4056488
BLAST score	487
E value	9.0e-49
Match length	186
% identity	55
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	124076
Contig ID	13023_1.R1010
5'-most EST	LIB23-023-Q1-E1-E4

Seq. No.	124077
Contig ID	13026_1.R1010
5'-most EST	jC-atX23023Q1E1E07b1
Method	BLASTX
NCBI GI	g4678322
BLAST score	404
E value	2.0e-39
Match length	146
% identity	58
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	124078
Contig ID	13033_1.R1010
5'-most EST	jC-atXLIB327429P3e10b2
Method	BLASTX
NCBI GI	g3122254
BLAST score	539
E value	6.0e-55
Match length	140
% identity	73
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) >gi_2642164 (AC003000) hypothetical protein [Arabidopsis

thaliana]

Seq. No.	124079
Contig ID	13033_2.R1010
5'-most EST	jC-atXLIB327404P1f11a1
Method	BLASTX
NCBI GI	g3122254
BLAST score	131
E value	1.0e-09
Match length	66
% identity	59
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) >gi_2642164 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124080
Contig ID	13034_1.R1010
5'-most EST	jC-atXLIB327414P1b12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	9.0e-09
Match length	40
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	124081
Contig ID	13036_1.R1010
5'-most EST	LIB23-023-Q1-E1-F7
Method	BLASTX
NCBI GI	g3386607
BLAST score	570
E value	1.0e-58
Match length	196
% identity	63
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124082
Contig ID	13040_1.R1010
5'-most EST	LIB3234-037-P1-K1-A9

Seq. No.	124083
Contig ID	13044_1.R1010
5'-most EST	jC-atXP68C214G4T7d1
Method	BLASTX
NCBI GI	g3236246
BLAST score	782
E value	1.0e-83
Match length	139
% identity	100
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	124084
Contig ID	13044_2.R1010
5'-most EST	g438324
Method	BLASTX
NCBI GI	g3236246

BLAST score	547
E value	2.0e-58
Match length	122
% identity	98
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	124085
Contig ID	13051_1.R1010
5'-most EST	LIB3168-025-P1-K1-C11
Method	BLASTN
NCBI GI	g4589409
BLAST score	173
E value	2.0e-92
Match length	505
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	124086
Contig ID	13052_1.R1010
5'-most EST	LIB23-023-Q1-E1-H2

Seq. No.	124087
Contig ID	13053_1.R1010
5'-most EST	LIB23-023-Q1-E1-H3
Method	BLASTN
NCBI GI	g2262155
BLAST score	470
E value	0.0e+00
Match length	470
% identity	100
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	124088
Contig ID	13056_1.R1010
5'-most EST	jC-atXLIB327431P2a11b1
Method	BLASTX
NCBI GI	g1532169
BLAST score	624
E value	7.0e-65
Match length	227
% identity	57
NCBI Description	(U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

Seq. No.	124089
Contig ID	13061_1.R1010
5'-most EST	jC-atXLIB327429P4d09b2
Method	BLASTN
NCBI GI	g3269280
BLAST score	489
E value	0.0e+00
Match length	489
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22

(ESSAII project)

Seq. No.	124090
Contig ID	13063_1.R1010
5'-most EST	jC-atXLIB327430P4e07b1
Method	BLASTN
NCBI GI	g4468103
BLAST score	338
E value	0.0e+00
Match length	928
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	124091
Contig ID	13070_1.R1010
5'-most EST	LIB24-072-Q1-E1-C10
Method	BLASTX
NCBI GI	g4467123
BLAST score	313
E value	8.0e-29
Match length	56
% identity	100
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124092
Contig ID	13075_1.R1010
5'-most EST	g936990
Method	BLASTN
NCBI GI	g4589446
BLAST score	166
E value	3.0e-88
Match length	470
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	124093
Contig ID	13077_1.R1010
5'-most EST	jC-atXLIB327431P1a09b1

Seq. No.	124094
Contig ID	13078_1.R1010
5'-most EST	LIB3234-080-P1-K1-A4

Seq. No.	124095
Contig ID	13081_1.R1010
5'-most EST	LIB25-083-Q1-E1-B10
Method	BLASTX
NCBI GI	g3150415
BLAST score	459
E value	1.0e-45
Match length	89
% identity	35
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	124096
Contig ID	13084_1.R1010
5'-most EST	jC-atXLIB327429P3f10b2
Method	BLASTX
NCBI GI	g1495366
BLAST score	356
E value	2.0e-33
Match length	192
% identity	35
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	124097
Contig ID	13089_1.R1010
5'-most EST	jC-atXLIB327407P1h05b2
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	3.0e-19
Match length	58
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	124098
Contig ID	13092_1.R1010
5'-most EST	jC-atXLIB327408P2g07b1
Method	BLASTX
NCBI GI	g1321731
BLAST score	185
E value	2.0e-13
Match length	151
% identity	38
NCBI Description	(Z72439) major allergen Cor a 1 [Corylus avellana]

Seq. No.	124099
Contig ID	13093_1.R1010
5'-most EST	jC-atXLIB327430P4h09b1
Method	BLASTN
NCBI GI	g3608126
BLAST score	499
E value	0.0e+00
Match length	503
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124100
Contig ID	13098_1.R1010
5'-most EST	jC-atXLIB327429P4c11b2
Method	BLASTN
NCBI GI	g4733953
BLAST score	456
E value	0.0e+00
Match length	468
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	124101
Contig ID	13100_1.R1010
5'-most EST	jC-atXLIB327429P4c12b2
Method	BLASTX
NCBI GI	g2289006
BLAST score	583
E value	2.0e-60
Match length	129
% identity	88
NCBI Description	(AC002335) glutathione perosidase isolog [Arabidopsis thaliana]

Seq. No.	124102
Contig ID	13106_1.R1010
5'-most EST	jC-atXLIB327420P3h02b1
Method	BLASTX
NCBI GI	g401621
BLAST score	262
E value	2.0e-22
Match length	184
% identity	38
NCBI Description	HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION >gi_290561 (L10328) o188 [Escherichia coli] >gi_1790149 (AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No.	124103
Contig ID	13109_1.R1010
5'-most EST	jC-atXP62C203A2T7d2
Method	BLASTX
NCBI GI	g2832629
BLAST score	390
E value	2.0e-37
Match length	254
% identity	36
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	124104
Contig ID	13110_1.R1010
5'-most EST	LIB23-025-Q1-E1-C1
Method	BLASTN
NCBI GI	g3928074
BLAST score	222
E value	1.0e-121
Match length	479
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124105
Contig ID	13112_1.R1010
5'-most EST	jC-atXLIB327431P2a01b1

Seq. No.	124106
Contig ID	13114_1.R1010
5'-most EST	jC-atXLIB327429P1d08b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	1.0e-20
Match length	65
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124107
Contig ID	13121_1.R1010
5'-most EST	jC-atXP73C223H5T7b1
Method	BLASTX
NCBI GI	g1854386
BLAST score	931
E value	1.0e-100
Match length	252
% identity	68
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	124108
Contig ID	13121_2.R1010
5'-most EST	LIB3176-037-P1-K1-H1
Method	BLASTX
NCBI GI	g1854386
BLAST score	570
E value	1.0e-58
Match length	184
% identity	59
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	124109
Contig ID	13127_1.R1010
5'-most EST	g502322
Method	BLASTX
NCBI GI	g3702323
BLAST score	955
E value	1.0e-104
Match length	191
% identity	96
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	124110
Contig ID	13132_1.R1010
5'-most EST	jC-atXLIB327431P2d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 124111

Contig ID	13132_4.R1010
5'-most EST	jC-atXLIB327427P2a05b1

Seq. No.	124112
Contig ID	13132_6.R1010
5'-most EST	jC-atX25108Q1E1C05a1
Method	BLASTN
NCBI GI	g4580745
BLAST score	340
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	124113
Contig ID	13132_7.R1010
5'-most EST	jC-atX23019Q1E1F06a1
Method	BLASTN
NCBI GI	g4580745
BLAST score	235
E value	1.0e-129
Match length	251
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	124114
Contig ID	13132_9.R1010
5'-most EST	jC-atXLIB327417P3e12a1
Method	BLASTN
NCBI GI	g4580745
BLAST score	232
E value	1.0e-128
Match length	264
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	124115
Contig ID	13132_11.R1010
5'-most EST	jC-atXLIB327431P2b05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	74
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	124116
Contig ID	13134_1.R1010
5'-most EST	jC-atXLIB327431P1a08b1
Method	BLASTX
NCBI GI	g2244850
BLAST score	722
E value	2.0e-76

Match length	146
% identity	99
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124117
Contig ID	13134_2.R1010
5'-most EST	LIB3175-006-P1-K1-E5
Method	BLASTN
NCBI GI	g2244829
BLAST score	132
E value	5.0e-68
Match length	306
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	124118
Contig ID	13136_1.R1010
5'-most EST	LIB23-025-Q1-E1-E2
Method	BLASTN
NCBI GI	g2656026
BLAST score	263
E value	1.0e-145
Match length	1039
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	124119
Contig ID	13139_1.R1010
5'-most EST	LIB23-025-Q1-E1-E6
Method	BLASTN
NCBI GI	g3367567
BLAST score	45
E value	5.0e-16
Match length	168
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	124120
Contig ID	13143_1.R1010
5'-most EST	LIB35-021-Q1-E1-G1
Method	BLASTX
NCBI GI	g1769970
BLAST score	541
E value	4.0e-55
Match length	166
% identity	66
NCBI Description	(Y10155) myrosinase-associated protein [Brassica napus]

Seq. No.	124121
Contig ID	13145_1.R1010
5'-most EST	jC-atXLIB327421P1e10b1
Method	BLASTX
NCBI GI	g1523796
BLAST score	340

E value	1.0e-31
Match length	107
% identity	62
NCBI Description	(X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	124122
Contig ID	13146_1.R1010
5'-most EST	jC-atXLIB327431P2a08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	67
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124123
Contig ID	13148_1.R1010
5'-most EST	jC-alXLIB327434P3c04b1
Method	BLASTX
NCBI GI	g3212871
BLAST score	569
E value	1.0e-58
Match length	147
% identity	80
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	124124
Contig ID	13156_1.R1010
5'-most EST	jC-atXLIB327429P3e03b2
Method	BLASTN
NCBI GI	g4220645
BLAST score	376
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	124125
Contig ID	13159_1.R1010
5'-most EST	LIB25-027-Q1-E1-D6
Method	BLASTX
NCBI GI	g2347187
BLAST score	357
E value	6.0e-34
Match length	73
% identity	99
NCBI Description	(AC002338) putative malonyl-CoA:Acyl carrier protein transacylase, 3' partial [Arabidopsis thaliana]

Seq. No.	124126
Contig ID	13162_1.R1010
5'-most EST	LIB23-025-Q1-E1-G7
Method	BLASTX

NCBI GI	g2829902
BLAST score	568
E value	2.0e-65
Match length	182
% identity	77
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	124127
Contig ID	13167_1.R1010
5'-most EST	LIB3175-003-P1-K1-A10
Method	BLASTX
NCBI GI	g3193298
BLAST score	170
E value	2.0e-11
Match length	134
% identity	29
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	124128
Contig ID	13168_1.R1010
5'-most EST	jC-atXLIB327431P3a11b1

Seq. No.	124129
Contig ID	13168_2.R1010
5'-most EST	jC-atXLIB327423P2c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	7.0e-09
Match length	41
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124130
Contig ID	13178_1.R1010
5'-most EST	jC-atXLIB327428P1e06b2
Method	BLASTX
NCBI GI	g4753655
BLAST score	427
E value	5.0e-42
Match length	123
% identity	64
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No.	124131
Contig ID	13178_2.R1010
5'-most EST	LIB23-026-Q1-E1-A3
Method	BLASTX
NCBI GI	g4753655
BLAST score	292
E value	3.0e-26
Match length	71
% identity	75
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis

thaliana]

Seq. No.	124132
Contig ID	13182_1.R1010
5'-most EST	jC-atXLIB327429P1f04b1
Method	BLASTX
NCBI GI	g4580389
BLAST score	921
E value	1.0e-99
Match length	217
% identity	81
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	124133
Contig ID	13184_1.R1010
5'-most EST	LIB3176-019-P1-K1-H12
Method	BLASTX
NCBI GI	g4490757
BLAST score	1159
E value	1.0e-127
Match length	242
% identity	93
NCBI Description	(AL035708) homeodomain-like protein [Arabidopsis thaliana]

Seq. No.	124134
Contig ID	13187_1.R1010
5'-most EST	LIB23-026-Q1-E1-B2
Method	BLASTN
NCBI GI	g3641835
BLAST score	215
E value	1.0e-117
Match length	611
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	124135
Contig ID	13194_1.R1010
5'-most EST	jC-atXP11C98A20T7038d1
Method	BLASTX
NCBI GI	g4544399
BLAST score	1062
E value	1.0e-116
Match length	273
% identity	71
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	124136
Contig ID	13194_2.R1010
5'-most EST	LIB24-106-Q1-E1-E11
Method	BLASTX
NCBI GI	g4544399
BLAST score	1053
E value	1.0e-115
Match length	343
% identity	57

NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	124137
Contig ID	13194_4.R1010
5'-most EST	g2062894

Seq. No.	124138
Contig ID	13207_1.R1010
5'-most EST	jC-atXLIB327431P2a04b1
Method	BLASTN
NCBI GI	g2832689
BLAST score	184
E value	7.0e-99
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	124139
Contig ID	13209_1.R1010
5'-most EST	jC-atX35015Q1E1B09b1
Method	BLASTX
NCBI GI	g4249391
BLAST score	694
E value	2.0e-73
Match length	145
% identity	87
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	124140
Contig ID	13212_1.R1010
5'-most EST	jC-atXLIB327431P1a03b1
Method	BLASTX
NCBI GI	g2499011
BLAST score	289
E value	8.0e-26
Match length	139
% identity	46
NCBI Description	HYDROXYETHYLTHIAZOLE KINASE (4-METHYL-5-BETA-HYDROXYETHYLTHIAZOLE KINASE) (THZ KINASE) (TH KINASE) >gi_1842117 (U87940) hydroxyethyl thiazole kinase [Salmonella typhimurium]

Seq. No.	124141
Contig ID	13213_1.R1010
5'-most EST	LIB23-038-Q1-E1-G6

Seq. No.	124142
Contig ID	13218_1.R1010
5'-most EST	LIB23-026-Q1-E1-E2
Method	BLASTN
NCBI GI	g4455168
BLAST score	345
E value	0.0e+00

Match length	526
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	124143
Contig ID	13220_1.R1010
5'-most EST	g949056
Method	BLASTX
NCBI GI	g3123712
BLAST score	197
E value	2.0e-55
Match length	201
% identity	49
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	124144
Contig ID	13220_2.R1010
5'-most EST	g2446064
Method	BLASTX
NCBI GI	g3123712
BLAST score	300
E value	5.0e-27
Match length	93
% identity	58
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	124145
Contig ID	13227_1.R1010
5'-most EST	LIB25-109-Q1-E1-G1
Method	BLASTX
NCBI GI	g2827709
BLAST score	779
E value	1.0e-87
Match length	215
% identity	79
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	124146
Contig ID	13228_1.R1010
5'-most EST	LIB25-078-Q1-E1-G2
Method	BLASTX
NCBI GI	g3080371
BLAST score	740
E value	1.0e-78
Match length	136
% identity	100
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	124147
Contig ID	13230_1.R1010
5'-most EST	LIB25-075-Q1-E1-A3

Seq. No.	124148
Contig ID	13236_1.R1010
5'-most EST	jC-atXLIB327429P4e03b2

Method	BLASTX
NCBI GI	g4455035
BLAST score	261
E value	3.0e-22
Match length	169
% identity	37
NCBI Description	(AF116238) pseudouridine synthase 1 [Homo sapiens]

Seq. No.	124149
Contig ID	13237_1.R1010
5'-most EST	jC-atXP94CG11C2T7070d1
Method	BLASTX
NCBI GI	g3834307
BLAST score	283
E value	5.0e-25
Match length	66
% identity	80
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	124150
Contig ID	13237_2.R1010
5'-most EST	jC-atXLIB327431P2a09b1
Method	BLASTN
NCBI GI	g3766106
BLAST score	59
E value	3.0e-24
Match length	196
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124151
Contig ID	13247_1.R1010
5'-most EST	LIB3176-122-P2-K1-F10
Method	BLASTX
NCBI GI	g2317911
BLAST score	510
E value	1.0e-51
Match length	119
% identity	87
NCBI Description	(U89959) similar to GTP-binding protein [Arabidopsis thaliana]

Seq. No.	124152
Contig ID	13252_1.R1010
5'-most EST	jC-atXLIB327405P2f12b2
Method	BLASTN
NCBI GI	g3869069
BLAST score	62
E value	5.0e-26
Match length	257
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	124153
Contig ID	13261_1.R1010
5'-most EST	LIB3168-072-P1-K1-D5
Method	BLASTX
NCBI GI	g3551425
BLAST score	187
E value	2.0e-13
Match length	180
% identity	32
NCBI Description	(AB015291) pyrrolidone carboxyl peptidase [Pyrococcus furiosus]

Seq. No.	124154
Contig ID	13265_1.R1010
5'-most EST	LIB23-027-Q1-E1-A9
Method	BLASTX
NCBI GI	g3021270
BLAST score	562
E value	3.0e-61
Match length	156
% identity	79
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No.	124155
Contig ID	13267_1.R1010
5'-most EST	LIB25-047-Q1-E1-B1
Method	BLASTN
NCBI GI	g4335744
BLAST score	360
E value	0.0e+00
Match length	608
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124156
Contig ID	13269_1.R1010
5'-most EST	g315674
Method	BLASTN
NCBI GI	g4531433
BLAST score	189
E value	1.0e-102
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	124157
Contig ID	13273_1.R1010
5'-most EST	LIB23-027-Q1-E1-B5
Method	BLASTX
NCBI GI	g3367591
BLAST score	214
E value	2.0e-17
Match length	64

% identity	66
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	124158
Contig ID	13278_1.R1010
5'-most EST	LIB3234-085-Q1-K1-E12

Seq. No.	124159
Contig ID	13289_1.R1010
5'-most EST	LIB23-027-Q1-E1-D10
Method	BLASTX
NCBI GI	g4261517
BLAST score	188
E value	5.0e-14
Match length	89
% identity	52
NCBI Description	(AF117334) cysteine proteinase inhibitor [Ipomoea batatas]

Seq. No.	124160
Contig ID	13300_1.R1010
5'-most EST	g931932

Seq. No.	124161
Contig ID	13306_1.R1010
5'-most EST	LIB23-027-Q1-E1-E5
Method	BLASTX
NCBI GI	g2760322
BLAST score	344
E value	3.0e-32
Match length	111
% identity	63
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	124162
Contig ID	13309_1.R1010
5'-most EST	jC-atX24037Q1E2B02b2
Method	BLASTN
NCBI GI	g3269280
BLAST score	360
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	124163
Contig ID	13318_1.R1010
5'-most EST	LIB3175-001-Q1-K1-C2

Seq. No.	124164
Contig ID	13319_1.R1010
5'-most EST	LIB23-027-Q1-E1-F8
Method	BLASTN
NCBI GI	g4490734
BLAST score	154
E value	5.0e-81
Match length	400

% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	124165
Contig ID	13321_1.R1010
5'-most EST	jC-atXLIB327420P4h05b1
Method	BLASTX
NCBI GI	g4741198
BLAST score	1006
E value	1.0e-109
Match length	189
% identity	100
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	124166
Contig ID	13330_1.R1010
5'-most EST	g1159410
Method	BLASTX
NCBI GI	g3193285
BLAST score	145
E value	6.0e-09
Match length	98
% identity	33
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	124167
Contig ID	13341_1.R1010
5'-most EST	jC-atXP98CH2G9T7b1
Method	BLASTX
NCBI GI	g4262167
BLAST score	298
E value	9.0e-27
Match length	121
% identity	34
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	124168
Contig ID	13343_1.R1010
5'-most EST	jC-atXLIB327421P4g06b1
Method	BLASTN
NCBI GI	g3241923
BLAST score	195
E value	1.0e-105
Match length	848
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	124169
Contig ID	13343_2.R1010
5'-most EST	LIB25-089-Q1-E1-D9
Method	BLASTN
NCBI GI	g3241923
BLAST score	287
E value	1.0e-160

Match length	573
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	124170
Contig ID	13355_1.R1010
5'-most EST	LIB23-028-Q1-E1-D11
Method	BLASTN
NCBI GI	g4567259
BLAST score	212
E value	1.0e-115
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	124171
Contig ID	13358_1.R1010
5'-most EST	LIB3176-070-P1-K1-A8
Method	BLASTN
NCBI GI	g3128137
BLAST score	622
E value	0.0e+00
Match length	659
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	124172
Contig ID	13359_1.R1010
5'-most EST	jC-atXLIB327402P3b10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	5.0e-21
Match length	69
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124173
Contig ID	13359_2.R1010
5'-most EST	jC-atXP39C162G17T7s1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	3.0e-18
Match length	49
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	124174
Contig ID	13361_1.R1010
5'-most EST	LIB23-028-Q1-E1-D8
Method	BLASTX
NCBI GI	g4454049

BLAST score	349
E value	5.0e-33
Match length	122
% identity	63
NCBI Description	(AL035394) 98b like protein [Arabidopsis thaliana]

Seq. No.	124175
Contig ID	13365_1.R1010
5'-most EST	LIB23-028-Q1-E1-E5
Method	BLASTN
NCBI GI	g4567259
BLAST score	73
E value	7.0e-33
Match length	138
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	124176
Contig ID	13376_1.R1010
5'-most EST	jC-atXP46C172F6T7067d1
Method	BLASTN
NCBI GI	g2739359
BLAST score	669
E value	0.0e+00
Match length	711
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124177
Contig ID	13377_1.R1010
5'-most EST	LIB23-028-Q1-E1-F7
Method	BLASTN
NCBI GI	g4115370
BLAST score	315
E value	1.0e-177
Match length	355
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124178
Contig ID	13382_1.R1010
5'-most EST	LIB23-028-Q1-E1-G4
Method	BLASTX
NCBI GI	g1903034
BLAST score	285
E value	2.0e-25
Match length	128
% identity	44
NCBI Description	(X94625) amp-binding protein [Brassica napus]

Seq. No.	124179
Contig ID	13383_1.R1010
5'-most EST	jC-atX24062Q1E1A04b1
Method	BLASTN

NCBI GI	g3366536
BLAST score	288
E value	1.0e-161
Match length	623
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	124180
Contig ID	13385_1.R1010
5'-most EST	LIB23-028-Q1-E1-G9
Method	BLASTX
NCBI GI	g4115913
BLAST score	277
E value	2.0e-24
Match length	98
% identity	49
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_ (AL049524) putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	124181
Contig ID	13387_1.R1010
5'-most EST	LIB23-028-Q1-E1-H4
Method	BLASTX
NCBI GI	g3738284
BLAST score	165
E value	2.0e-11
Match length	43
% identity	70
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	124182
Contig ID	13389_1.R1010
5'-most EST	jC-atXLIB327409P1b09b1
Method	BLASTX
NCBI GI	g4262149
BLAST score	1581
E value	1.0e-177
Match length	290
% identity	100
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	124183
Contig ID	13389_2.R1010
5'-most EST	jC-atXLIB327408P4c12b1
Method	BLASTX
NCBI GI	g4262149
BLAST score	616
E value	1.0e-109
Match length	235
% identity	83
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	124184
Contig ID	13399_1.R1010
5'-most EST	LIB23-029-Q1-E1-B10
Method	BLASTX
NCBI GI	g464621
BLAST score	402
E value	2.0e-83
Match length	230
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	124185
Contig ID	13399_2.R1010
5'-most EST	jC-atXLIB327415P3b11b1
Method	BLASTX
NCBI GI	g464621
BLAST score	867
E value	3.0e-93
Match length	228
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	124186
Contig ID	13399_3.R1010
5'-most EST	LIB3176-023-P1-K1-A2
Method	BLASTX
NCBI GI	g464621
BLAST score	459
E value	8.0e-46
Match length	138
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	124187
Contig ID	13399_4.R1010
5'-most EST	g1053900
Method	BLASTX
NCBI GI	g464621
BLAST score	321
E value	1.0e-29
Match length	134
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	124188
Contig ID	13401_1.R1010
5'-most EST	jC-atXP78CF6H8T7b1
Method	BLASTX
NCBI GI	g2493132
BLAST score	192
E value	1.0e-163
Match length	354
% identity	84
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi_167110 (L11873) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No.	124189
Contig ID	13401_6.R1010
5'-most EST	LIB23-051-Q1-E1-D11
Method	BLASTX
NCBI GI	g4467138
BLAST score	643
E value	2.0e-67
Match length	127
% identity	100
NCBI Description	(AL035540) probable H+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	124190
Contig ID	13408_1.R1010
5'-most EST	jC-atXLIB327416P3g08b1
Method	BLASTN
NCBI GI	g2160155
BLAST score	199
E value	1.0e-108
Match length	402
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	124191
Contig ID	13411_1.R1010
5'-most EST	jC-atXLIB327423P1h02b1
Method	BLASTX
NCBI GI	g2947062
BLAST score	446
E value	5.0e-44
Match length	199
% identity	58
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	124192
Contig ID	13416_1.R1010
5'-most EST	ARABLI-14-Q1-B1-G6
Method	BLASTX
NCBI GI	g1888557
BLAST score	417
E value	8.0e-41
Match length	113
% identity	61

NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]
Seq. No.	124193
Contig ID	13418_1.R1010
5'-most EST	LIB23-029-Q1-E1-D3
Method	BLASTN
NCBI GI	g2760168
BLAST score	470
E value	0.0e+00
Match length	661
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.	124194
Contig ID	13422_1.R1010
5'-most EST	jC-atXLIB327428P4a10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	62
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	124195
Contig ID	13427_1.R1010
5'-most EST	LIB3234-009-P1-K1-A9
Method	BLASTX
NCBI GI	g2352921
BLAST score	575
E value	3.0e-59
Match length	155
% identity	75
NCBI Description	(AF012862) cytosolic glucose-6-phosphate dehydrogenase 1 [Petroselinum crispum]
Seq. No.	124196
Contig ID	13428_1.R1010
5'-most EST	LIB23-029-Q1-E1-E7
Method	BLASTN
NCBI GI	g4741184
BLAST score	201
E value	1.0e-109
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)
Seq. No.	124197
Contig ID	13437_1.R1010
5'-most EST	LIB3176-073-P1-K1-E2
Method	BLASTX
NCBI GI	g1652134
BLAST score	306

E value	1.0e-27
Match length	131
% identity	48
NCBI Description	(D90903) FKBP-type peptidyl-prolyl cis-trans isomerase [Synechocystis sp.]

Seq. No.	124198
Contig ID	13454_1.R1010
5'-most EST	LIB23-029-Q1-E1-H8

Seq. No.	124199
Contig ID	13456_1.R1010
5'-most EST	LIB35-042-Q1-E1-G1

Seq. No.	124200
Contig ID	13464_1.R1010
5'-most EST	LIB23-030-Q1-E1-B11
Method	BLASTX
NCBI GI	g1730560
BLAST score	515
E value	2.0e-52
Match length	127
% identity	77
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]

Seq. No.	124201
Contig ID	13472_1.R1010
5'-most EST	LIB23-030-Q1-E1-C12
Method	BLASTX
NCBI GI	g4063751
BLAST score	175
E value	4.0e-13
Match length	141
% identity	30
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	124202
Contig ID	13475_1.R1010
5'-most EST	LIB23-030-Q1-E1-C8
Method	BLASTN
NCBI GI	g2182286
BLAST score	325
E value	0.0e+00
Match length	398
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	124203
Contig ID	13482_1.R1010
5'-most EST	jC-alXLIB327435P4e07b1
Method	BLASTX
NCBI GI	g3881189

BLAST score	633
E value	9.0e-66
Match length	183
% identity	61
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No.	124204
Contig ID	13482_2.R1010
5'-most EST	jC-atXP89C244P18T7067d1
Method	BLASTX
NCBI GI	g3881189
BLAST score	640
E value	1.0e-66
Match length	183
% identity	62
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No.	124205
Contig ID	13486_1.R1010
5'-most EST	g1158654
Method	BLASTX
NCBI GI	g2190550
BLAST score	743
E value	6.0e-79
Match length	157
% identity	92
NCBI Description	(AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]

Seq. No.	124206
Contig ID	13489_1.R1010
5'-most EST	LIB23-030-Q1-E1-F11
Method	BLASTN
NCBI GI	g4115930
BLAST score	101
E value	2.0e-49
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	124207
Contig ID	13496_1.R1010
5'-most EST	g2748494
Method	BLASTN
NCBI GI	g3860166
BLAST score	46
E value	1.0e-16
Match length	94
% identity	88
NCBI Description	Arabidopsis thaliana disease resistance protein RPP1-WsC gene, partial cds

Seq. No.	124208
Contig ID	13499_1.R1010
5'-most EST	LIB23-030-Q1-E1-H9
Method	BLASTN
NCBI GI	g2642152
BLAST score	344
E value	0.0e+00
Match length	360
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124209
Contig ID	13500_1.R1010
5'-most EST	jC-atXLIB327401P4b04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	7.0e-13
Match length	72
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124210
Contig ID	13500_2.R1010
5'-most EST	g958159
Method	BLASTX
NCBI GI	g1653508
BLAST score	216
E value	5.0e-17
Match length	109
% identity	43
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	124211
Contig ID	13505_1.R1010
5'-most EST	g930591
Method	BLASTX
NCBI GI	g2911085
BLAST score	564
E value	1.0e-66
Match length	196
% identity	77
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	124212
Contig ID	13505_2.R1010
5'-most EST	g2581659
Method	BLASTX
NCBI GI	g2911085
BLAST score	554
E value	1.0e-56

Match length	115
% identity	97
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	124213
Contig ID	13505_3.R1010
5'-most EST	g905833
Method	BLASTX
NCBI GI	g2911085
BLAST score	487
E value	7.0e-49
Match length	128
% identity	83
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	124214
Contig ID	13505_7.R1010
5'-most EST	g2576671
Method	BLASTX
NCBI GI	g4583542
BLAST score	272
E value	9.0e-24
Match length	178
% identity	46
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	124215
Contig ID	13508_1.R1010
5'-most EST	LIB25-097-Q1-E1-E8

Seq. No.	124216
Contig ID	13512_1.R1010
5'-most EST	g2722711
Method	BLASTN
NCBI GI	g3650026
BLAST score	314
E value	1.0e-176
Match length	581
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124217
Contig ID	13512_2.R1010
5'-most EST	LIB3175-061-P1-K1-B5
Method	BLASTN
NCBI GI	g3650026
BLAST score	223
E value	1.0e-122
Match length	335

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124218
Contig ID	13512_3.R1010
5'-most EST	g2722238
Method	BLASTN
NCBI GI	g16214
BLAST score	50
E value	8.0e-19
Match length	50
% identity	100
NCBI Description	A.thaliana mRNA for catalase

Seq. No.	124219
Contig ID	13517_2.R1010
5'-most EST	LIB24-103-Q1-E2-A10

Seq. No.	124220
Contig ID	13521_1.R1010
5'-most EST	LIB23-031-Q1-E1-C3

Seq. No.	124221
Contig ID	13525_1.R1010
5'-most EST	jC-atXLIB327427P4d02b2
Method	BLASTX
NCBI GI	g418507
BLAST score	242
E value	6.0e-20
Match length	163
% identity	32
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	124222
Contig ID	13526_1.R1010
5'-most EST	jC-atXLIB327418P4h07b1
Method	BLASTX
NCBI GI	g3687249
BLAST score	581
E value	7.0e-60
Match length	122
% identity	89
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	124223
Contig ID	13526_2.R1010
5'-most EST	g2393667
Method	BLASTX
NCBI GI	g3687249

BLAST score	167
E value	2.0e-11
Match length	119
% identity	33
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	124224
Contig ID	13526_3.R1010
5'-most EST	jC-atXP101CE2B5T7093d1
Method	BLASTX
NCBI GI	g3687249
BLAST score	249
E value	4.0e-51
Match length	119
% identity	86
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	124225
Contig ID	13529_1.R1010
5'-most EST	LIB23-031-Q1-E1-D4
Method	BLASTX
NCBI GI	g4760370
BLAST score	391
E value	1.0e-37
Match length	159
% identity	57
NCBI Description	(AF082565) ATP dependent copper transporter [Arabidopsis thaliana] >gi_4760380_gb_AAD29115.1_ (AF091112) ATP dependent copper transporter [Arabidopsis thaliana]

Seq. No.	124226
Contig ID	13530_1.R1010
5'-most EST	jC-atXLIB327406P1c04b1
Method	BLASTX
NCBI GI	g3269288
BLAST score	849
E value	4.0e-91
Match length	204
% identity	82
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	124227
Contig ID	13533_1.R1010
5'-most EST	LIB24-099-Q1-E1-E11
Method	BLASTX
NCBI GI	g3355471
BLAST score	229
E value	8.0e-19
Match length	88
% identity	47
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	124228
Contig ID	13539_1.R1010

5'-most EST	LIB3175-007-P1-K1-E7
Method	BLASTX
NCBI GI	g3075399
BLAST score	162
E value	1.0e-10
Match length	63
% identity	56
NCBI Description	(AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No.	124229
Contig ID	13557_1.R1010
5'-most EST	LIB23-046-Q1-E1-E9
Method	BLASTN
NCBI GI	g3335356
BLAST score	366
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124230
Contig ID	13563_1.R1010
5'-most EST	LIB3175-055-P1-K1-H7

Seq. No.	124231
Contig ID	13576_1.R1010
5'-most EST	LIB23-032-Q1-E1-A10
Method	BLASTN
NCBI GI	g4519190
BLAST score	201
E value	1.0e-109
Match length	493
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	124232
Contig ID	13577_1.R1010
5'-most EST	jC-atXP32C146O7T7d2
Method	BLASTN
NCBI GI	g2351068
BLAST score	349
E value	0.0e+00
Match length	426
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	124233
Contig ID	13577_2.R1010
5'-most EST	jC-alXLIB327436P2a07b1
Method	BLASTN
NCBI GI	g2351068
BLAST score	468
E value	0.0e+00
Match length	501

% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No. 124234
Contig ID 13578_1.R1010
5'-most EST LIB23-038-Q1-E1-H8

Seq. No. 124235
Contig ID 13583_1.R1010
5'-most EST jC-atXLIB327408P1g09b1
Method BLASTX
NCBI GI g2895188
BLAST score 150
E value 2.0e-09
Match length 112
% identity 22
NCBI Description (AF016011) CONSTANS homolog [Brassica napus]

Seq. No. 124236
Contig ID 13584_1.R1010
5'-most EST LIB23-032-Q1-E1-A8
Method BLASTX
NCBI GI g2887437
BLAST score 101
E value 5.0e-09
Match length 196
% identity 32
NCBI Description (AB007893) KIAA0433 [Homo sapiens]

Seq. No. 124237
Contig ID 13586_1.R1010
5'-most EST LIB23-032-Q1-E1-F5
Method BLASTX
NCBI GI g2245070
BLAST score 195
E value 2.0e-15
Match length 216
% identity 29
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 124238
Contig ID 13587_1.R1010
5'-most EST jC-atXP96C249H15T7b1
Method BLASTX
NCBI GI g4033349
BLAST score 702
E value 5.0e-74
Match length 145
% identity 95
NCBI Description (AJ223496) phosphoenolpyrovate carboxylase [Brassica juncea]

Seq. No. 124239
Contig ID 13587_2.R1010
5'-most EST LIB3176-016-P1-K1-F11
Method BLASTX

NCBI GI	g4033351
BLAST score	61
E value	1.0e-144
Match length	282
% identity	91
NCBI Description	(AJ223497) phosphoenolpyruvate carboxylase [Brassica juncea]

Seq. No.	124240
Contig ID	13588_1.R1010
5'-most EST	LIB3177-076-P1-K1-G2
Method	BLASTX
NCBI GI	g3337361
BLAST score	338
E value	1.0e-31
Match length	146
% identity	50
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	124241
Contig ID	13590_1.R1010
5'-most EST	LIB23-032-Q1-E1-B5
Method	BLASTN
NCBI GI	g2062705
BLAST score	24
E value	2.0e-03
Match length	47
% identity	56
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	124242
Contig ID	13597_1.R1010
5'-most EST	LIB23-046-Q1-E1-G8

Seq. No.	124243
Contig ID	13599_1.R1010
5'-most EST	jC-atXP53C183N22T7059a1
Method	BLASTX
NCBI GI	g4741962
BLAST score	1047
E value	1.0e-114
Match length	265
% identity	82
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	124244
Contig ID	13599_2.R1010
5'-most EST	g1158271
Method	BLASTN
NCBI GI	g4741961
BLAST score	323
E value	0.0e+00
Match length	447
% identity	95
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

Seq. No.	124245

Contig ID	13603_1.R1010
5'-most EST	jC-atXP37C157G22T7d2
Method	BLASTX
NCBI GI	g2281111
BLAST score	89
E value	1.0e-59
Match length	117
% identity	95
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana] >gi_2288991 (AC002335) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	124246
Contig ID	13603_2.R1010
5'-most EST	g936047
Method	BLASTX
NCBI GI	g2281111
BLAST score	1047
E value	1.0e-114
Match length	218
% identity	87
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana] >gi_2288991 (AC002335) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	124247
Contig ID	13611_1.R1010
5'-most EST	LIB23-060-Q1-E1-H1

Seq. No.	124248
Contig ID	13612_1.R1010
5'-most EST	g1054356
Method	BLASTN
NCBI GI	g2894591
BLAST score	192
E value	1.0e-103
Match length	326
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	124249
Contig ID	13612_3.R1010
5'-most EST	jC-atXLIB327418P4g08b1
Method	BLASTN
NCBI GI	g2894591
BLAST score	219
E value	1.0e-120
Match length	465
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	124250
Contig ID	13612_4.R1010
5'-most EST	LIB23-032-Q1-E1-E10
Method	BLASTN

NCBI GI	g2894591
BLAST score	212
E value	1.0e-115
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	124251
Contig ID	13613_1.R1010
5'-most EST	LIB24-035-Q1-E1-E11
Method	BLASTX
NCBI GI	g3334756
BLAST score	143
E value	9.0e-09
Match length	71
% identity	39
NCBI Description	(Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]

Seq. No.	124252
Contig ID	13616_1.R1010
5'-most EST	LIB23-032-Q1-E1-E5
Method	BLASTN
NCBI GI	g4757662
BLAST score	338
E value	0.0e+00
Match length	490
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	124253
Contig ID	13618_1.R1010
5'-most EST	LIB24-017-Q1-E1-D1
Method	BLASTN
NCBI GI	g4510338
BLAST score	571
E value	0.0e+00
Match length	575
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	124254
Contig ID	13619_1.R1010
5'-most EST	LIB23-032-Q1-E1-E9
Method	BLASTN
NCBI GI	g4512690
BLAST score	373
E value	0.0e+00
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No. 124255

Contig ID	13623_1.R1010
5'-most EST	jC-atXLIB327431P3h08a1
Method	BLASTX
NCBI GI	g1707981
BLAST score	360
E value	1.0e-35
Match length	97
% identity	79
NCBI Description	GLUTAREDOXIN >gi_1076561_pir__S54825 glutaredoxin - castor bean

Seq. No.	124256
Contig ID	13625_1.R1010
5'-most EST	jC-alXLIB327434P2h05b1
Method	BLASTX
NCBI GI	g2827524
BLAST score	459
E value	1.0e-45
Match length	81
% identity	100
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	124257
Contig ID	13625_2.R1010
5'-most EST	LIB25-070-Q1-E1-G6
Method	BLASTN
NCBI GI	g2827513
BLAST score	174
E value	5.0e-93
Match length	294
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	124258
Contig ID	13628_1.R1010
5'-most EST	LIB23-074-Q1-E1-C2
Method	BLASTN
NCBI GI	g3702736
BLAST score	43
E value	1.0e-14
Match length	203
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	124259
Contig ID	13630_1.R1010
5'-most EST	jC-alXLIB327436P4h01b1
Method	BLASTX
NCBI GI	g1723511
BLAST score	103
E value	1.0e-14
Match length	106
% identity	52
NCBI Description	PUTATIVE ENDONUCLEASE C1F12.06C >gi_2130239_pir__S67449 hypothetical protein - fission yeast (Schizosaccharomyces

pombe) >gi_1217980_emb_CAA93810_ (Z69944) unknown [Schizosaccharomyces pombe]

Seq. No. 124260
Contig ID 13630_2.R1010
5'-most EST LIB23-032-Q1-E1-F9

Seq. No. 124261
Contig ID 13631_1.R1010
5'-most EST jC-atXP86CG4G5T7d2
Method BLASTN
NCBI GI g2828278
BLAST score 378
E value 0.0e+00
Match length 730
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No. 124262
Contig ID 13631_2.R1010
5'-most EST jC-atXLIB327426P2b08b1
Method BLASTN
NCBI GI g2828278
BLAST score 194
E value 1.0e-104
Match length 426
% identity 93
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No. 124263
Contig ID 13636_1.R1010
5'-most EST LIB24-014-Q1-E1-B12
Method BLASTX
NCBI GI g2642153
BLAST score 203
E value 4.0e-51
Match length 370
% identity 38
NCBI Description (AC003000) unknown protein [Arabidopsis thaliana] >gi_2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No. 124264
Contig ID 13636_2.R1010
5'-most EST LIB3168-014-P1-K1-F7
Method BLASTX
NCBI GI g2245012
BLAST score 99
E value 5.0e-09
Match length 142
% identity 37
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 124265
Contig ID 13636_3.R1010

5'-most EST	jC-atXP71C222019T7069d1
Method	BLASTN
NCBI GI	g4589436
BLAST score	129
E value	6.0e-66
Match length	300
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	124266
Contig ID	13636_4.R1010
5'-most EST	LIB25-036-Q1-E1-F1

Seq. No.	124267
Contig ID	13636_7.R1010
5'-most EST	g2733672

Seq. No.	124268
Contig ID	13642_1.R1010
5'-most EST	jC-atXLIB327409P1d01b1
Method	BLASTN
NCBI GI	g4469002
BLAST score	318
E value	1.0e-178
Match length	1021
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	124269
Contig ID	13644_1.R1010
5'-most EST	jC-atXLIB327409P2d10a1
Method	BLASTX
NCBI GI	g3434986
BLAST score	225
E value	5.0e-51
Match length	174
% identity	28
NCBI Description	(AB016895) Pop3 [Schizosaccharomyces pombe]

Seq. No.	124270
Contig ID	13645_1.R1010
5'-most EST	LIB3234-053-P1-K1-D5
Method	BLASTX
NCBI GI	g2921323
BLAST score	143
E value	1.0e-15
Match length	60
% identity	63
NCBI Description	(AF034112) beta-1,3-glucanase 7 [Glycine max]

Seq. No.	124271
Contig ID	13647_1.R1010
5'-most EST	LIB3175-020-P1-K1-E3
Method	BLASTN
NCBI GI	g4589409

BLAST score	399
E value	0.0e+00
Match length	523
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	124272
Contig ID	13647_2.R1010
5'-most EST	g1159044
Method	BLASTN
NCBI GI	g4589409
BLAST score	375
E value	0.0e+00
Match length	521
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	124273
Contig ID	13651_1.R1010
5'-most EST	LIB23-033-Q1-E1-G4
Method	BLASTX
NCBI GI	g3668080
BLAST score	345
E value	1.0e-54
Match length	139
% identity	82
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	124274
Contig ID	13659_1.R1010
5'-most EST	LIB24-116-Q1-E1-C5
Method	BLASTX
NCBI GI	g3980411
BLAST score	516
E value	1.0e-52
Match length	102
% identity	100
NCBI Description	(AC004561) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	124275
Contig ID	13665_1.R1010
5'-most EST	LIB23-033-Q1-E1-B8
Method	BLASTN
NCBI GI	g2264312
BLAST score	421
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	124276
Contig ID	13667_1.R1010
5'-most EST	jC-atXP111C119K22T7d1

Seq. No.	124277
Contig ID	13669_1.R1010
5'-most EST	jC-atXP30C142L2T7d2
Method	BLASTN
NCBI GI	g4732169
BLAST score	265
E value	1.0e-147
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana BAC T3E15

Seq. No.	124278
Contig ID	13671_1.R1010
5'-most EST	g438356
Method	BLASTX
NCBI GI	g3122724
BLAST score	351
E value	4.0e-33
Match length	69
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	124279
Contig ID	13673_1.R1010
5'-most EST	LIB25-076-Q1-E1-F2
Method	BLASTN
NCBI GI	g2264309
BLAST score	305
E value	1.0e-171
Match length	480
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	124280
Contig ID	13678_1.R1010
5'-most EST	jC-atXP39C158N17T7s1
Method	BLASTX
NCBI GI	g2459421
BLAST score	278
E value	1.0e-24
Match length	53
% identity	96
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	124281
Contig ID	13678_2.R1010
5'-most EST	LIB35-045-Q1-E1-E9
Method	BLASTX
NCBI GI	g2459421
BLAST score	1096
E value	1.0e-120
Match length	236
% identity	89

NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	124282
Contig ID	13683_1.R1010
5'-most EST	LIB23-033-Q1-E1-D6
Method	BLASTX
NCBI GI	g4220514
BLAST score	932
E value	1.0e-100
Match length	360
% identity	61
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	124283
Contig ID	13699_1.R1010
5'-most EST	LIB23-033-Q1-E1-F10
Method	BLASTN
NCBI GI	g3600045
BLAST score	279
E value	1.0e-155
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	124284
Contig ID	13700_1.R1010
5'-most EST	jC-atXLIB327402P1a01b1
Method	BLASTN
NCBI GI	g3702731
BLAST score	644
E value	0.0e+00
Match length	671
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	124285
Contig ID	13701_1.R1010
5'-most EST	LIB23-033-Q1-E1-F12
Method	BLASTX
NCBI GI	g2245063
BLAST score	307
E value	4.0e-54
Match length	108
% identity	96
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124286
Contig ID	13710_1.R1010
5'-most EST	LIB3176-019-P1-K1-C3
Method	BLASTX
NCBI GI	g2244852
BLAST score	482
E value	2.0e-48
Match length	114
% identity	87

NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	124287
Contig ID	13712_1.R1010
5'-most EST	jC-atXP87CG8H3T7b1
Method	BLASTX
NCBI GI	g1871195
BLAST score	344
E value	3.0e-32
Match length	109
% identity	65
NCBI Description	(U90439) Ca++ dependent protein kinase isolog [Arabidopsis thaliana] >gi_2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.	124288
Contig ID	13713_1.R1010
5'-most EST	LIB24-083-Q1-E1-H1
Method	BLASTN
NCBI GI	g3510338
BLAST score	206
E value	1.0e-112
Match length	470
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21I16, complete sequence [Arabidopsis thaliana]
Seq. No.	124289
Contig ID	13714_1.R1010
5'-most EST	jC-atXP87CG10G10T7b1
Method	BLASTX
NCBI GI	g2462832
BLAST score	279
E value	1.0e-24
Match length	92
% identity	58
NCBI Description	(AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
Seq. No.	124290
Contig ID	13717_1.R1010
5'-most EST	LIB23-033-Q1-E1-G5
Method	BLASTN
NCBI GI	g3868723
BLAST score	262
E value	1.0e-145
Match length	668
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	124291
Contig ID	13728_1.R1010
5'-most EST	LIB25-070-Q1-E1-C8
Method	BLASTX
NCBI GI	g2262110
BLAST score	469
E value	7.0e-47

Match length	102
% identity	85
NCBI Description	(AC002343) zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	124292
Contig ID	13733_1.R1010
5'-most EST	jC-atXLIB327420P1a02b1
Method	BLASTN
NCBI GI	g4589432
BLAST score	551
E value	0.0e+00
Match length	1379
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMJ24, complete sequence

Seq. No.	124293
Contig ID	13737_1.R1010
5'-most EST	jC-atXLIB327426P2g04b1
Method	BLASTX
NCBI GI	g1076440
BLAST score	378
E value	4.0e-36
Match length	84
% identity	87
NCBI Description	acyl-CoA binding protein - rape >gi_1076441_pir__S49102 acyl-CoA binding protein - rape >gi_509265_emb_CAA54390_ (X77134) acyl-CoA binding protein [Brassica napus]

Seq. No.	124294
Contig ID	13737_2.R1010
5'-most EST	jC-atXLIB327408P2g04b1
Method	BLASTX
NCBI GI	g1076440
BLAST score	323
E value	1.0e-29
Match length	73
% identity	86
NCBI Description	acyl-CoA binding protein - rape >gi_1076441_pir__S49102 acyl-CoA binding protein - rape >gi_509265_emb_CAA54390_ (X77134) acyl-CoA binding protein [Brassica napus]

Seq. No.	124295
Contig ID	13739_1.R1010
5'-most EST	jC-atXLIB327424P4g08b1
Method	BLASTX
NCBI GI	g4262240
BLAST score	306
E value	1.0e-27
Match length	144
% identity	49
NCBI Description	(AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No.	124296
Contig ID	13740_1.R1010
5'-most EST	g2762672

Method	BLASTX
NCBI GI	g4508077
BLAST score	644
E value	2.0e-67
Match length	136
% identity	90
NCBI Description	(AC005882) 62114 [Arabidopsis thaliana]

Seq. No.	124297
Contig ID	13744_1.R1010
5'-most EST	LIB23-034-Q1-E1-B6

Seq. No.	124298
Contig ID	13745_1.R1010
5'-most EST	LIB23-034-Q1-E1-B7

Seq. No.	124299
Contig ID	13749_1.R1010
5'-most EST	jC-atXP89C242K4T7025d1
Method	BLASTN
NCBI GI	g4455348
BLAST score	277
E value	1.0e-154
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	124300
Contig ID	13750_1.R1010
5'-most EST	jC-atXLIB327404P1b03b1
Method	BLASTN
NCBI GI	g3868723
BLAST score	221
E value	1.0e-121
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	124301
Contig ID	13754_1.R1010
5'-most EST	g906381
Method	BLASTN
NCBI GI	g4572664
BLAST score	434
E value	0.0e+00
Match length	438
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	124302
Contig ID	13755_1.R1010
5'-most EST	jC-alXLIB327436P4b01b1
Method	BLASTN
NCBI GI	g3510247

BLAST score	282
E value	1.0e-157
Match length	527
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124303
Contig ID	13755_2.R1010
5'-most EST	g2047491
Method	BLASTN
NCBI GI	g3510247
BLAST score	170
E value	3.0e-90
Match length	788
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124304
Contig ID	13759_1.R1010
5'-most EST	jC-atXLIB327438P1f11a1

Seq. No.	124305
Contig ID	13760_1.R1010
5'-most EST	jC-atXLIB327416P2f03b1
Method	BLASTN
NCBI GI	g4559319
BLAST score	286
E value	1.0e-160
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	124306
Contig ID	13766_1.R1010
5'-most EST	LIB23-034-Q1-E1-E1
Method	BLASTN
NCBI GI	g2618677
BLAST score	183
E value	3.0e-98
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	124307
Contig ID	13769_1.R1010
5'-most EST	LIB23-034-Q1-E1-E12
Method	BLASTX
NCBI GI	g4337207
BLAST score	826
E value	2.0e-88
Match length	176
% identity	91
NCBI Description	(AC006403) putative zinc-finger protein [Arabidopsis

thaliana] >gi_4585205_gb_AAD25324.1_AF095588_1 (AF095588)
C2H2 zinc finger protein FZF [Arabidopsis thaliana]

Seq. No.	124308
Contig ID	13774_1.R1010
5'-most EST	jC-atXLIB327431P4b12a1
Method	BLASTX
NCBI GI	g4490311
BLAST score	370
E value	3.0e-35
Match length	122
% identity	61
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	124309
Contig ID	13777_1.R1010
5'-most EST	jC-atXP22C119I8T7076a1
Method	BLASTX
NCBI GI	g224293
BLAST score	386
E value	5.0e-37
Match length	78
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	124310
Contig ID	13777_2.R1010
5'-most EST	jC-atX24103Q1E1H06b1
Method	BLASTX
NCBI GI	g224293
BLAST score	386
E value	4.0e-37
Match length	78
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	124311
Contig ID	13779_1.R1010
5'-most EST	jC-atXLIB327402P1e03b1

Seq. No.	124312
Contig ID	13784_1.R1010
5'-most EST	jC-atXLIB327408P2h05b1
Method	BLASTX
NCBI GI	g3328619
BLAST score	177
E value	4.0e-12
Match length	191
% identity	27
NCBI Description	(AE001295) hypothetical protein [Chlamydia trachomatis]

Seq. No.	124313
Contig ID	13789_1.R1010
5'-most EST	g2763090
Method	BLASTN
NCBI GI	g3702734
BLAST score	175

E value	2.0e-93
Match length	842
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	124314
Contig ID	13791_1.R1010
5'-most EST	LIB3176-030-P1-K1-C6

Seq. No.	124315
Contig ID	13793_1.R1010
5'-most EST	jC-atXLIB327406P4b02b2
Method	BLASTX
NCBI GI	g4105772
BLAST score	833
E value	3.0e-89
Match length	180
% identity	81
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	124316
Contig ID	13794_1.R1010
5'-most EST	LIB23-034-Q1-E1-H2
Method	BLASTX
NCBI GI	g2735841
BLAST score	141
E value	1.0e-08
Match length	74
% identity	47
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	124317
Contig ID	13802_1.R1010
5'-most EST	LIB3175-018-P1-K1-C5
Method	BLASTX
NCBI GI	g4559346
BLAST score	625
E value	3.0e-65
Match length	121
% identity	99
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	124318
Contig ID	13804_1.R1010
5'-most EST	LIB23-035-Q1-E1-B12
Method	BLASTN
NCBI GI	g4539309
BLAST score	336
E value	0.0e+00
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	124319
Contig ID	13805_1.R1010

5'-most EST	jC-atXLIB327425P3e11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	3.0e-30
Match length	76
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124320
Contig ID	13807_1.R1010
5'-most EST	jC-atXP39C160P23T7d1
Method	BLASTN
NCBI GI	g2564044
BLAST score	658
E value	0.0e+00
Match length	1011
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	124321
Contig ID	13814_1.R1010
5'-most EST	LIB23-062-Q1-E1-H3
Method	BLASTX
NCBI GI	g4678944
BLAST score	666
E value	5.0e-70
Match length	138
% identity	63
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	124322
Contig ID	13816_1.R1010
5'-most EST	jC-atXP95CG11F3T7022d1
Method	BLASTN
NCBI GI	g3193311
BLAST score	452
E value	0.0e+00
Match length	460
% identity	95
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	124323
Contig ID	13823_1.R1010
5'-most EST	jC-atXLIB327408P3h07b1
Method	BLASTX
NCBI GI	g2832616
BLAST score	401
E value	1.0e-38
Match length	134
% identity	63
NCBI Description	(AL021711) heat shock transcription factor - like protein [Arabidopsis thaliana]

Seq. No. 124324

Contig ID	13830_1.R1010
5'-most EST	LIB23-035-Q1-E112-A6
Seq. No.	124325
Contig ID	13839_1.R1010
5'-most EST	LIB23-035-Q1-E112-B7
Seq. No.	124326
Contig ID	13843_1.R1010
5'-most EST	LIB23-035-Q1-E112-C3
Method	BLASTN
NCBI GI	g2827698
BLAST score	350
E value	0.0e+00
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)
Seq. No.	124327
Contig ID	13843_2.R1010
5'-most EST	LIB25-011-Q1-E1-G5
Method	BLASTX
NCBI GI	g2827713
BLAST score	657
E value	6.0e-69
Match length	143
% identity	93
NCBI Description	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]
Seq. No.	124328
Contig ID	13853_1.R1010
5'-most EST	LIB3176-042-P1-K1-D12
Seq. No.	124329
Contig ID	13854_1.R1010
5'-most EST	LIB23-035-Q1-E112-D6
Seq. No.	124330
Contig ID	13856_1.R1010
5'-most EST	jC-atXP115C250F18T7061d1
Method	BLASTX
NCBI GI	g3786008
BLAST score	246
E value	2.0e-20
Match length	173
% identity	38
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	124331
Contig ID	13860_1.R1010
5'-most EST	jC-atXP85CG4D3T7b1
Method	BLASTN
NCBI GI	g4678340
BLAST score	87
E value	7.0e-41

Match length	256
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)

Seq. No.	124332
Contig ID	13864_1.R1010
5'-most EST	jC-atXP73CF3A10T7d2
Method	BLASTX
NCBI GI	g4091804
BLAST score	286
E value	5.0e-25
Match length	142
% identity	51
NCBI Description	(AF052584) CONSTANS-like protein 1 [Malus domestica]

Seq. No.	124333
Contig ID	13864_2.R1010
5'-most EST	jC-atXP100CE3F1T7b1
Method	BLASTX
NCBI GI	g4557093
BLAST score	268
E value	4.0e-23
Match length	106
% identity	57
NCBI Description	(AF001136) zinc finger protein [Pinus radiata]

Seq. No.	124334
Contig ID	13864_3.R1010
5'-most EST	jC-atXP75C225K13T7d1
Method	BLASTX
NCBI GI	g4091806
BLAST score	396
E value	3.0e-38
Match length	185
% identity	46
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	124335
Contig ID	13864_8.R1010
5'-most EST	LIB23-035-Q1-E112-F1
Method	BLASTX
NCBI GI	g4091806
BLAST score	248
E value	4.0e-21
Match length	79
% identity	63
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	124336
Contig ID	13868_1.R1010
5'-most EST	LIB23-035-Q1-E112-F6
Method	BLASTX
NCBI GI	g1934730
BLAST score	523
E value	2.0e-53
Match length	121

% identity	81
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	124337
Contig ID	13873_1.R1010
5'-most EST	jC-atX24022Q1E1H02b1
Method	BLASTX
NCBI GI	g3738327
BLAST score	526
E value	1.0e-98
Match length	321
% identity	56
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	124338
Contig ID	13877_1.R1010
5'-most EST	LIB24-074-Q1-E1-B8
Method	BLASTX
NCBI GI	g2213590
BLAST score	497
E value	3.0e-50
Match length	150
% identity	64
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	124339
Contig ID	13879_1.R1010
5'-most EST	LIB23-035-Q1-E112-H3
Method	BLASTX
NCBI GI	g3152605
BLAST score	608
E value	3.0e-63
Match length	124
% identity	100
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124340
Contig ID	13882_1.R1010
5'-most EST	LIB23-035-Q1-E112-H7

Seq. No.	124341
Contig ID	13884_1.R1010
5'-most EST	jC-atXLIB327403P3g08b1
Method	BLASTX
NCBI GI	g2129640
BLAST score	881
E value	6.0e-95
Match length	215
% identity	81
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	124342
Contig ID	13884_2.R1010
5'-most EST	jC-atXLIB327421P3h10b1

Method	BLASTX
NCBI GI	g2129640
BLAST score	1234
E value	1.0e-136
Match length	246
% identity	98
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	124343
Contig ID	13884_3.R1010
5'-most EST	g2749632
Method	BLASTX
NCBI GI	g2129640
BLAST score	469
E value	9.0e-47
Match length	91
% identity	99
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	124344
Contig ID	13884_4.R1010
5'-most EST	g398668
Method	BLASTX
NCBI GI	g2129640
BLAST score	169
E value	4.0e-68
Match length	152
% identity	97
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	124345
Contig ID	13884_5.R1010
5'-most EST	LIB3176-028-P1-K1-C9
Method	BLASTX
NCBI GI	g2129640
BLAST score	1207
E value	1.0e-133
Match length	299
% identity	85
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	124346
Contig ID	13889_1.R1010
5'-most EST	LIB23-036-Q1-E1-A5
Method	BLASTX
NCBI GI	g3128191
BLAST score	1047
E value	1.0e-114
Match length	191

% identity	99
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	124347
Contig ID	13892_1.R1010
5'-most EST	LIB23-036-Q1-E1-A9
Method	BLASTX
NCBI GI	g2459445
BLAST score	473
E value	2.0e-47
Match length	91
% identity	54
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	124348
Contig ID	13903_1.R1010
5'-most EST	jC-alXLIB327434P3f02b1
Method	BLASTN
NCBI GI	g4757392
BLAST score	361
E value	0.0e+00
Match length	739
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	124349
Contig ID	13905_1.R1010
5'-most EST	jC-atXLIB327422P2d09b2
Method	BLASTX
NCBI GI	g3075397
BLAST score	1056
E value	1.0e-115
Match length	198
% identity	100
NCBI Description	(AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124350
Contig ID	13907_1.R1010
5'-most EST	LIB23-036-Q1-E1-C2
Method	BLASTX
NCBI GI	g3451071
BLAST score	628
E value	1.0e-65
Match length	138
% identity	93
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	124351
Contig ID	13915_2.R1010
5'-most EST	LIB23-036-Q1-E1-D1

Seq. No.	124352
Contig ID	13916_1.R1010
5'-most EST	LIB24-123-Q1-E1-D6

Method	BLASTN
NCBI GI	g3985952
BLAST score	607
E value	0.0e+00
Match length	631
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	124353
Contig ID	13930_1.R1010
5'-most EST	jC-atXLIB327415P3d04b1
Method	BLASTN
NCBI GI	g2832667
BLAST score	427
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	124354
Contig ID	13938_1.R1010
5'-most EST	LIB3176-074-P1-K1-H12
Method	BLASTX
NCBI GI	g3236242
BLAST score	492
E value	1.0e-49
Match length	112
% identity	89
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	124355
Contig ID	13938_2.R1010
5'-most EST	g2597584
Method	BLASTX
NCBI GI	g3236242
BLAST score	467
E value	1.0e-46
Match length	106
% identity	91
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	124356
Contig ID	13938_3.R1010
5'-most EST	LIB25-041-Q1-E1-D3
Method	BLASTX
NCBI GI	g3236242
BLAST score	557
E value	2.0e-57
Match length	113
% identity	100
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	124357
Contig ID	13941_1.R1010
5'-most EST	jC-atXLIB327409P1a07b1
Method	BLASTX
NCBI GI	g3335337
BLAST score	631
E value	1.0e-65
Match length	126
% identity	100
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No.	124358
Contig ID	13943_1.R1010
5'-most EST	LIB3176-064-P1-K1-B7
Method	BLASTX
NCBI GI	g461550
BLAST score	803
E value	2.0e-89
Match length	234
% identity	78
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	124359
Contig ID	13945_1.R1010
5'-most EST	LIB3168-073-P1-K1-A6
Method	BLASTX
NCBI GI	g2388582
BLAST score	467
E value	1.0e-46
Match length	94
% identity	97
NCBI Description	(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No.	124360
Contig ID	13948_1.R1010
5'-most EST	g2762781
Method	BLASTX
NCBI GI	g4467099
BLAST score	590
E value	4.0e-61
Match length	130
% identity	90
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	124361
Contig ID	13948_2.R1010
5'-most EST	jC-atXLIB327421P1a02b1

Method	BLASTX
NCBI GI	g4467099
BLAST score	457
E value	4.0e-47
Match length	99
% identity	100
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	124362
Contig ID	13949_1.R1010
5'-most EST	g2749307
Method	BLASTN
NCBI GI	g4512690
BLAST score	383
E value	0.0e+00
Match length	433
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	124363
Contig ID	13952_1.R1010
5'-most EST	LIB24-089-Q1-E1-F3
Method	BLASTX
NCBI GI	g4633656
BLAST score	250
E value	3.0e-21
Match length	117
% identity	46
NCBI Description	(AF123263) phenylalanyl tRNA synthetase beta subunit [Mus musculus]

Seq. No.	124364
Contig ID	13958_1.R1010
5'-most EST	LIB24-085-Q1-E1-B6
Method	BLASTX
NCBI GI	g3287270
BLAST score	1308
E value	1.0e-145
Match length	356
% identity	71
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	124365
Contig ID	13966_1.R1010
5'-most EST	g937375
Method	BLASTX
NCBI GI	g4049349
BLAST score	508
E value	3.0e-51
Match length	122
% identity	86
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No. 124366

Contig ID	13966_2.R1010
5'-most EST	jC-atXP91C247C5T7b1
Method	BLASTX
NCBI GI	g4049349
BLAST score	449
E value	3.0e-44
Match length	116
% identity	81
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	124367
Contig ID	13970_1.R1010
5'-most EST	jC-atXLIB327405P2g03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	5.0e-13
Match length	76
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124368
Contig ID	13974_1.R1010
5'-most EST	jC-atXP73C223K20T7d2
Method	BLASTX
NCBI GI	g1168977
BLAST score	289
E value	1.0e-25
Match length	98
% identity	60
NCBI Description	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (ENDOPEPTIDASE CLP) >gi_1073886_pir__D64088 ATP-dependent proteinase clpP (proteolytic component) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1573716 (U32754) ATP-dependent Clp protease, proteolytic subunit (clpP) [Haemophilus influenzae Rd]

Seq. No.	124369
Contig ID	13979_1.R1010
5'-most EST	LIB23-037-Q1-E1-A7
Method	BLASTX
NCBI GI	g4006848
BLAST score	672
E value	2.0e-70
Match length	209
% identity	63
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	124370
Contig ID	13980_1.R1010
5'-most EST	LIB23-038-Q1-E1-B4
Method	BLASTN
NCBI GI	g2262097
BLAST score	351

E value	0.0e+00
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	124371
Contig ID	13983_1.R1010
5'-most EST	jC-atXLIB327404P2g11b1
Method	BLASTX
NCBI GI	g2842491
BLAST score	195
E value	1.0e-14
Match length	111
% identity	41
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	124372
Contig ID	13989_1.R1010
5'-most EST	jC-atXLIB327408P1f09b1
Method	BLASTN
NCBI GI	g3510336
BLAST score	226
E value	1.0e-124
Match length	480
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	124373
Contig ID	13989_2.R1010
5'-most EST	LIB23-037-Q1-E1-B7
Method	BLASTN
NCBI GI	g3510336
BLAST score	98
E value	1.0e-47
Match length	241
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	124374
Contig ID	13996_1.R1010
5'-most EST	LIB24-070-Q1-E1-E10
Method	BLASTX
NCBI GI	g4741197
BLAST score	609
E value	2.0e-63
Match length	117
% identity	100
NCBI Description	(AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	124375
Contig ID	14001_1.R1010
5'-most EST	jC-atXP19C111J24T7d2
Method	BLASTX

NCBI GI	g2662377
BLAST score	366
E value	1.0e-34
Match length	150
% identity	48
NCBI Description	(D89063) oligosaccharyltransferase [Mus musculus]

Seq. No.	124376
Contig ID	14002_1.R1010
5'-most EST	g907133
Method	BLASTN
NCBI GI	g2924733
BLAST score	400
E value	0.0e+00
Match length	471
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	124377
Contig ID	14009_1.R1010
5'-most EST	jC-atX23026Q1E1E05a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	333
E value	0.0e+00
Match length	367
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	124378
Contig ID	14011_1.R1010
5'-most EST	jC-atXP24C123M11T7055d1

Seq. No.	124379
Contig ID	14011_3.R1010
5'-most EST	g2576803
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	61
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	124380
Contig ID	14012_1.R1010
5'-most EST	jC-atXLIB327408P4d06b1
Method	BLASTN
NCBI GI	g3763944
BLAST score	314
E value	1.0e-176
Match length	814
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	124381
Contig ID	14012_2.R1010
5'-most EST	g2733206
Method	BLASTX
NCBI GI	g2911047
BLAST score	549
E value	2.0e-56
Match length	116
% identity	96
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	124382
Contig ID	14026_1.R1010
5'-most EST	LIB24-038-Q1-E1-A1
Method	BLASTX
NCBI GI	g4006860
BLAST score	1217
E value	1.0e-134
Match length	261
% identity	91
NCBI Description	(Z99707) thiol-disulfide interchange like protein [Arabidopsis thaliana]

Seq. No.	124383
Contig ID	14027_1.R1010
5'-most EST	jC-atXP71C221J1T7s2
Method	BLASTN
NCBI GI	g4191760
BLAST score	351
E value	0.0e+00
Match length	501
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	124384
Contig ID	14030_1.R1010
5'-most EST	jC-atX35008Q1E1H12b1
Method	BLASTN
NCBI GI	g4415928
BLAST score	47
E value	3.0e-17
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124385
Contig ID	14034_1.R1010
5'-most EST	jC-atXP89C245D3T7032d1
Method	BLASTX
NCBI GI	g3914442
BLAST score	503
E value	9.0e-51
Match length	145
% identity	69

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	124386
Contig ID	14034_2.R1010
5'-most EST	jC-atXP34C150M14T7d1
Method	BLASTX
NCBI GI	g407355
BLAST score	373
E value	2.0e-35
Match length	96
% identity	71
NCBI Description	(D21055) PSI-H precursor [Nicotiana sylvestris]

Seq. No.	124387
Contig ID	14034_3.R1010
5'-most EST	jC-atXP108C181L2T7007d1
Method	BLASTX
NCBI GI	g3914442
BLAST score	545
E value	1.0e-55
Match length	145
% identity	75
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	124388
Contig ID	14034_5.R1010
5'-most EST	jC-atXP100CE3F8T7b1
Method	BLASTX
NCBI GI	g3914442
BLAST score	352
E value	4.0e-33
Match length	90
% identity	76
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	124389
Contig ID	14034_6.R1010
5'-most EST	LIB3177-081-P1-K1-G10
Method	BLASTX
NCBI GI	g3914442
BLAST score	56
E value	6.0e-34
Match length	140
% identity	55
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	124390
Contig ID	14035_1.R1010
5'-most EST	g510781

Seq. No.	124391
Contig ID	14037_1.R1010
5'-most EST	LIB3176-118-P2-K1-C10
Method	BLASTX
NCBI GI	g3080393
BLAST score	1050
E value	1.0e-114
Match length	295
% identity	74
NCBI Description	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	124392
Contig ID	14046_1.R1010
5'-most EST	LIB23-037-Q1-E1-H1
Method	BLASTX
NCBI GI	g4538929
BLAST score	377
E value	5.0e-36
Match length	157
% identity	49
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	124393
Contig ID	14056_1.R1010
5'-most EST	jC-atXP89CG6D10T7038d1
Method	BLASTX
NCBI GI	g4099090
BLAST score	160
E value	1.0e-10
Match length	79
% identity	52
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	124394
Contig ID	14056_2.R1010
5'-most EST	LIB25-029-Q1-E1-C8

Seq. No.	124395
Contig ID	14057_1.R1010
5'-most EST	jC-atXLIB327408P1g02b1
Method	BLASTN
NCBI GI	g4589411
BLAST score	265
E value	1.0e-147
Match length	455
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F5H8, complete sequence

Seq. No.	124396
Contig ID	14057_2.R1010
5'-most EST	g315513
Method	BLASTX
NCBI GI	g129960

BLAST score	221
E value	7.0e-18
Match length	92
% identity	46
NCBI Description	4-NITROPHENYLPHOSPHATASE (PNPPASE)

Seq. No.	124397
Contig ID	14060_1.R1010
5'-most EST	jC-atXP33C151A15T7d2
Method	BLASTX
NCBI GI	g1483222
BLAST score	501
E value	1.0e-50
Match length	141
% identity	81
NCBI Description	(X99097) peroxidase [Arabidopsis thaliana]

Seq. No.	124398
Contig ID	14060_2.R1010
5'-most EST	g507015
Method	BLASTX
NCBI GI	g1483222
BLAST score	785
E value	7.0e-84
Match length	157
% identity	97
NCBI Description	(X99097) peroxidase [Arabidopsis thaliana]

Seq. No.	124399
Contig ID	14065_1.R1010
5'-most EST	jC-atXLIB327415P1c04b1
Method	BLASTX
NCBI GI	g3036808
BLAST score	565
E value	8.0e-66
Match length	134
% identity	98
NCBI Description	(AL022373) DnaJ-like protein [Arabidopsis thaliana]

Seq. No.	124400
Contig ID	14065_2.R1010
5'-most EST	g1269393
Method	BLASTX
NCBI GI	g3036808
BLAST score	326
E value	1.0e-67
Match length	134
% identity	99
NCBI Description	(AL022373) DnaJ-like protein [Arabidopsis thaliana]

Seq. No.	124401
Contig ID	14066_1.R1010
5'-most EST	jC-atXLIB327414P2c04a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	508
E value	0.0e+00

Match length	508
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	124402
Contig ID	14067_1.R1010
5'-most EST	LIB25-069-Q1-E1-D12
Method	BLASTN
NCBI GI	g3702735
BLAST score	246
E value	1.0e-136
Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	124403
Contig ID	14071_1.R1010
5'-most EST	jC-atXLIB327421P3c04b1
Method	BLASTN
NCBI GI	g3128142
BLAST score	389
E value	0.0e+00
Match length	717
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	124404
Contig ID	14071_2.R1010
5'-most EST	g2048168
Method	BLASTN
NCBI GI	g3128142
BLAST score	312
E value	1.0e-175
Match length	328
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	124405
Contig ID	14071_3.R1010
5'-most EST	g957646
Method	BLASTN
NCBI GI	g3128142
BLAST score	360
E value	0.0e+00
Match length	472
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	124406
Contig ID	14071_4.R1010
5'-most EST	g1520883
Method	BLASTN

NCBI GI	g3128142
BLAST score	319
E value	1.0e-179
Match length	323
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	124407
Contig ID	14073_1.R1010
5'-most EST	LIB3234-085-Q1-K1-F5
Method	BLASTX
NCBI GI	g3176874
BLAST score	1545
E value	1.0e-172
Match length	551
% identity	58
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	124408
Contig ID	14079_1.R1010
5'-most EST	LIB24-091-Q1-E1-H5

Seq. No.	124409
Contig ID	14082_1.R1010
5'-most EST	LIB25-110-Q1-E1-C7
Method	BLASTX
NCBI GI	g2832643
BLAST score	168
E value	6.0e-12
Match length	102
% identity	51
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124410
Contig ID	14086_1.R1010
5'-most EST	LIB23-038-Q1-E1-D10
Method	BLASTN
NCBI GI	g2351065
BLAST score	318
E value	1.0e-179
Match length	555
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	124411
Contig ID	14092_1.R1010
5'-most EST	LIB23-038-Q1-E1-D7

Seq. No.	124412
Contig ID	14093_1.R1010
5'-most EST	LIB23-038-Q1-E1-D9
Method	BLASTX
NCBI GI	g1931652
BLAST score	370

E value	3.0e-35
Match length	85
% identity	81
NCBI Description	(U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No.	124413
Contig ID	14101_1.R1010
5'-most EST	LIB3177-060-P1-K1-E4
Method	BLASTN
NCBI GI	g2351064
BLAST score	462
E value	0.0e+00
Match length	511
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	124414
Contig ID	14102_1.R1010
5'-most EST	jC-atXLIB327422P2f12b2
Method	BLASTN
NCBI GI	g2264314
BLAST score	283
E value	1.0e-158
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	124415
Contig ID	14105_1.R1010
5'-most EST	jC-atXLIB327421P2d05b1
Method	BLASTN
NCBI GI	g3643588
BLAST score	366
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124416
Contig ID	14106_1.R1010
5'-most EST	LIB23-038-Q1-E1-F1
Method	BLASTX
NCBI GI	g2492863
BLAST score	324
E value	6.0e-32
Match length	108
% identity	63
NCBI Description	ORNITHINE AMINOTRANSFERASE (ORNITHINE--OXO-ACID AMINOTRANSFERASE) >gi_4416517_gb_AAB18259_ (U74303) ornithine transaminase [Emericella nidulans]

Seq. No.	124417
Contig ID	14109_1.R1010

5'-most EST	ARABL1-039-Q1-B1-C11
Method	BLASTX
NCBI GI	g3540181
BLAST score	190
E value	5.0e-14
Match length	160
% identity	29
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	124418
Contig ID	14113_1.R1010
5'-most EST	LIB23-038-Q1-E1-F7
Method	BLASTN
NCBI GI	g3399678
BLAST score	314
E value	1.0e-176
Match length	322
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124419
Contig ID	14115_1.R1010
5'-most EST	jC-atXLIB327408P3g09b1
Method	BLASTX
NCBI GI	g3080415
BLAST score	632
E value	1.0e-136
Match length	357
% identity	69
NCBI Description	(AL022604) cysteine proteinase-like protein [Arabidopsis thaliana]

Seq. No.	124420
Contig ID	14116_1.R1010
5'-most EST	LIB23-038-Q1-E1-G1

Seq. No.	124421
Contig ID	14118_1.R1010
5'-most EST	jC-atXLIB327415P1d04b1
Method	BLASTN
NCBI GI	g2264306
BLAST score	42
E value	4.0e-14
Match length	74
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	124422
Contig ID	14126_1.R1010
5'-most EST	jC-alXLIB327434P1d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74

% identity 97
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 124423
Contig ID 14128_1.R1010
5'-most EST g3868953
Method BLASTX
NCBI GI g3953471
BLAST score 240
E value 6.0e-20
Match length 179
% identity 36
NCBI Description (AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No. 124424
Contig ID 14131_1.R1010
5'-most EST LIB3175-035-P1-K1-E4

Seq. No. 124425
Contig ID 14132_1.R1010
5'-most EST LIB23-038-Q1-E1-H6
Method BLASTX
NCBI GI g3859659
BLAST score 733
E value 5.0e-78
Match length 193
% identity 82
NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No. 124426
Contig ID 14136_1.R1010
5'-most EST jC-atXP38C158J6T7d1
Method BLASTX
NCBI GI g3650033
BLAST score 1697
E value 0.0e+00
Match length 369
% identity 92
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 124427
Contig ID 14137_1.R1010
5'-most EST jC-atXLIB327409P3c07b1
Method BLASTN
NCBI GI g2582640
BLAST score 48
E value 1.0e-17
Match length 60
% identity 95
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 124428
Contig ID 14139_1.R1010
5'-most EST jC-alXLIB327435P3d06b1

Method	BLASTX
NCBI GI	g4586111
BLAST score	470
E value	7.0e-47
Match length	149
% identity	62
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	124429
Contig ID	14140_1.R1010
5'-most EST	jC-alXLIB327435P3f10b1
Method	BLASTX
NCBI GI	g3024500
BLAST score	818
E value	4.0e-97
Match length	226
% identity	84
NCBI Description	RAS-RELATED PROTEIN RAB11A >gi_1370142_emb_CAA98177_ (Z73949) RAB11A [Lotus japonicus]

Seq. No.	124430
Contig ID	14155_1.R1010
5'-most EST	LIB23-039-Q1-E1-F9
Method	BLASTN
NCBI GI	g2980757
BLAST score	336
E value	0.0e+00
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	124431
Contig ID	14159_1.R1010
5'-most EST	jC-atXP112C129F10T7a1
Method	BLASTX
NCBI GI	g4741966
BLAST score	562
E value	2.0e-57
Match length	140
% identity	78
NCBI Description	(AF134133) Lil3 protein [Arabidopsis thaliana]

Seq. No.	124432
Contig ID	14159_2.R1010
5'-most EST	jC-atXP112C129F10T7d2
Method	BLASTX
NCBI GI	g2245118
BLAST score	1080
E value	1.0e-118
Match length	255
% identity	83
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124433
Contig ID	14159_3.R1010
5'-most EST	g2413116

Method	BLASTX
NCBI GI	g4741966
BLAST score	158
E value	2.0e-10
Match length	63
% identity	67
NCBI Description	(AF134133) Lil3 protein [Arabidopsis thaliana]

Seq. No.	124434
Contig ID	14159_4.R1010
5'-most EST	g1520834
Method	BLASTX
NCBI GI	g2245118
BLAST score	475
E value	2.0e-47
Match length	125
% identity	76
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124435
Contig ID	14159_5.R1010
5'-most EST	g1103333
Method	BLASTN
NCBI GI	g2245073
BLAST score	141
E value	2.0e-73
Match length	221
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	124436
Contig ID	14167_1.R1010
5'-most EST	LIB25-035-Q1-E1-D12
Method	BLASTX
NCBI GI	g3184082
BLAST score	411
E value	5.0e-40
Match length	153
% identity	48
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	124437
Contig ID	14168_1.R1010
5'-most EST	jC-atXLIB327419P4b09b1
Method	BLASTX
NCBI GI	g2828296
BLAST score	865
E value	5.0e-93
Match length	168
% identity	53
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	124438
Contig ID	14168_2.R1010
5'-most EST	LIB23-040-Q1-E1-A7

Method	BLASTX
NCBI GI	g2828296
BLAST score	1054
E value	1.0e-115
Match length	246
% identity	47
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	124439
Contig ID	14171_1.R1010
5'-most EST	LIB3234-058-P1-K1-H12

Seq. No.	124440
Contig ID	14173_1.R1010
5'-most EST	LIB23-040-Q1-E1-A8
Method	BLASTX
NCBI GI	g2492603
BLAST score	178
E value	3.0e-12
Match length	245
% identity	24
NCBI Description	WHITE PROTEIN HOMOLOG >gi_1107730_emb_CAA88636_ (Z48745) ABC8 [Mus musculus] >gi_1314279 (U34920) white homolog [Mus musculus]

Seq. No.	124441
Contig ID	14176_1.R1010
5'-most EST	LIB23-040-Q1-E1-B2
Method	BLASTN
NCBI GI	g1946354
BLAST score	328
E value	0.0e+00
Match length	365
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	124442
Contig ID	14180_1.R1010
5'-most EST	LIB23-040-Q1-E1-C10
Method	BLASTN
NCBI GI	g3128143
BLAST score	189
E value	1.0e-102
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	124443
Contig ID	14181_1.R1010
5'-most EST	LIB25-098-Q1-E1-A5
Method	BLASTX
NCBI GI	g2146740
BLAST score	484
E value	9.0e-49
Match length	109

% identity	84
NCBI Description	inner mitochondrial membrane protein - Arabidopsis thaliana >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No.	124444
Contig ID	14183_1.R1010
5'-most EST	jC-atXLIB327430P2e12b1
Method	BLASTN
NCBI GI	g2924731
BLAST score	352
E value	0.0e+00
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSI17, complete sequence [Arabidopsis thaliana]

Seq. No.	124445
Contig ID	14186_1.R1010
5'-most EST	LIB3177-005-P1-K2-E9
Method	BLASTN
NCBI GI	g3643588
BLAST score	453
E value	0.0e+00
Match length	469
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124446
Contig ID	14187_1.R1010
5'-most EST	jC-atXLIB327423P1b08b1
Method	BLASTX
NCBI GI	g4587543
BLAST score	715
E value	2.0e-75
Match length	186
% identity	75
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. EST gb_AB015099 comes from this gene. [Arabidopsis thaliana]

Seq. No.	124447
Contig ID	14191_1.R1010
5'-most EST	g906707
Method	BLASTN
NCBI GI	g2160155
BLAST score	181
E value	5.0e-97
Match length	539
% identity	98
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	124448
Contig ID	14192_1.R1010
5'-most EST	LIB25-039-Q1-E1-D7

Method	BLASTX
NCBI GI	g4115377
BLAST score	840
E value	4.0e-90
Match length	205
% identity	77
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	124449
Contig ID	14200_1.R1010
5'-most EST	jC-atXP73C223I3T7b1
Method	BLASTX
NCBI GI	g1323704
BLAST score	278
E value	3.0e-24
Match length	205
% identity	35
NCBI Description	(U55387) similar to C. elegans F38E1.9 gene product encoded by GenBank Accession Number U41996 [Cricetulus griseus]

Seq. No.	124450
Contig ID	14203_1.R1010
5'-most EST	jC-atXLIB327421P4g02b1
Method	BLASTX
NCBI GI	g4101574
BLAST score	198
E value	6.0e-15
Match length	129
% identity	36
NCBI Description	(AF004876) 54TMp [Homo sapiens]

Seq. No.	124451
Contig ID	14218_1.R1010
5'-most EST	LIB25-040-Q1-E1-H6
Method	BLASTX
NCBI GI	g2622711
BLAST score	147
E value	4.0e-09
Match length	47
% identity	55
NCBI Description	(AE000918) ferripyochelin binding protein [Methanobacterium thermoautotrophicum]

Seq. No.	124452
Contig ID	14220_1.R1010
5'-most EST	LIB23-040-Q1-E1-G5
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	124453
Contig ID	14222_1.R1010
5'-most EST	jC-atXLIB327418P3b11b1

Method	BLASTX
NCBI GI	g2982466
BLAST score	349
E value	1.0e-32
Match length	76
% identity	89
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	124454
Contig ID	14222_2.R1010
5'-most EST	LIB23-040-Q1-E1-G7
Method	BLASTX
NCBI GI	g4204263
BLAST score	177
E value	6.0e-13
Match length	45
% identity	71
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	124455
Contig ID	14225_1.R1010
5'-most EST	jC-atXLIB327405P2b06b2
Method	BLASTX
NCBI GI	g2829920
BLAST score	297
E value	5.0e-57
Match length	195
% identity	68
NCBI Description	(AC002291) Similar to 'MADS box' transcription factors [Arabidopsis thaliana]

Seq. No.	124456
Contig ID	14225_2.R1010
5'-most EST	g2762514
Method	BLASTX
NCBI GI	g2829920
BLAST score	437
E value	4.0e-43
Match length	133
% identity	72
NCBI Description	(AC002291) Similar to 'MADS box' transcription factors [Arabidopsis thaliana]

Seq. No.	124457
Contig ID	14225_3.R1010
5'-most EST	LIB25-027-Q1-E1-D7
Method	BLASTX
NCBI GI	g4469408
BLAST score	236
E value	9.0e-20
Match length	81
% identity	59
NCBI Description	(AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana]

Seq. No.	124458

Contig ID	14236_1.R1010
5'-most EST	g2597770
Seq. No.	124459
Contig ID	14238_1.R1010
5'-most EST	LIB35-024-Q1-E1-B10
Seq. No.	124460
Contig ID	14240_1.R1010
5'-most EST	LIB23-041-Q1-E1-B4
Method	BLASTX
NCBI GI	g2462837
BLAST score	285
E value	1.0e-25
Match length	111
% identity	55
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.	124461
Contig ID	14241_1.R1010
5'-most EST	LIB3176-089-P1-K1-F8
Method	BLASTN
NCBI GI	g3702734
BLAST score	200
E value	1.0e-108
Match length	725
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.	124462
Contig ID	14250_1.R1010
5'-most EST	LIB24-033-Q1-E1-A2
Seq. No.	124463
Contig ID	14253_1.R1010
5'-most EST	LIB23-041-Q1-E1-D1
Method	BLASTX
NCBI GI	g2459445
BLAST score	299
E value	7.0e-27
Match length	94
% identity	30
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]
Seq. No.	124464
Contig ID	14258_1.R1010
5'-most EST	LIB35-027-Q1-E1-B9
Seq. No.	124465
Contig ID	14265_1.R1010
5'-most EST	LIB23-041-Q1-E1-E12
Method	BLASTX
NCBI GI	g2829911
BLAST score	427
E value	4.0e-42

Match length	116
% identity	72
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	124466
Contig ID	14274_1.R1010
5'-most EST	LIB25-061-Q1-E1-G6
Method	BLASTX
NCBI GI	g4539419
BLAST score	483
E value	2.0e-48
Match length	119
% identity	82
NCBI Description	(AL049171) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	124467
Contig ID	14280_1.R1010
5'-most EST	jC-atXLIB327408P2h01b1
Method	BLASTN
NCBI GI	g3643588
BLAST score	793
E value	0.0e+00
Match length	1400
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124468
Contig ID	14283_1.R1010
5'-most EST	LIB3234-054-P1-K1-D2
Method	BLASTX
NCBI GI	g4115931
BLAST score	666
E value	5.0e-70
Match length	159
% identity	81
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	124469
Contig ID	14288_1.R1010
5'-most EST	LIB25-082-Q1-E1-G12
Method	BLASTN
NCBI GI	g3513725
BLAST score	332
E value	0.0e+00
Match length	399
% identity	96
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	124470
Contig ID	14299_1.R1010
5'-most EST	jC-atXP55C187E2T7d2
Method	BLASTX
NCBI GI	g3582342
BLAST score	1513

E value	1.0e-169
Match length	305
% identity	95
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	124471
Contig ID	14305_1.R1010
5'-most EST	g936085
Method	BLASTX
NCBI GI	g2062156
BLAST score	283
E value	6.0e-25
Match length	125
% identity	17
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	124472
Contig ID	14311_1.R1010
5'-most EST	LIB25-094-Q1-E1-F4

Seq. No.	124473
Contig ID	14314_1.R1010
5'-most EST	jC-atXP90C245M8T7d2
Method	BLASTX
NCBI GI	g2467274
BLAST score	337
E value	4.0e-31
Match length	157
% identity	52
NCBI Description	(Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	124474
Contig ID	14318_1.R1010
5'-most EST	LIB23-042-Q1-E1-C3

Seq. No.	124475
Contig ID	14325_1.R1010
5'-most EST	g2733651
Method	BLASTX
NCBI GI	g3738336
BLAST score	371
E value	2.0e-35
Match length	120
% identity	66
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	124476
Contig ID	14327_1.R1010
5'-most EST	LIB23-042-Q1-E1-D12
Method	BLASTN
NCBI GI	g4519188
BLAST score	257
E value	1.0e-142
Match length	458
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	124477
Contig ID	14332_1.R1010
5'-most EST	LIB23-042-Q1-E1-D7
Method	BLASTX
NCBI GI	g266936
BLAST score	376
E value	3.0e-36
Match length	111
% identity	71
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	124478
Contig ID	14339_1.R1010
5'-most EST	LIB3175-052-P1-K1-A2

Seq. No.	124479
Contig ID	14341_1.R1010
5'-most EST	LIB23-042-Q1-E1-E6
Method	BLASTX
NCBI GI	g4455322
BLAST score	805
E value	1.0e-98
Match length	206
% identity	87
NCBI Description	(AL035525) putative protein kinase [Arabidopsis thaliana]

Seq. No.	124480
Contig ID	14352_1.R1010
5'-most EST	ARABL1-02-Q1-B1-E8
Method	BLASTX
NCBI GI	g4559369
BLAST score	796
E value	7.0e-88
Match length	185
% identity	89
NCBI Description	(AC006585) putative Rieske iron-sulfur protein [Arabidopsis thaliana]

Seq. No.	124481
Contig ID	14356_1.R1010
5'-most EST	jC-atXLIB327418P1g10b1
Method	BLASTX
NCBI GI	g2739168
BLAST score	467
E value	2.0e-46
Match length	177
% identity	49
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	124482
Contig ID	14358_1.R1010
5'-most EST	jC-atXLIB327407P1a09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	7.0e-22
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124483
Contig ID	14360_1.R1010
5'-most EST	LIB3176-088-P1-K1-D12
Method	BLASTX
NCBI GI	g4630748
BLAST score	343
E value	2.0e-32
Match length	80
% identity	79
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	124484
Contig ID	14362_1.R1010
5'-most EST	LIB23-042-Q1-E1-G9

Seq. No.	124485
Contig ID	14363_1.R1010
5'-most EST	g949626
Method	BLASTX
NCBI GI	g2213584
BLAST score	672
E value	1.0e-70
Match length	132
% identity	98
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	124486
Contig ID	14364_1.R1010
5'-most EST	LIB23-042-Q1-E1-H10
Method	BLASTN
NCBI GI	g3241925
BLAST score	628
E value	0.0e+00
Match length	636
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	124487
Contig ID	14370_1.R1010
5'-most EST	LIB24-003-Q1-E1-D10
Method	BLASTN
NCBI GI	g3821780
BLAST score	35

E value 4.0e-10
Match length 35
% identity 59
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 124488
Contig ID 14373_1.R1010
5'-most EST LIB23-069-Q1-E1-G4
Method BLASTN
NCBI GI g3176701
BLAST score 79
E value 3.0e-36
Match length 115
% identity 92
NCBI Description Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 124489
Contig ID 14378_1.R1010
5'-most EST LIB23-043-Q1-E1-A3
Method BLASTN
NCBI GI g4587986
BLAST score 57
E value 3.0e-23
Match length 69
% identity 96
NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No. 124490
Contig ID 14379_1.R1010
5'-most EST jC-atXP19C109J8T7029a1

Seq. No. 124491
Contig ID 14379_2.R1010
5'-most EST LIB23-043-Q1-E1-A4

Seq. No. 124492
Contig ID 14379_3.R1010
5'-most EST g634513

Seq. No. 124493
Contig ID 14380_1.R1010
5'-most EST LIB23-043-Q1-E1-A5
Method BLASTX
NCBI GI g2492784
BLAST score 166
E value 1.0e-11
Match length 54
% identity 57
NCBI Description 2-ISOPROPYLMALATE SYNTHASE (ALPHA-ISOPROPYLMALATE SYNTHASE) (ALPHA-IPM SYNTHETASE) >gi_1770069_emb_CAA99531_ (Z75208) 2-isopropylmalate synthase [Bacillus subtilis] >gi_2635293_emb_CAB14788_ (Z99118) 2-isopropylmalate synthase [Bacillus subtilis]

Seq. No. 124494

Contig ID	14385_1.R1010
5'-most EST	g2756996
Method	BLASTX
NCBI GI	g4455312
BLAST score	804
E value	7.0e-86
Match length	197
% identity	80
NCBI Description	(AL035528) DnaJ-like protein [Arabidopsis thaliana]

Seq. No.	124495
Contig ID	14393_1.R1010
5'-most EST	g2413859
Method	BLASTN
NCBI GI	g2618604
BLAST score	231
E value	1.0e-127
Match length	488
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No.	124496
Contig ID	14393_2.R1010
5'-most EST	jC-atXmonuni26Dc08b1
Method	BLASTX
NCBI GI	g1706476
BLAST score	207
E value	3.0e-16
Match length	69
% identity	61
NCBI Description	DNAJ-LIKE PROTEIN SLR0093 >gi_1001729_dbj_BAA10566_ (D64004) DnaJ [Synechocystis sp.]

Seq. No.	124497
Contig ID	14394_1.R1010
5'-most EST	jC-alX24071Q1E1H04b1
Method	BLASTX
NCBI GI	g2558664
BLAST score	754
E value	2.0e-80
Match length	148
% identity	100
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124498
Contig ID	14396_1.R1010
5'-most EST	LIB3177-004-P1-K2-F7
Method	BLASTX
NCBI GI	g4510396
BLAST score	175
E value	2.0e-12
Match length	96
% identity	44
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No. 124499

Contig ID	14397_1.R1010
5'-most EST	LIB23-043-Q1-E1-C6
Method	BLASTX
NCBI GI	g4581856
BLAST score	678
E value	2.0e-72
Match length	236
% identity	66
NCBI Description	(AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Mentha x piperita]

Seq. No.	124500
Contig ID	14397_2.R1010
5'-most EST	jC-atXLIB327430P3d08b1
Method	BLASTN
NCBI GI	g2656029
BLAST score	125
E value	1.0e-63
Match length	379
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	124501
Contig ID	14400_1.R1010
5'-most EST	LIB3175-056-P1-K1-H9
Method	BLASTX
NCBI GI	g4587549
BLAST score	1552
E value	1.0e-173
Match length	390
% identity	76
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	124502
Contig ID	14407_1.R1010
5'-most EST	jC-atXLIB327431P1d11a1
Method	BLASTX
NCBI GI	g2827712
BLAST score	733
E value	7.0e-78
Match length	138
% identity	100
NCBI Description	(AL021684) endoxyloglucan tranferase-like protein [Arabidopsis thaliana]

Seq. No.	124503
Contig ID	14407_2.R1010
5'-most EST	jC-atXLIB327414P3a04a1
Method	BLASTX
NCBI GI	g2827712
BLAST score	568
E value	1.0e-58
Match length	110

% identity	100
NCBI Description	(AL021684) endoxyloglucan tranferase-like protein [Arabidopsis thaliana]

Seq. No.	124504
Contig ID	14410_1.R1010
5'-most EST	LIB3177-093-P1-K1-F6
Method	BLASTX
NCBI GI	g2245144
BLAST score	457
E value	3.0e-45
Match length	138
% identity	65
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	124505
Contig ID	14410_2.R1010
5'-most EST	jC-atXP46C173F21T7042a1
Method	BLASTX
NCBI GI	g2245144
BLAST score	270
E value	2.0e-23
Match length	117
% identity	50
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	124506
Contig ID	14410_3.R1010
5'-most EST	g2749259
Method	BLASTN
NCBI GI	g2243121
BLAST score	45
E value	7.0e-16
Match length	93
% identity	88
NCBI Description	Brassica juncea mRNA for O-acetylserine(thiol) lyase, clone OAS-TL5

Seq. No.	124507
Contig ID	14415_1.R1010
5'-most EST	LIB23-043-Q1-E1-E7
Method	BLASTN
NCBI GI	g4519193
BLAST score	317
E value	1.0e-178
Match length	457
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	124508
Contig ID	14427_1.R1010
5'-most EST	LIB23-043-Q1-E1-F9
Method	BLASTX
NCBI GI	g2911066
BLAST score	575
E value	2.0e-59

Match length	118
% identity	96
NCBI Description	(AL021960) adrenodoxin-like protein [Arabidopsis thaliana]

Seq. No.	124509
Contig ID	14429_1.R1010
5'-most EST	jC-atXLIB327415P4c12b1
Method	BLASTN
NCBI GI	g4734011
BLAST score	277
E value	1.0e-154
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24C20 genomic sequence, complete sequence

Seq. No.	124510
Contig ID	14433_1.R1010
5'-most EST	LIB3176-099-P1-K1-H2
Method	BLASTX
NCBI GI	g2982301
BLAST score	348
E value	6.0e-38
Match length	159
% identity	55
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	124511
Contig ID	14442_1.R1010
5'-most EST	LIB3168-058-P1-K1-C10
Method	BLASTX
NCBI GI	g3549670
BLAST score	463
E value	4.0e-53
Match length	111
% identity	100
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	124512
Contig ID	14451_1.R1010
5'-most EST	LIB24-063-Q1-E1-E7
Method	BLASTN
NCBI GI	g4220644
BLAST score	41
E value	1.0e-13
Match length	105
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	124513
Contig ID	14454_1.R1010
5'-most EST	LIB23-044-Q1-E2-A4
Method	BLASTN
NCBI GI	g2244829
BLAST score	175
E value	1.0e-93

Match length	301
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	124514
Contig ID	14457_1.R1010
5'-most EST	jC-atXP115C247A22T7049d1
Method	BLASTX
NCBI GI	g4218123
BLAST score	454
E value	6.0e-45
Match length	143
% identity	67
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	124515
Contig ID	14457_2.R1010
5'-most EST	jC-atXP115C248M12T7068d1
Method	BLASTX
NCBI GI	g4218123
BLAST score	448
E value	3.0e-44
Match length	143
% identity	66
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	124516
Contig ID	14457_3.R1010
5'-most EST	jC-atXLIB327414P1b07a1
Method	BLASTX
NCBI GI	g4218123
BLAST score	310
E value	5.0e-34
Match length	143
% identity	62
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	124517
Contig ID	14457_4.R1010
5'-most EST	g2414019
Method	BLASTX
NCBI GI	g4218123
BLAST score	303
E value	2.0e-27
Match length	109
% identity	65
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	124518
Contig ID	14457_5.R1010
5'-most EST	g2750042
Method	BLASTX

NCBI GI	g4218123
BLAST score	207
E value	1.0e-22
Match length	126
% identity	55
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	124519
Contig ID	14457_7.R1010
5'-most EST	jC-atX25021Q1E1G07b1
Method	BLASTN
NCBI GI	g4218109
BLAST score	437
E value	0.0e+00
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	124520
Contig ID	14461_1.R1010
5'-most EST	LIB23-044-Q1-E2-B4
Method	BLASTN
NCBI GI	g3046856
BLAST score	232
E value	1.0e-127
Match length	381
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	124521
Contig ID	14464_1.R1010
5'-most EST	LIB23-044-Q1-E2-C11

Seq. No.	124522
Contig ID	14467_1.R1010
5'-most EST	jC-atXLIB327422P1g03b1
Method	BLASTN
NCBI GI	g4325336
BLAST score	338
E value	0.0e+00
Match length	638
% identity	98
NCBI Description	Arabidopsis thaliana BAC F15P23

Seq. No.	124523
Contig ID	14468_1.R1010
5'-most EST	LIB23-044-Q1-E2-D1
Method	BLASTN
NCBI GI	g3241927
BLAST score	336
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	124524
Contig ID	14473_1.R1010
5'-most EST	LIB23-044-Q1-E1-E11
Method	BLASTX
NCBI GI	g2494266
BLAST score	260
E value	1.0e-22
Match length	57
% identity	89
NCBI Description	GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871_ (D90917) LepA [Synechocystis sp.]

Seq. No.	124525
Contig ID	14474_1.R1010
5'-most EST	LIB23-044-Q1-E2-E3

Seq. No.	124526
Contig ID	14478_1.R1010
5'-most EST	LIB23-044-Q1-E1-F9
Method	BLASTX
NCBI GI	g1362055
BLAST score	605
E value	1.0e-62
Match length	239
% identity	59
NCBI Description	phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - alfalfa >gi_603221 (U18239) 6-phosphogluconate dehydrogenase [Medicago sativa subsp. sativa]

Seq. No.	124527
Contig ID	14479_1.R1010
5'-most EST	LIB3234-078-P1-K1-C2
Method	BLASTN
NCBI GI	g4220468
BLAST score	318
E value	1.0e-179
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124528
Contig ID	14484_1.R1010
5'-most EST	jC-atXmonuni27Ba02b1
Method	BLASTN
NCBI GI	g3228389
BLAST score	162
E value	7.0e-86
Match length	313
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	124529
Contig ID	14485_1.R1010

5'-most EST	LIB23-044-Q1-E1-H11
Method	BLASTX
NCBI GI	g3859659
BLAST score	420
E value	2.0e-41
Match length	126
% identity	63
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	124530
Contig ID	14514_1.R1010
5'-most EST	LIB23-044-Q1-E2-E10

Seq. No.	124531
Contig ID	14523_1.R1010
5'-most EST	LIB23-044-Q1-E2-F2

Seq. No.	124532
Contig ID	14543_1.R1010
5'-most EST	LIB24-074-Q1-E1-A3
Method	BLASTX
NCBI GI	g3327870
BLAST score	329
E value	1.0e-30
Match length	104
% identity	64
NCBI Description	(AB012913) COP1-Interacting ProteinI 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	124533
Contig ID	14544_1.R1010
5'-most EST	LIB23-044-Q1-E2-H3
Method	BLASTN
NCBI GI	g4467094
BLAST score	225
E value	1.0e-123
Match length	289
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	124534
Contig ID	14546_1.R1010
5'-most EST	LIB23-044-Q1-E2-H6
Method	BLASTX
NCBI GI	g3152590
BLAST score	1121
E value	1.0e-123
Match length	228
% identity	98
NCBI Description	(AC002986) Similar to protein serine/threonine kinase NPK15 gb_D31737 from Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No.	124535
Contig ID	14554_1.R1010
5'-most EST	LIB23-047-Q1-E1-D8

Method	BLASTX
NCBI GI	g4689474
BLAST score	564
E value	3.0e-58
Match length	112
% identity	100
NCBI Description	(AC007213) unknown protein [Arabidopsis thaliana]

Seq. No.	124536
Contig ID	14556_1.R1010
5'-most EST	jC-atXLIB327422P3f03b2

Seq. No.	124537
Contig ID	14559_1.R1010
5'-most EST	LIB23-045-Q1-E1-B1
Method	BLASTX
NCBI GI	g4505499
BLAST score	116
E value	1.0e-05
Match length	119
% identity	55
NCBI Description	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) >gi_2266994 (U77413) O-linked GlcNAc transferase [Homo sapiens]

Seq. No.	124538
Contig ID	14561_1.R1010
5'-most EST	LIB3177-087-P1-K1-D6
Method	BLASTX
NCBI GI	g1363492
BLAST score	575
E value	2.0e-59
Match length	147
% identity	73
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.	124539
Contig ID	14565_1.R1010
5'-most EST	LIB25-039-Q1-E1-E9
Method	BLASTN
NCBI GI	g3702730
BLAST score	225
E value	1.0e-123
Match length	569
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence [Arabidopsis thaliana]

Seq. No.	124540
Contig ID	14569_1.R1010
5'-most EST	LIB24-083-Q1-E1-E4
Method	BLASTN
NCBI GI	g4544405

BLAST score	286
E value	1.0e-160
Match length	286
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	124541
Contig ID	14576_1.R1010
5'-most EST	LIB3175-061-P1-K1-B4
Method	BLASTX
NCBI GI	g2281635
BLAST score	336
E value	2.0e-31
Match length	135
% identity	62
NCBI Description	(AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]

Seq. No.	124542
Contig ID	14577_1.R1010
5'-most EST	g2748385

Seq. No.	124543
Contig ID	14578_1.R1010
5'-most EST	ARABL1-02-Q1-B1-H12
Method	BLASTX
NCBI GI	g4105131
BLAST score	144
E value	1.0e-08
Match length	113
% identity	35
NCBI Description	(AF043539) ClpC protease [Spinacia oleracea]

Seq. No.	124544
Contig ID	14579_1.R1010
5'-most EST	jC-atX24067Q1E1F04b1
Method	BLASTX
NCBI GI	g3152606
BLAST score	580
E value	7.0e-60
Match length	147
% identity	72
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	124545
Contig ID	14582_1.R1010
5'-most EST	jC-atXLIB327408P2c07b1
Method	BLASTX
NCBI GI	g2244865
BLAST score	149
E value	3.0e-09
Match length	70
% identity	40
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124546
Contig ID	14586_1.R1010
5'-most EST	LIB23-045-Q1-E1-D3
Method	BLASTX
NCBI GI	g4371282
BLAST score	762
E value	6.0e-81
Match length	152
% identity	99
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	124547
Contig ID	14586_2.R1010
5'-most EST	g2750094
Method	BLASTX
NCBI GI	g4371282
BLAST score	424
E value	2.0e-41
Match length	100
% identity	88
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	124548
Contig ID	14599_1.R1010
5'-most EST	jC-atXLIB327438P2c12a1
Method	BLASTX
NCBI GI	g4704730
BLAST score	274
E value	1.0e-23
Match length	140
% identity	38
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	124549
Contig ID	14600_1.R1010
5'-most EST	g2758767
Method	BLASTX
NCBI GI	g4210334
BLAST score	97
E value	1.0e-118
Match length	251
% identity	89
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	124550
Contig ID	14601_1.R1010
5'-most EST	LIB23-045-Q1-E1-E7
Method	BLASTN
NCBI GI	g2244747
BLAST score	127
E value	5.0e-65
Match length	437
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No.	124551
Contig ID	14609_1.R1010
5'-most EST	jC-atXLIB327423P4f09b1
Method	BLASTN
NCBI GI	g3128137
BLAST score	267
E value	1.0e-148
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	124552
Contig ID	14609_2.R1010
5'-most EST	LIB3176-050-P1-K1-F3
Method	BLASTN
NCBI GI	g3128137
BLAST score	281
E value	1.0e-157
Match length	416
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	124553
Contig ID	14610_1.R1010
5'-most EST	LIB23-045-Q1-E1-F5

Seq. No.	124554
Contig ID	14617_1.R1010
5'-most EST	g2749667
Method	BLASTX
NCBI GI	g4335724
BLAST score	519
E value	1.0e-52
Match length	93
% identity	99
NCBI Description	(AC006248) putative RING-H2 finger protein [Arabidopsis thaliana]

Seq. No.	124555
Contig ID	14617_2.R1010
5'-most EST	g906632
Method	BLASTN
NCBI GI	g4335711
BLAST score	344
E value	0.0e+00
Match length	598
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124556
Contig ID	14617_3.R1010
5'-most EST	jC-atXLIB327405P2g04b2

Method	BLASTN
NCBI GI	g4335711
BLAST score	192
E value	1.0e-103
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124557
Contig ID	14620_1.R1010
5'-most EST	LIB3176-033-P1-K1-H10
Method	BLASTX
NCBI GI	g16245
BLAST score	1149
E value	1.0e-126
Match length	264
% identity	88
NCBI Description	(X51514) precursor acetolactate synthase (670 AA) [Arabidopsis thaliana]

Seq. No.	124558
Contig ID	14632_1.R1010
5'-most EST	LIB3168-048-P1-K1-B6
Method	BLASTX
NCBI GI	g4651202
BLAST score	361
E value	2.0e-34
Match length	156
% identity	44
NCBI Description	(AB026253) copper amine oxidase [Pisum sativum]

Seq. No.	124559
Contig ID	14633_1.R1010
5'-most EST	LIB23-046-Q1-E1-A1
Method	BLASTX
NCBI GI	g2244913
BLAST score	206
E value	8.0e-68
Match length	287
% identity	80
NCBI Description	(Z97339) similar to SEN1 protein - yeast [Arabidopsis thaliana]

Seq. No.	124560
Contig ID	14635_1.R1010
5'-most EST	jC-atXP115C251D4T7078d1
Method	BLASTN
NCBI GI	g3264774
BLAST score	91
E value	3.0e-43
Match length	475
% identity	88
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 124561

Contig ID	14637_1.R1010
5'-most EST	LIB23-046-Q1-E1-A4
Method	BLASTX
NCBI GI	g3928758
BLAST score	182
E value	3.0e-13
Match length	53
% identity	55
NCBI Description	(AB007987) Lipoic acid synthase [Arabidopsis thaliana] >gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid synthase [Arabidopsis thaliana]

Seq. No.	124562
Contig ID	14638_1.R1010
5'-most EST	g2048730
Method	BLASTN
NCBI GI	g4539309
BLAST score	218
E value	1.0e-119
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	124563
Contig ID	14638_2.R1010
5'-most EST	jC-atXLIB327416P1c12b1
Method	BLASTX
NCBI GI	g4539323
BLAST score	932
E value	1.0e-114
Match length	295
% identity	75
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	124564
Contig ID	14638_3.R1010
5'-most EST	jC-atXLIB327425P3b10b1
Method	BLASTX
NCBI GI	g4539323
BLAST score	471
E value	3.0e-47
Match length	118
% identity	84
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	124565
Contig ID	14639_1.R1010
5'-most EST	LIB3234-008-P1-K1-H7
Method	BLASTX
NCBI GI	g2618688
BLAST score	1519
E value	1.0e-169
Match length	284
% identity	100
NCBI Description	(AC002510) putative esterase D [Arabidopsis thaliana]

Seq. No.	124566
Contig ID	14640_1.R1010
5'-most EST	LIB23-046-Q1-E1-A8
Method	BLASTX
NCBI GI	g131143
BLAST score	398
E value	9.0e-39
Match length	74
% identity	97
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi_72670_pir__A1NTP7 photosystem I P700 apoprotein A1 - common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044) PSI P700 apoprotein A1 [Nicotiana tabacum] >gi_225198_prf__1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum]

Seq. No.	124567
Contig ID	14642_1.R1010
5'-most EST	jC-alXLIB327436P1f06b1
Method	BLASTX
NCBI GI	g2388583
BLAST score	834
E value	2.0e-89
Match length	195
% identity	87
NCBI Description	(AC000098) Similar to Synechocystis hypothetical protein (gb_D90908). [Arabidopsis thaliana]

Seq. No.	124568
Contig ID	14644_1.R1010
5'-most EST	LIB23-046-Q1-E1-B2
Method	BLASTX
NCBI GI	g3184281
BLAST score	496
E value	4.0e-50
Match length	121
% identity	82
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	124569
Contig ID	14645_1.R1010
5'-most EST	LIB23-046-Q1-E1-B3
Method	BLASTX
NCBI GI	g2388581
BLAST score	419
E value	5.0e-41
Match length	75
% identity	99
NCBI Description	(AC000098) Similar to Zea DWARF3 (gb_U32579). [Arabidopsis thaliana]

Seq. No.	124570
Contig ID	14652_1.R1010
5'-most EST	LIB25-082-Q1-E1-H10

Seq. No.	124571
Contig ID	14654_1.R1010

5'-most EST	LIB23-046-Q1-E1-C12
Seq. No.	124572
Contig ID	14656_1.R1010
5'-most EST	g905787
Method	BLASTX
NCBI GI	g4538928
BLAST score	184
E value	4.0e-13
Match length	137
% identity	36
NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]
Seq. No.	124573
Contig ID	14660_1.R1010
5'-most EST	LIB23-046-Q1-E1-C8
Seq. No.	124574
Contig ID	14673_1.R1010
5'-most EST	jC-atXLIB327427P1c03b1
Method	BLASTX
NCBI GI	g2245109
BLAST score	675
E value	5.0e-71
Match length	130
% identity	100
NCBI Description	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]
Seq. No.	124575
Contig ID	14673_2.R1010
5'-most EST	LIB3176-042-P1-K1-A5
Method	BLASTX
NCBI GI	g3551425
BLAST score	177
E value	3.0e-12
Match length	181
% identity	32
NCBI Description	(AB015291) pyrrolidone carboxyl peptidase [Pyrococcus furiosus]
Seq. No.	124576
Contig ID	14680_1.R1010
5'-most EST	jC-atXLIB327423P2f07b1
Method	BLASTX
NCBI GI	g3687239
BLAST score	747
E value	2.0e-79
Match length	143
% identity	100
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]
Seq. No.	124577
Contig ID	14686_1.R1010
5'-most EST	LIB23-046-Q1-E1-F2
Method	BLASTN

NCBI GI g2494110
BLAST score 374
E value 0.0e+00
Match length 401
% identity 98
NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 124578
Contig ID 14698_1.R1010
5'-most EST g17500

Seq. No. 124579
Contig ID 14706_1.R1010
5'-most EST jC-atXLIB327424P4d05b1
Method BLASTN
NCBI GI g2828187
BLAST score 227
E value 1.0e-124
Match length 369
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No. 124580
Contig ID 14710_1.R1010
5'-most EST LIB23-046-Q1-E1-H8
Method BLASTN
NCBI GI g2244950
BLAST score 136
E value 2.0e-70
Match length 371
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 124581
Contig ID 14719_1.R1010
5'-most EST LIB23-047-Q1-E1-A7
Method BLASTN
NCBI GI g3449327
BLAST score 274
E value 1.0e-152
Match length 431
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 124582
Contig ID 14720_1.R1010
5'-most EST LIB23-047-Q1-E1-A8
Method BLASTX
NCBI GI g2842615
BLAST score 337
E value 2.0e-31
Match length 128
% identity 55

NCBI Description	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE) >gi_1359593_emb_CAA66607_ (X97964) aspartate-semialdehyde dehydrogenase [Campylobacter jejuni]

Seq. No.	124583
Contig ID	14727_1.R1010
5'-most EST	jC-atXLIB327429P4h05a2
Method	BLASTX
NCBI GI	g4314401
BLAST score	646
E value	1.0e-107
Match length	224
% identity	92
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	124584
Contig ID	14728_1.R1010
5'-most EST	jC-atXLIB327429P4g08a2
Method	BLASTX
NCBI GI	g4582441
BLAST score	220
E value	1.0e-17
Match length	94
% identity	55
NCBI Description	(AC007142) unknown protein [Arabidopsis thaliana]

Seq. No.	124585
Contig ID	14729_1.R1010
5'-most EST	LIB23-047-Q1-E1-B7
Method	BLASTX
NCBI GI	g4263527
BLAST score	289
E value	1.0e-25
Match length	129
% identity	43
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124586
Contig ID	14738_1.R1010
5'-most EST	jC-atXLIB327403P3b08b2

Seq. No.	124587
Contig ID	14747_1.R1010
5'-most EST	LIB25-014-Q1-E1-F4
Method	BLASTN
NCBI GI	g3046855
BLAST score	243
E value	1.0e-134
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	124588
Contig ID	14754_1.R1010
5'-most EST	LIB23-047-Q1-E1-E10

Method	BLASTX
NCBI GI	g1871174
BLAST score	369
E value	2.0e-46
Match length	122
% identity	75
NCBI Description	(U90439) actin isolog [Arabidopsis thaliana]

Seq. No.	124589
Contig ID	14755_1.R1010
5'-most EST	LIB23-047-Q1-E1-E11

Seq. No.	124590
Contig ID	14756_1.R1010
5'-most EST	ARABL1-07-Q1-B1-H3
Method	BLASTX
NCBI GI	g130261
BLAST score	781
E value	2.0e-83
Match length	171
% identity	92
NCBI Description	PLASTOCYANIN PRECURSOR >gi_65841_pir__CUMUM plastocyanin precursor - Arabidopsis thaliana >gi_166790 (M20937) plastocyanin [Arabidopsis thaliana]

Seq. No.	124591
Contig ID	14758_1.R1010
5'-most EST	jC-atXLIB327418P3e04b1
Method	BLASTX
NCBI GI	g3603011
BLAST score	119
E value	2.0e-05
Match length	234
% identity	53
NCBI Description	(AF041468) elongation factor Ts [Guillardia theta]

Seq. No.	124592
Contig ID	14761_1.R1010
5'-most EST	LIB25-008-Q1-E1-A4
Method	BLASTX
NCBI GI	g2979559
BLAST score	342
E value	5.0e-32
Match length	80
% identity	80
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	124593
Contig ID	14765_1.R1010
5'-most EST	LIB23-047-Q1-E1-F11
Method	BLASTX
NCBI GI	g872116
BLAST score	247
E value	5.0e-21
Match length	125
% identity	15

NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	124594
Contig ID	14772_1.R1010
5'-most EST	jC-atXLIB327423P2d05b1
Method	BLASTX
NCBI GI	g4249386
BLAST score	641
E value	6.0e-67
Match length	145
% identity	88
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	124595
Contig ID	14773_1.R1010
5'-most EST	jC-alXLIB327436P4e11b1
Method	BLASTX
NCBI GI	g2501555
BLAST score	225
E value	4.0e-18
Match length	79
% identity	56
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	124596
Contig ID	14777_1.R1010
5'-most EST	jC-atXP115C124I15T7072d1
Method	BLASTN
NCBI GI	g2924651
BLAST score	513
E value	0.0e+00
Match length	517
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	124597
Contig ID	14777_3.R1010
5'-most EST	jC-atXLIB327403P3c12a2
Method	BLASTN
NCBI GI	g2924651
BLAST score	815
E value	0.0e+00
Match length	815
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	124598
Contig ID	14780_1.R1010
5'-most EST	jC-alXLIB327436P1g07b1
Method	BLASTX
NCBI GI	g549977
BLAST score	477

E value 7.0e-48
Match length 129
% identity 74
NCBI Description (U12859) cDNA-5-encoded protein [Arabidopsis thaliana]

Seq. No. 124599
Contig ID 14780_2.R1010
5'-most EST LIB35-046-Q1-E1-G12
Method BLASTX
NCBI GI g4538942
BLAST score 353
E value 2.0e-33
Match length 96
% identity 73
NCBI Description (AL049483) uncharacterized protein [Arabidopsis thaliana]

Seq. No. 124600
Contig ID 14781_1.R1010
5'-most EST ARABL1-032-Q1-B1-F4

Seq. No. 124601
Contig ID 14793_1.R1010
5'-most EST LIB317-049-P1-K2-B2

Seq. No. 124602
Contig ID 14794_1.R1010
5'-most EST LIB23-048-Q1-E1-A3
Method BLASTN
NCBI GI g2618605
BLAST score 154
E value 3.0e-81
Match length 310
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 124603
Contig ID 14802_1.R1010
5'-most EST LIB23-048-Q1-E1-B10
Method BLASTX
NCBI GI g3033379
BLAST score 370
E value 5.0e-35
Match length 173
% identity 48
NCBI Description (AC004238) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 124604
Contig ID 14804_1.R1010
5'-most EST g4239693
Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 1.0e-18
Match length 58
% identity 98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	124605
Contig ID	14810_1.R1010
5'-most EST	jC-atXLIB327438P1h12a1
Method	BLASTN
NCBI GI	g3297806
BLAST score	303
E value	1.0e-170
Match length	370
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)
Seq. No.	124606
Contig ID	14812_1.R1010
5'-most EST	jC-atXLIB327422P2h04b2
Method	BLASTX
NCBI GI	g4336325
BLAST score	174
E value	4.0e-12
Match length	121
% identity	33
NCBI Description	(AF081282) small membrane protein 1 [Homo sapiens]
Seq. No.	124607
Contig ID	14816_1.R1010
5'-most EST	jC-atXP32C148A24T7d2
Method	BLASTX
NCBI GI	g3687235
BLAST score	206
E value	3.0e-31
Match length	123
% identity	62
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
Seq. No.	124608
Contig ID	14816_2.R1010
5'-most EST	g931338
Method	BLASTX
NCBI GI	g3687235
BLAST score	352
E value	7.0e-35
Match length	116
% identity	70
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
Seq. No.	124609
Contig ID	14816_3.R1010
5'-most EST	g2749494
Method	BLASTN
NCBI GI	g3687221
BLAST score	34
E value	2.0e-09
Match length	54

% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124610
Contig ID	14816_4.R1010
5'-most EST	jC-atXLIB327410P4e12b1
Method	BLASTX
NCBI GI	g3687235
BLAST score	717
E value	1.0e-75
Match length	149
% identity	97
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	124611
Contig ID	14817_1.R1010
5'-most EST	jC-atXLIB327408P3h06b1
Method	BLASTX
NCBI GI	g4512709
BLAST score	550
E value	3.0e-56
Match length	145
% identity	79
NCBI Description	(AC006569) putative photosystem I reaction center subunit IV precursor [Arabidopsis thaliana]

Seq. No.	124612
Contig ID	14829_1.R1010
5'-most EST	LIB23-048-Q1-E1-D5
Method	BLASTX
NCBI GI	g1906830
BLAST score	826
E value	1.0e-88
Match length	247
% identity	74
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	124613
Contig ID	14830_2.R1010
5'-most EST	jC-atXP111C126H5T7d1
Method	BLASTN
NCBI GI	g4519193
BLAST score	103
E value	2.0e-50
Match length	784
% identity	53
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	124614
Contig ID	14837_1.R1010
5'-most EST	jC-atXP91CH1D9T7b1
Method	BLASTX
NCBI GI	g3377813
BLAST score	321

E value 7.0e-49
Match length 183
% identity 52
NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]

Seq. No. 124615
Contig ID 14837_2.R1010
5'-most EST LIB23-048-Q1-E1-E12

Seq. No. 124616
Contig ID 14840_1.R1010
5'-most EST jC-atXLIB327407P4d10b1
Method BLASTN
NCBI GI g3228389
BLAST score 635
E value 0.0e+00
Match length 978
% identity 98
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No. 124617
Contig ID 14848_1.R1010
5'-most EST jC-atXLIB327408P3b05b1
Method BLASTX
NCBI GI g2289003
BLAST score 344
E value 6.0e-32
Match length 203
% identity 30
NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No. 124618
Contig ID 14848_2.R1010
5'-most EST LIB23-048-Q1-E1-F12
Method BLASTX
NCBI GI g2289003
BLAST score 467
E value 1.0e-46
Match length 111
% identity 86
NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No. 124619
Contig ID 14855_1.R1010
5'-most EST jC-atXLIB327405P4c04b1
Method BLASTX
NCBI GI g3201618
BLAST score 1018
E value 1.0e-111
Match length 210
% identity 92
NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No. 124620

Contig ID	14855_2.R1010
5'-most EST	LIB25-111-Q1-E1-C12
Method	BLASTX
NCBI GI	g3201618
BLAST score	464
E value	2.0e-46
Match length	87
% identity	99
NCBI Description	(AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No.	124621
Contig ID	14856_1.R1010
5'-most EST	jC-alXLIB327435P4c01b1

Seq. No.	124622
Contig ID	14859_1.R1010
5'-most EST	jC-atXLIB327419P4h12b1
Method	BLASTX
NCBI GI	g4185505
BLAST score	465
E value	3.0e-46
Match length	112
% identity	79
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	124623
Contig ID	14861_1.R1010
5'-most EST	LIB3176-083-P1-K1-D9
Method	BLASTN
NCBI GI	g2253009
BLAST score	338
E value	0.0e+00
Match length	338
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for MAP3K delta-1 protein kinase, partial

Seq. No.	124624
Contig ID	14863_1.R1010
5'-most EST	jC-atXLIB327420P3f03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124625
Contig ID	14866_1.R1010
5'-most EST	jC-alXLIB327435P3f06b1
Method	BLASTX
NCBI GI	g4586047
BLAST score	473
E value	3.0e-81

Match length	258
% identity	57
NCBI Description	(AC007020) putative ferritin protein [Arabidopsis thaliana] >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279) hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No.	124626
Contig ID	14866_2.R1010
5'-most EST	jC-atXLIB327408P4a11b1
Method	BLASTX
NCBI GI	g4586047
BLAST score	333
E value	6.0e-31
Match length	106
% identity	68
NCBI Description	(AC007020) putative ferritin protein [Arabidopsis thaliana] >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279) hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No.	124627
Contig ID	14868_1.R1010
5'-most EST	jC-atXLIB327440P4f09b2

Seq. No.	124628
Contig ID	14868_2.R1010
5'-most EST	jC-atX24061Q1E1G10b1

Seq. No.	124629
Contig ID	14869_1.R1010
5'-most EST	jC-atXLIB327420P3h03b1
Method	BLASTX
NCBI GI	g1666173
BLAST score	423
E value	2.0e-41
Match length	146
% identity	61
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	124630
Contig ID	14870_1.R1010
5'-most EST	LIB3234-072-P1-K1-F8

Seq. No.	124631
Contig ID	14873_1.R1010
5'-most EST	g2733541

Seq. No.	124632
Contig ID	14873_2.R1010
5'-most EST	LIB23-048-Q1-E1-H3

Seq. No.	124633
Contig ID	14874_1.R1010
5'-most EST	jC-atXLIB327422P2h11a2
Method	BLASTX
NCBI GI	g2494144
BLAST score	335
E value	7.0e-31

Match length	112
% identity	25
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	124634
Contig ID	14874_3.R1010
5'-most EST	LIB23-048-Q1-E1-H4
Method	BLASTX
NCBI GI	g2494144
BLAST score	494
E value	1.0e-49
Match length	136
% identity	17
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	124635
Contig ID	14876_1.R1010
5'-most EST	LIB24-078-Q1-E1-F7
Method	BLASTX
NCBI GI	g4587595
BLAST score	708
E value	5.0e-75
Match length	141
% identity	98
NCBI Description	(AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	124636
Contig ID	14885_1.R1010
5'-most EST	LIB23-049-Q1-E1-A7
Method	BLASTX
NCBI GI	g2827551
BLAST score	592
E value	2.0e-61
Match length	120
% identity	95
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	124637
Contig ID	14891_1.R1010
5'-most EST	g2758484
Method	BLASTN
NCBI GI	g4262221
BLAST score	51
E value	1.0e-19
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124638
Contig ID	14893_1.R1010
5'-most EST	jC-atXLIB327431P3h02a1
Method	BLASTX
NCBI GI	g2341039

BLAST score	612
E value	2.0e-63
Match length	155
% identity	81
NCBI Description	(AC000104) Similar to Nicotiana lesion-inducing ORF (gb_U66269). [Arabidopsis thaliana]

Seq. No.	124639
Contig ID	14902_1.R1010
5'-most EST	LIB24-121-Q1-E1-D2
Method	BLASTN
NCBI GI	g2264316
BLAST score	311
E value	1.0e-175
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	124640
Contig ID	14908_1.R1010
5'-most EST	jC-atXP41C164N9T7s1
Method	BLASTX
NCBI GI	g2702268
BLAST score	232
E value	6.0e-19
Match length	202
% identity	93
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	124641
Contig ID	14915_1.R1010
5'-most EST	jC-atXLIB327408P3h02b1
Method	BLASTN
NCBI GI	g3420042
BLAST score	225
E value	1.0e-123
Match length	595
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124642
Contig ID	14915_2.R1010
5'-most EST	LIB3176-070-P1-K1-A2
Method	BLASTN
NCBI GI	g3420042
BLAST score	136
E value	2.0e-70
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124643
Contig ID	14923_1.R1010
5'-most EST	jC-atXLIB327409P3b01b1

Method	BLASTN
NCBI GI	g2760164
BLAST score	70
E value	2.0e-30
Match length	473
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	124644
Contig ID	14923_2.R1010
5'-most EST	g905683
Method	BLASTN
NCBI GI	g2760164
BLAST score	62
E value	4.0e-26
Match length	360
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	124645
Contig ID	14926_1.R1010
5'-most EST	g2762575
Method	BLASTN
NCBI GI	g4417264
BLAST score	243
E value	1.0e-134
Match length	329
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124646
Contig ID	14929_1.R1010
5'-most EST	LIB3176-086-P1-K1-E5

Seq. No.	124647
Contig ID	14933_1.R1010
5'-most EST	LIB3177-098-P1-K1-D1

Seq. No.	124648
Contig ID	14934_1.R1010
5'-most EST	jC-atXLIB327431P4f11a1

Seq. No.	124649
Contig ID	14934_2.R1010
5'-most EST	LIB23-049-Q1-E1-F3

Seq. No.	124650
Contig ID	14937_1.R1010
5'-most EST	jC-atXLIB327420P3e10b1
Method	BLASTX
NCBI GI	g4185505
BLAST score	467
E value	2.0e-46
Match length	115

% identity	77
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	124651
Contig ID	14938_1.R1010
5'-most EST	LIB35-005-Q1-E1-F9
Method	BLASTN
NCBI GI	g4519188
BLAST score	383
E value	0.0e+00
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	124652
Contig ID	14941_1.R1010
5'-most EST	jC-alXLIB327434P4a08b1
Method	BLASTX
NCBI GI	g4538920
BLAST score	815
E value	3.0e-87
Match length	168
% identity	98
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	124653
Contig ID	14942_1.R1010
5'-most EST	jC-atXLIB327421P4b09b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	679
E value	1.0e-71
Match length	146
% identity	92
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	124654
Contig ID	14951_1.R1010
5'-most EST	LIB24-005-Q1-E1-B5
Method	BLASTX
NCBI GI	g4538902
BLAST score	457
E value	2.0e-55
Match length	120
% identity	90
NCBI Description	(AL049482) rab7-like protein [Arabidopsis thaliana]

Seq. No.	124655
Contig ID	14954_1.R1010
5'-most EST	LIB3177-092-P1-K1-H1
Method	BLASTX
NCBI GI	g687844
BLAST score	272
E value	1.0e-32

Match length	158
% identity	51
NCBI Description	(U21320) contains TPR domain-like repeats [Caenorhabditis elegans]

Seq. No.	124656
Contig ID	14960_1.R1010
5'-most EST	jC-atXLIB327406P4f02b2
Method	BLASTX
NCBI GI	g3878105
BLAST score	215
E value	3.0e-17
Match length	142
% identity	37
NCBI Description	(AL024499) cDNA EST EMBL:C10123 comes from this gene [Caenorhabditis elegans]

Seq. No.	124657
Contig ID	14960_2.R1010
5'-most EST	jC-atXLIB327408P4g01b1
Method	BLASTN
NCBI GI	g4519192
BLAST score	142
E value	1.0e-73
Match length	631
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	124658
Contig ID	14970_1.R1010
5'-most EST	LIB23-050-Q1-E1-E4
Method	BLASTX
NCBI GI	g4204263
BLAST score	704
E value	2.0e-74
Match length	157
% identity	88
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	124659
Contig ID	14979_1.R1010
5'-most EST	LIB23-050-Q1-E1-H3
Method	BLASTX
NCBI GI	g2208903
BLAST score	519
E value	3.0e-64
Match length	138
% identity	94
NCBI Description	(AB004798) ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	124660
Contig ID	14983_1.R1010
5'-most EST	LIB24-104-Q1-E1-C2
Method	BLASTX
NCBI GI	g4324409
BLAST score	126

E value 1.0e-15
Match length 192
% identity 30
NCBI Description (AF104119) intracellular chloride ion channel protein p64H1 [Rattus norvegicus]

Seq. No. 124661
Contig ID 14985_1.R1010
5'-most EST LIB25-024-Q1-E1-H5
Method BLASTX
NCBI GI g3212849
BLAST score 1124
E value 1.0e-123
Match length 227
% identity 95
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 124662
Contig ID 14985_2.R1010
5'-most EST jC-alXLIB327435P4e10b1
Method BLASTX
NCBI GI g3212849
BLAST score 201
E value 2.0e-15
Match length 40
% identity 100
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 124663
Contig ID 14988_1.R1010
5'-most EST LIB23-051-Q1-E1-A4
Method BLASTX
NCBI GI g3892704
BLAST score 520
E value 6.0e-53
Match length 120
% identity 81
NCBI Description (AL033545) RCc3-like protein [Arabidopsis thaliana]

Seq. No. 124664
Contig ID 14992_1.R1010
5'-most EST LIB3234-078-P1-K1-F4
Method BLASTX
NCBI GI g4218002
BLAST score 597
E value 6.0e-62
Match length 122
% identity 99
NCBI Description (AC006135) putative UTP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 124665
Contig ID 15001_1.R1010
5'-most EST LIB23-051-Q1-E1-B8
Method BLASTX
NCBI GI g1363325
BLAST score 259

E value	3.0e-22
Match length	102
% identity	52
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	124666
Contig ID	15002_1.R1010
5'-most EST	LIB35-009-Q1-E1-D4
Method	BLASTX
NCBI GI	g2425123
BLAST score	176
E value	1.0e-12
Match length	120
% identity	37
NCBI Description	(AF019986) PksB [Dictyostelium discoideum]

Seq. No.	124667
Contig ID	15006_2.R1010
5'-most EST	LIB25-052-Q1-E1-B7
Method	BLASTN
NCBI GI	g2244829
BLAST score	263
E value	1.0e-146
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	124668
Contig ID	15007_1.R1010
5'-most EST	jC-atXLIB327405P3c12b1
Method	BLASTX
NCBI GI	g4678947
BLAST score	713
E value	3.0e-75
Match length	195
% identity	64
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	124669
Contig ID	15007_2.R1010
5'-most EST	LIB23-051-Q1-E1-C2
Method	BLASTN
NCBI GI	g4691223
BLAST score	140
E value	1.0e-72
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	124670
Contig ID	15008_1.R1010
5'-most EST	LIB35-033-Q1-E1-C8

Seq. No.	124671

Contig ID	15008_2.R1010
5'-most EST	jC-alXLIB327436P1g06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124672
Contig ID	15011_1.R1010
5'-most EST	LIB24-047-Q1-E1-A5
Method	BLASTX
NCBI GI	g2811028
BLAST score	546
E value	4.0e-56
Match length	125
% identity	90
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188 (AF007271) similar to S. cerevisiae SIK1P (PID:g984964) [Arabidopsis thaliana]

Seq. No.	124673
Contig ID	15018_1.R1010
5'-most EST	LIB23-054-Q1-E1-A12
Method	BLASTX
NCBI GI	g4337174
BLAST score	545
E value	4.0e-56
Match length	108
% identity	99
NCBI Description	(AC006416) Similar to gi_1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb_U32764. [Arabidopsis thaliana]

Seq. No.	124674
Contig ID	15026_1.R1010
5'-most EST	jC-atXLIB327404P1f01b1
Method	BLASTX
NCBI GI	g2827621
BLAST score	608
E value	6.0e-63
Match length	177
% identity	65
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	124675
Contig ID	15031_1.R1010
5'-most EST	LIB23-051-Q1-E1-E3
Method	BLASTX
NCBI GI	g4503521
BLAST score	545
E value	2.0e-55
Match length	176
% identity	62

NCBI Description	murine mammary tumor integration site 6 (oncogene homolog) >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens]
Seq. No.	124676
Contig ID	15035_1.R1010
5'-most EST	jC-atXLIB327418P4a06b1
Method	BLASTX
NCBI GI	g3875304
BLAST score	282
E value	9.0e-25
Match length	82
% identity	62
NCBI Description	(Z74030) predicted using Genefinder; cDNA EST EMBL:C07609 comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com
Seq. No.	124677
Contig ID	15036_1.R1010
5'-most EST	LIB23-051-Q1-E1-E9
Method	BLASTX
NCBI GI	g1619300
BLAST score	458
E value	1.0e-45
Match length	142
% identity	65
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]
Seq. No.	124678
Contig ID	15038_1.R1010
5'-most EST	LIB23-051-Q1-E1-F10
Method	BLASTX
NCBI GI	g4678269
BLAST score	873
E value	3.0e-98
Match length	211
% identity	88
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]
Seq. No.	124679
Contig ID	15058_1.R1010
5'-most EST	LIB3176-093-P1-K1-E5
Method	BLASTN
NCBI GI	g2264312
BLAST score	355
E value	0.0e+00
Match length	419
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
Seq. No.	124680

Contig ID	15063_1.R1010
5'-most EST	LIB23-060-Q1-E1-B7
Seq. No.	124681
Contig ID	15066_1.R1010
5'-most EST	LIB23-051-Q1-E1-H5
Method	BLASTN
NCBI GI	g3299824
BLAST score	153
E value	1.0e-80
Match length	379
% identity	92
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	124682
Contig ID	15068_2.R1010
5'-most EST	LIB3175-045-P1-K1-D1
Method	BLASTX
NCBI GI	g3128187
BLAST score	397
E value	1.0e-38
Match length	92
% identity	78
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]
Seq. No.	124683
Contig ID	15069_1.R1010
5'-most EST	LIB23-051-Q1-E1-H8
Method	BLASTX
NCBI GI	g3858939
BLAST score	68
E value	1.0e-65
Match length	171
% identity	84
NCBI Description	(AL021636) serine/threonine protein kinase like protein [Arabidopsis thaliana]
Seq. No.	124684
Contig ID	15070_1.R1010
5'-most EST	g1159738
Method	BLASTX
NCBI GI	g2632252
BLAST score	169
E value	1.0e-11
Match length	64
% identity	52
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.	124685
Contig ID	15073_1.R1010
5'-most EST	LIB23-052-Q1-E1-A11
Method	BLASTX
NCBI GI	g4314378
BLAST score	841
E value	2.0e-90
Match length	167

% identity	97
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	124686
Contig ID	15075_1.R1010
5'-most EST	g576972
Method	BLASTN
NCBI GI	g2583106
BLAST score	223
E value	1.0e-122
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124687
Contig ID	15080_1.R1010
5'-most EST	jC-atXLIB327408P3f03b1
Method	BLASTX
NCBI GI	g3169173
BLAST score	341
E value	1.0e-134
Match length	342
% identity	62
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124688
Contig ID	15080_2.R1010
5'-most EST	jC-atXLIB327408P4b02b1
Method	BLASTX
NCBI GI	g3169172
BLAST score	1138
E value	1.0e-125
Match length	209
% identity	100
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445214 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124689
Contig ID	15080_3.R1010
5'-most EST	jC-alXLIB327435P4e03b1
Method	BLASTX
NCBI GI	g3169173
BLAST score	875
E value	3.0e-94
Match length	221
% identity	77
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124690
Contig ID	15080_5.R1010
5'-most EST	jC-atXLIB327408P2f06a1

Method	BLASTX
NCBI GI	g3169174
BLAST score	510
E value	1.0e-51
Match length	95
% identity	98
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124691
Contig ID	15080_8.R1010
5'-most EST	jC-atXLIB327408P2f06b1
Method	BLASTX
NCBI GI	g3169171
BLAST score	93
E value	1.0e-145
Match length	310
% identity	83
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124692
Contig ID	15080_9.R1010
5'-most EST	jC-atXLIB327408P2e09b1
Method	BLASTX
NCBI GI	g3169173
BLAST score	347
E value	1.0e-32
Match length	101
% identity	70
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124693
Contig ID	15080_10.R1010
5'-most EST	jC-atXLIB327408P4e10b1
Method	BLASTX
NCBI GI	g3169172
BLAST score	505
E value	4.0e-51
Match length	111
% identity	86
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445214 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	124694
Contig ID	15080_11.R1010
5'-most EST	jC-atXLIB327424P1h09b2
Method	BLASTX
NCBI GI	g3169171
BLAST score	154
E value	5.0e-46
Match length	102
% identity	96

NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]
Seq. No.	124695
Contig ID	15081_1.R1010
5'-most EST	LIB23-052-Q1-E1-B12
Method	BLASTN
NCBI GI	g4469002
BLAST score	243
E value	1.0e-134
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)
Seq. No.	124696
Contig ID	15092_1.R1010
5'-most EST	jC-atXLIB327405P3c03a1
Method	BLASTX
NCBI GI	g2618686
BLAST score	170
E value	7.0e-12
Match length	63
% identity	46
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.	124697
Contig ID	15093_1.R1010
5'-most EST	jC-atXLIB327423P2c07b1
Method	BLASTX
NCBI GI	g2245110
BLAST score	383
E value	3.0e-36
Match length	357
% identity	34
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	124698
Contig ID	15100_1.R1010
5'-most EST	jC-atXLIB327409P2a12b1
Seq. No.	124699
Contig ID	15102_1.R1010
5'-most EST	LIB23-052-Q1-E1-D7
Seq. No.	124700
Contig ID	15103_1.R1010
5'-most EST	g506996
Method	BLASTX
NCBI GI	g3834310
BLAST score	341
E value	2.0e-31
Match length	152
% identity	59
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,

gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	124701
Contig ID	15103_2.R1010
5'-most EST	jC-atXP91C247D9T7b1
Method	BLASTX
NCBI GI	g3834310
BLAST score	712
E value	4.0e-75
Match length	141
% identity	99
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	124702
Contig ID	15103_3.R1010
5'-most EST	LIB35-014-Q1-E1-H10
Method	BLASTX
NCBI GI	g3834310
BLAST score	716
E value	5.0e-82
Match length	160
% identity	99
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	124703
Contig ID	15103_5.R1010
5'-most EST	jC-atXP121C96P20T7045d1
Method	BLASTX
NCBI GI	g3834310
BLAST score	448
E value	7.0e-66
Match length	146
% identity	95
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	124704
Contig ID	15103_6.R1010
5'-most EST	jC-atXP121C132H9T7050d1
Method	BLASTX
NCBI GI	g3834310
BLAST score	137
E value	2.0e-20
Match length	58
% identity	95
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No.	124705
Contig ID	15104_1.R1010
5'-most EST	LIB23-052-Q1-E1-D9
Method	BLASTX
NCBI GI	g419760
BLAST score	925
E value	1.0e-100
Match length	195
% identity	49
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	124706
Contig ID	15112_1.R1010
5'-most EST	jC-atXLIB327406P2a08b1
Method	BLASTX
NCBI GI	g1532165
BLAST score	764
E value	2.0e-81
Match length	162
% identity	98
NCBI Description	(U63815) similar to dehydrogenase encoded by GenBank Accession Number S39508; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop

Seq. No.	124707
Contig ID	15115_1.R1010
5'-most EST	LIB23-052-Q1-E1-F1

Seq. No.	124708
Contig ID	15117_1.R1010
5'-most EST	jC-atXP118C144G12T7045d2
Method	BLASTX
NCBI GI	g2245125
BLAST score	167
E value	3.0e-11
Match length	78
% identity	49
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124709
Contig ID	15118_1.R1010
5'-most EST	LIB23-052-Q1-E1-F12

Seq. No.	124710
Contig ID	15126_1.R1010
5'-most EST	jC-alXLIB327436P3h10b1
Method	BLASTX
NCBI GI	g2317908
BLAST score	1154
E value	1.0e-127
Match length	243

% identity	93
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	124711
Contig ID	15127_1.R1010
5'-most EST	jC-atXLIB327426P3h12b1
Method	BLASTX
NCBI GI	g4581141
BLAST score	424
E value	3.0e-41
Match length	168
% identity	60
NCBI Description	(AC006919) unknown protein [Arabidopsis thaliana]

Seq. No.	124712
Contig ID	15129_1.R1010
5'-most EST	jC-atXLIB327409P2b04b1
Method	BLASTX
NCBI GI	g4469023
BLAST score	720
E value	6.0e-76
Match length	192
% identity	74
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	124713
Contig ID	15132_1.R1010
5'-most EST	jC-atXLIB327427P3c05b2
Method	BLASTX
NCBI GI	g4432845
BLAST score	226
E value	2.0e-18
Match length	142
% identity	36
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	124714
Contig ID	15133_1.R1010
5'-most EST	LIB23-052-Q1-E1-G8
Method	BLASTX
NCBI GI	g1085002
BLAST score	232
E value	5.0e-19
Match length	83
% identity	19
NCBI Description	mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115) carrier protein (c1) [Caenorhabditis elegans] >gi_829102_emb_CAA88283_ (Z48240) DIF-1 [Caenorhabditis elegans]

Seq. No.	124715
Contig ID	15135_1.R1010
5'-most EST	jC-atXLIB327419P2b10b2

Seq. No.	124716
Contig ID	15135_2.R1010

5'-most EST	g2048358
Seq. No.	124717
Contig ID	15135_3.R1010
5'-most EST	LIB23-052-Q1-E1-H1
Seq. No.	124718
Contig ID	15142_1.R1010
5'-most EST	LIB24-082-Q1-E1-G12
Method	BLASTX
NCBI GI	g3152581
BLAST score	302
E value	2.0e-27
Match length	94
% identity	68
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]
Seq. No.	124719
Contig ID	15143_1.R1010
5'-most EST	LIB3177-042-P1-K2-G12
Method	BLASTN
NCBI GI	g4539290
BLAST score	204
E value	1.0e-111
Match length	603
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)
Seq. No.	124720
Contig ID	15145_1.R1010
5'-most EST	jC-atXLIB327424P2e02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	59
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	124721
Contig ID	15147_1.R1010
5'-most EST	jC-atXLIB327421P2d12b1
Method	BLASTN
NCBI GI	g3885325
BLAST score	430
E value	0.0e+00
Match length	471
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	124722
Contig ID	15155_1.R1010

5'-most EST	LIB23-053-Q1-E1-B12
Seq. No.	124723
Contig ID	15157_1.R1010
5'-most EST	jC-atXLIB327431P3h04a1
Method	BLASTX
NCBI GI	g3450842
BLAST score	452
E value	3.0e-46
Match length	281
% identity	43
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
Seq. No.	124724
Contig ID	15177_1.R1010
5'-most EST	jC-atX25025Q1E1D06b1
Method	BLASTN
NCBI GI	g2337888
BLAST score	174
E value	6.0e-93
Match length	518
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
Seq. No.	124725
Contig ID	15179_1.R1010
5'-most EST	LIB23-075-Q1-E1-F12
Seq. No.	124726
Contig ID	15186_1.R1010
5'-most EST	jC-atXLIB327421P3a06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	8.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	124727
Contig ID	15189_1.R1010
5'-most EST	g315966
Method	BLASTN
NCBI GI	g2351069
BLAST score	501
E value	0.0e+00
Match length	596
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	124728
Contig ID	15190_1.R1010
5'-most EST	jC-atXLIB327424P1a05b2

Method	BLASTX
NCBI GI	g2695703
BLAST score	146
E value	5.0e-09
Match length	61
% identity	26
NCBI Description	(Y10555) CONSTANS [Arabidopsis thaliana] >gi_2695705_emb_CAA71588_ (Y10556) CONSTANS [Arabidopsis thaliana]

Seq. No.	124729
Contig ID	15193_1.R1010
5'-most EST	LIB23-053-Q1-E1-E7
Method	BLASTX
NCBI GI	g2194129
BLAST score	168
E value	1.0e-11
Match length	54
% identity	59
NCBI Description	(AC002062) EST gb_T21469 comes from this gene. [Arabidopsis thaliana]

Seq. No.	124730
Contig ID	15202_1.R1010
5'-most EST	ARABLI-11-Q1-B1-C1
Method	BLASTX
NCBI GI	g3212866
BLAST score	722
E value	6.0e-76
Match length	217
% identity	65
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	124731
Contig ID	15205_1.R1010
5'-most EST	LIB23-053-Q1-E1-F9
Method	BLASTX
NCBI GI	g4544369
BLAST score	243
E value	2.0e-20
Match length	154
% identity	39
NCBI Description	(AC006920) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124732
Contig ID	15210_1.R1010
5'-most EST	g2393186
Method	BLASTX
NCBI GI	g1495804
BLAST score	66
E value	1.0e-105
Match length	279
% identity	70
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	124733
Contig ID	15218_1.R1010

5'-most EST	g2749334
Method	BLASTX
NCBI GI	g4490330
BLAST score	68
E value	3.0e-31
Match length	99
% identity	66
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	124734
Contig ID	15218_2.R1010
5'-most EST	g937869
Method	BLASTX
NCBI GI	g4490330
BLAST score	1273
E value	1.0e-140
Match length	431
% identity	64
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	124735
Contig ID	15226_1.R1010
5'-most EST	LIB23-053-Q1-E1-H9
Method	BLASTX
NCBI GI	g4406778
BLAST score	326
E value	3.0e-30
Match length	167
% identity	6
NCBI Description	(AC006532) putative brassinosteroid insensitive protein [Arabidopsis thaliana]

Seq. No.	124736
Contig ID	15227_1.R1010
5'-most EST	LIB23-070-Q1-E1-A8
Method	BLASTX
NCBI GI	g4220512
BLAST score	510
E value	8.0e-52
Match length	124
% identity	74
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	124737
Contig ID	15228_1.R1010
5'-most EST	jC-alXLIB327434P4a05b1
Method	BLASTX
NCBI GI	g4689366
BLAST score	434
E value	1.0e-42
Match length	153
% identity	56
NCBI Description	(AF134155) RING finger protein [Arabidopsis thaliana]

Seq. No.	124738

Contig ID	15228_2.R1010
5'-most EST	LIB3176-007-P1-K1-D7
Method	BLASTX
NCBI GI	g4689366
BLAST score	429
E value	6.0e-42
Match length	151
% identity	56
NCBI Description	(AF134155) RING finger protein [Arabidopsis thaliana]

Seq. No.	124739
Contig ID	15233_1.R1010
5'-most EST	LIB23-054-Q1-E1-A4
Method	BLASTX
NCBI GI	g2494034
BLAST score	462
E value	3.0e-46
Match length	129
% identity	71
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	124740
Contig ID	15236_1.R1010
5'-most EST	g2748603
Method	BLASTN
NCBI GI	g3075383
BLAST score	276
E value	1.0e-154
Match length	508
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124741
Contig ID	15236_2.R1010
5'-most EST	LIB23-054-Q1-E1-A7
Method	BLASTN
NCBI GI	g3075383
BLAST score	220
E value	1.0e-120
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124742
Contig ID	15238_1.R1010
5'-most EST	LIB35-045-Q1-E1-H10
Method	BLASTN
NCBI GI	g4519183
BLAST score	232
E value	1.0e-127
Match length	472
% identity	72

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence
Seq. No.	124743
Contig ID	15241_1.R1010
5'-most EST	LIB3176-045-P1-K1-H10
Method	BLASTX
NCBI GI	g4586249
BLAST score	915
E value	1.0e-103
Match length	203
% identity	97
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]
Seq. No.	124744
Contig ID	15241_2.R1010
5'-most EST	g2581720
Method	BLASTN
NCBI GI	g4586241
BLAST score	507
E value	0.0e+00
Match length	626
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)
Seq. No.	124745
Contig ID	15241_3.R1010
5'-most EST	LIB3175-016-P1-K1-D6
Method	BLASTX
NCBI GI	g4586249
BLAST score	1086
E value	1.0e-119
Match length	213
% identity	100
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]
Seq. No.	124746
Contig ID	15244_1.R1010
5'-most EST	LIB23-054-Q1-E1-B3
Method	BLASTX
NCBI GI	g4091810
BLAST score	1437
E value	1.0e-160
Match length	274
% identity	100
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]
Seq. No.	124747
Contig ID	15260_1.R1010
5'-most EST	jC-atXLIB327420P3c05b1
Method	BLASTX
NCBI GI	g3668082
BLAST score	563

E value	6.0e-58
Match length	143
% identity	76
NCBI Description	(AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No.	124748
Contig ID	15263_1.R1010
5'-most EST	LIB3168-004-P1-K1-E7
Method	BLASTX
NCBI GI	g3395431
BLAST score	266
E value	5.0e-23
Match length	118
% identity	46
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	124749
Contig ID	15266_1.R1010
5'-most EST	LIB3176-074-P1-K1-B5
Method	BLASTN
NCBI GI	g4662609
BLAST score	516
E value	0.0e+00
Match length	619
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	124750
Contig ID	15269_1.R1010
5'-most EST	jC-atXP63C205C11T7d2
Method	BLASTN
NCBI GI	g3337347
BLAST score	365
E value	0.0e+00
Match length	563
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124751
Contig ID	15277_1.R1010
5'-most EST	jC-atXP43C169G2T7015d1
Method	BLASTX
NCBI GI	g3341723
BLAST score	344
E value	5.0e-32
Match length	163
% identity	50
NCBI Description	(AF052690) CONSTANS-like 1 protein [Raphanus sativus]

Seq. No.	124752
Contig ID	15277_2.R1010
5'-most EST	g2748116
Method	BLASTN
NCBI GI	g3212102
BLAST score	139

E value	5.0e-72
Match length	290
% identity	96
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	124753
Contig ID	15277_3.R1010
5'-most EST	jC-atXP52C181L14T7d2
Method	BLASTN
NCBI GI	g3212102
BLAST score	366
E value	0.0e+00
Match length	422
% identity	97
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	124754
Contig ID	15278_1.R1010
5'-most EST	jC-atXP69C219O3T7079d1
Method	BLASTX
NCBI GI	g228456
BLAST score	1195
E value	1.0e-131
Match length	272
% identity	86
NCBI Description	Gln synthetase [Arabidopsis thaliana]

Seq. No.	124755
Contig ID	15278_2.R1010
5'-most EST	LIB3168-094-P1-K1-D12
Method	BLASTX
NCBI GI	g99698
BLAST score	527
E value	1.0e-53
Match length	157
% identity	73
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgskb6) - Arabidopsis thaliana

Seq. No.	124756
Contig ID	15304_1.R1010
5'-most EST	jC-atXLIB327403P1h03b1
Method	BLASTN
NCBI GI	g4371278
BLAST score	81
E value	2.0e-37
Match length	193
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124757
Contig ID	15308_1.R1010
5'-most EST	jC-atX24136Q1E1D12b1
Method	BLASTX

NCBI GI g3881836
BLAST score 755
E value 2.0e-80
Match length 209
% identity 71
NCBI Description (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240); cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this ge

Seq. No. 124758
Contig ID 15312_1.R1010
5'-most EST g2047849
Method BLASTN
NCBI GI g3668073
BLAST score 297
E value 1.0e-166
Match length 500
% identity 93
NCBI Description Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 124759
Contig ID 15315_1.R1010
5'-most EST LIB23-072-Q1-E1-A1

Seq. No. 124760
Contig ID 15318_1.R1010
5'-most EST jC-atXLIB327421P4g07b1
Method BLASTX
NCBI GI g3355476
BLAST score 639
E value 7.0e-67
Match length 133
% identity 93
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 124761
Contig ID 15320_1.R1010
5'-most EST jC-alXLIB327436P4d08b1
Method BLASTN
NCBI GI g2582640
BLAST score 57
E value 4.0e-23
Match length 73
% identity 95
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 124762
Contig ID 15330_1.R1010
5'-most EST LIB23-055-Q1-E1-B2

Seq. No. 124763
Contig ID 15332_1.R1010
5'-most EST LIB23-072-Q1-E1-F3

Method	BLASTX
NCBI GI	g3023849
BLAST score	509
E value	9.0e-52
Match length	131
% identity	25
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF ACTIVATED PROTEIN KINASE C) (RACK) >gi_2558964 (AF025330) receptor for activated protein kinase C [Danio rerio]

Seq. No.	124764
Contig ID	15340_1.R1010
5'-most EST	LIB24-107-Q1-E1-H3
Method	BLASTX
NCBI GI	g1172754
BLAST score	639
E value	9.0e-67
Match length	194
% identity	71
NCBI Description	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) >gi_541885_pir__JQ2256 phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) precursor - Arabidopsis thaliana >gi_289188 (L12457) 5'-phosphoribosyl-5-aminoimidazole synthetase [Arabidopsis thaliana]

Seq. No.	124765
Contig ID	15341_1.R1010
5'-most EST	jC-alXLIB327434P4f09b1
Method	BLASTN
NCBI GI	g2098816
BLAST score	268
E value	1.0e-149
Match length	492
% identity	98
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	124766
Contig ID	15344_1.R1010
5'-most EST	ARABL1-039-Q1-B1-A10
Method	BLASTX
NCBI GI	g2507426
BLAST score	622
E value	6.0e-65
Match length	141
% identity	84
NCBI Description	ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (ALANINE--TRNA LIGASE) (ALARS) >gi_1673365_emb_CAA80380_ (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No.	124767
Contig ID	15345_1.R1010
5'-most EST	jC-alX24088Q1E1D07b1
Method	BLASTX

NCBI GI	g4115918
BLAST score	437
E value	7.0e-43
Match length	135
% identity	67
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	124768
Contig ID	15345_2.R1010
5'-most EST	jC-atXLIB327408P2f03b1
Method	BLASTX
NCBI GI	g4539408
BLAST score	414
E value	3.0e-40
Match length	148
% identity	59
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	124769
Contig ID	15345_3.R1010
5'-most EST	LIB35-038-Q1-E1-C2
Method	BLASTX
NCBI GI	g4115918
BLAST score	363
E value	3.0e-34
Match length	140
% identity	56
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	124770
Contig ID	15359_1.R1010
5'-most EST	LIB3175-079-P1-K1-A4

Seq. No.	124771
Contig ID	15369_1.R1010
5'-most EST	jC-atXLIB327419P3c02b2
Method	BLASTX
NCBI GI	g4490758
BLAST score	380
E value	3.0e-36
Match length	212
% identity	43
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	124772
Contig ID	15381_1.R1010
5'-most EST	LIB23-055-Q1-E1-G11
Method	BLASTX
NCBI GI	g4185599
BLAST score	173
E value	3.0e-12
Match length	129
% identity	32
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	124773
Contig ID	15384_1.R1010
5'-most EST	jC-atXLIB327408P1e02b1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	6.0e-16
Match length	53
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	124774
Contig ID	15388_1.R1010
5'-most EST	jC-atXLIB327418P1g09b1
Method	BLASTN
NCBI GI	g2264304
BLAST score	520
E value	0.0e+00
Match length	603
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	124775
Contig ID	15394_1.R1010
5'-most EST	jC-atXLIB327427P1b09b1
Method	BLASTN
NCBI GI	g4376087
BLAST score	232
E value	1.0e-127
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	124776
Contig ID	15406_1.R1010
5'-most EST	LIB23-056-Q1-E1-A12
Method	BLASTX
NCBI GI	g3550427
BLAST score	203
E value	2.0e-15
Match length	153
% identity	30
NCBI Description	(Y18007) seven transmembrane domain protein [Homo sapiens]

Seq. No.	124777
Contig ID	15413_1.R1010
5'-most EST	jC-atXLIB327406P2e08b1
Method	BLASTX
NCBI GI	g3738302
BLAST score	627
E value	5.0e-65
Match length	287
% identity	46
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	124778
Contig ID	15413_2.R1010
5'-most EST	jC-atXP17C110E22T7s3
Method	BLASTX
NCBI GI	g4309738
BLAST score	362
E value	3.0e-34
Match length	92
% identity	72
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	124779
Contig ID	15421_1.R1010
5'-most EST	LIB23-056-Q1-E1-B5
Method	BLASTX
NCBI GI	g2982303
BLAST score	1221
E value	1.0e-134
Match length	267
% identity	84
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	124780
Contig ID	15425_1.R1010
5'-most EST	jC-atXLIB327407P1f07b2
Method	BLASTX
NCBI GI	g4335759
BLAST score	529
E value	1.0e-53
Match length	108
% identity	97
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	124781
Contig ID	15425_2.R1010
5'-most EST	jC-atXmonuni27Cd04b1
Method	BLASTX
NCBI GI	g4335771
BLAST score	980
E value	1.0e-106
Match length	191
% identity	99
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	124782
Contig ID	15425_3.R1010
5'-most EST	jC-atXLIB327427P4d04b2
Method	BLASTX
NCBI GI	g4335771
BLAST score	786
E value	1.0e-83
Match length	181
% identity	83
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	124783
Contig ID	15428_1.R1010
5'-most EST	jC-atXP11C98P9T7084d1
Method	BLASTX
NCBI GI	g2098709
BLAST score	355
E value	4.0e-54
Match length	199
% identity	55
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	124784
Contig ID	15436_1.R1010
5'-most EST	LIB3234-091-P1-K1-B9
Method	BLASTN
NCBI GI	g4519195
BLAST score	172
E value	8.0e-92
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	124785
Contig ID	15440_1.R1010
5'-most EST	LIB23-056-Q1-E1-D12
Method	BLASTX
NCBI GI	g2642448
BLAST score	588
E value	4.0e-61
Match length	119
% identity	100
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124786
Contig ID	15443_1.R1010
5'-most EST	LIB23-056-Q1-E1-D4
Method	BLASTN
NCBI GI	g4220635
BLAST score	172
E value	6.0e-92
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	124787
Contig ID	15468_2.R1010
5'-most EST	LIB23-056-Q1-E1-F6
Method	BLASTX
NCBI GI	g2995370
BLAST score	69
E value	1.0e-12
Match length	177

% identity	31
NCBI Description	(AL022245) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	124788
Contig ID	15470_1.R1010
5'-most EST	LIB23-056-Q1-E1-F8
Method	BLASTX
NCBI GI	g2980773
BLAST score	941
E value	1.0e-102
Match length	184
% identity	71
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	124789
Contig ID	15481_1.R1010
5'-most EST	jC-atXLIB327419P4g11b1
Method	BLASTX
NCBI GI	g544134
BLAST score	317
E value	4.0e-61
Match length	409
% identity	42
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	124790
Contig ID	15484_1.R1010
5'-most EST	LIB35-039-Q1-E1-B9
Method	BLASTX
NCBI GI	g1361155
BLAST score	271
E value	2.0e-23
Match length	200
% identity	36
NCBI Description	hypothetical protein o215b - Escherichia coli >gi_537235 (U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi_1790856 (AE000509) phosphoglyceromutase 2 [Escherichia coli]

Seq. No.	124791
Contig ID	15489_1.R1010
5'-most EST	LIB3176-097-P1-K1-B1
Method	BLASTN
NCBI GI	g3449334
BLAST score	191
E value	1.0e-103
Match length	232
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	124792
Contig ID	15490_1.R1010
5'-most EST	LIB3234-011-P1-K1-D1

Seq. No.	124793
Contig ID	15497_1.R1010
5'-most EST	LIB23-073-Q1-E1-B4
Method	BLASTX
NCBI GI	g3025194
BLAST score	88
E value	1.0e-09
Match length	95
% identity	35
NCBI Description	HYPOTHETICAL PROTEIN IN HYDROGENASE 1 5'REGION >gi_481588_pir__S38903 hypothetical protein 1 - Clostridium pasteurianum (fragment) >gi_431947_emb_CAA82208_ (Z28353) Similar to ABC1 gene of yeast (SW: ABC1_Yeast) [Clostridium pasteurianum]

Seq. No.	124794
Contig ID	15498_2.R1010
5'-most EST	LIB25-029-Q1-E1-H5

Seq. No.	124795
Contig ID	15506_1.R1010
5'-most EST	jC-atXLIB327419P4a08b1
Method	BLASTN
NCBI GI	g4325365
BLAST score	323
E value	0.0e+00
Match length	483
% identity	98
NCBI Description	Arabidopsis thaliana BAC T3H13

Seq. No.	124796
Contig ID	15506_2.R1010
5'-most EST	LIB35-047-Q1-E1-A10
Method	BLASTN
NCBI GI	g4325365
BLAST score	276
E value	1.0e-154
Match length	351
% identity	98
NCBI Description	Arabidopsis thaliana BAC T3H13

Seq. No.	124797
Contig ID	15507_1.R1010
5'-most EST	LIB23-074-Q1-E1-F4

Seq. No.	124798
Contig ID	15512_1.R1010
5'-most EST	LIB23-057-Q1-E1-C10

Seq. No.	124799
Contig ID	15514_1.R1010
5'-most EST	jC-atXLIB327431P1f10a1
Method	BLASTN
NCBI GI	g2924651
BLAST score	491
E value	0.0e+00

Match length	495
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	124800
Contig ID	15514_2.R1010
5'-most EST	LIB23-062-Q1-E1-F11
Method	BLASTX
NCBI GI	g4539333
BLAST score	392
E value	6.0e-38
Match length	164
% identity	47
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No.	124801
Contig ID	15516_1.R1010
5'-most EST	jC-atXLIB327417P4c05b1
Method	BLASTN
NCBI GI	g4757414
BLAST score	447
E value	0.0e+00
Match length	483
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	124802
Contig ID	15520_1.R1010
5'-most EST	LIB23-057-Q1-E1-D1
Method	BLASTX
NCBI GI	g2982463
BLAST score	701
E value	3.0e-74
Match length	148
% identity	87
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	124803
Contig ID	15527_1.R1010
5'-most EST	jC-atXLIB327409P2a05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124804
Contig ID	15530_1.R1010
5'-most EST	jC-atXP115C246O8T7034d1
Method	BLASTX
NCBI GI	g417148

BLAST score	559
E value	3.0e-57
Match length	184
% identity	59
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir__A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No.	124805
Contig ID	15530_2.R1010
5'-most EST	g1517411
Method	BLASTX
NCBI GI	g417148
BLAST score	172
E value	1.0e-20
Match length	104
% identity	47
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir__A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No.	124806
Contig ID	15536_1.R1010
5'-most EST	LIB23-057-Q1-E1-E6
Method	BLASTN
NCBI GI	g4159706
BLAST score	453
E value	0.0e+00
Match length	508
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	124807
Contig ID	15537_1.R1010
5'-most EST	LIB25-061-Q1-E1-A6
Method	BLASTN
NCBI GI	g3985934
BLAST score	332
E value	0.0e+00
Match length	410
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	124808
Contig ID	15537_2.R1010
5'-most EST	jC-atXP67C214A2T7088a1
Method	BLASTN
NCBI GI	g3985934
BLAST score	416
E value	0.0e+00
Match length	436
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	124809
Contig ID	15542_1.R1010
5'-most EST	jC-atXLIB327421P2h09b1
Method	BLASTX
NCBI GI	g2244796
BLAST score	741
E value	2.0e-78
Match length	314
% identity	58
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124810
Contig ID	15544_1.R1010
5'-most EST	LIB23-073-Q1-E1-G5
Method	BLASTX
NCBI GI	g3176718
BLAST score	562
E value	4.0e-58
Match length	109
% identity	99
NCBI Description	(AC002392) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124811
Contig ID	15545_1.R1010
5'-most EST	jC-alX25089Q1E1G07b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	814
E value	3.0e-87
Match length	209
% identity	75
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	124812
Contig ID	15552_1.R1010
5'-most EST	LIB3176-056-P1-K1-H4

Seq. No.	124813
Contig ID	15553_1.R1010
5'-most EST	jC-atXLIB327416P2e08b1
Method	BLASTX
NCBI GI	g2463509
BLAST score	575
E value	5.0e-59
Match length	143
% identity	73
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	124814
Contig ID	15553_2.R1010
5'-most EST	jC-alXLIB327436P2a01a1

Seq. No.	124815
Contig ID	15555_1.R1010
5'-most EST	LIB25-026-Q1-E1-E5

Seq. No.	124816

Contig ID	15558_1.R1010
5'-most EST	jC-atXLIB327416P2g06b1
Method	BLASTX
NCBI GI	g2245129
BLAST score	205
E value	2.0e-15
Match length	279
% identity	31
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124817
Contig ID	15558_2.R1010
5'-most EST	LIB3175-018-P1-K1-F11
Method	BLASTN
NCBI GI	g4584841
BLAST score	36
E value	1.0e-10
Match length	474
% identity	68
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	124818
Contig ID	15558_5.R1010
5'-most EST	LIB3168-077-P1-K1-G3
Method	BLASTN
NCBI GI	g4584841
BLAST score	30
E value	4.0e-07
Match length	476
% identity	45
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	124819
Contig ID	15564_1.R1010
5'-most EST	jC-atXLIB327407P1c02b2
Method	BLASTX
NCBI GI	g4337175
BLAST score	625
E value	6.0e-65
Match length	166
% identity	77
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	124820
Contig ID	15592_1.R1010
5'-most EST	LIB24-051-Q1-E1-C11
Method	BLASTX
NCBI GI	g2947068
BLAST score	463
E value	2.0e-46
Match length	102
% identity	99

NCBI Description	(AC002521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124821
Contig ID	15595_1.R1010
5'-most EST	LIB23-058-Q1-E1-D1
Method	BLASTX
NCBI GI	g3157951
BLAST score	410
E value	5.0e-81
Match length	174
% identity	98
NCBI Description	(AC002131) Contains similarity to vesicle trafficking protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb_F14097 come from this gene. [Arabidopsis thaliana]

Seq. No.	124822
Contig ID	15597_1.R1010
5'-most EST	LIB24-096-Q1-E1-B4
Method	BLASTN
NCBI GI	g4159710
BLAST score	242
E value	1.0e-133
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSD23, complete sequence

Seq. No.	124823
Contig ID	15605_1.R1010
5'-most EST	g509440
Method	BLASTX
NCBI GI	g4262147
BLAST score	437
E value	3.0e-43
Match length	164
% identity	53
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	124824
Contig ID	15613_1.R1010
5'-most EST	jC-atXLIB327423P2g09b1
Method	BLASTN
NCBI GI	g2341023
BLAST score	191
E value	1.0e-103
Match length	442
% identity	99
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	124825
Contig ID	15615_1.R1010
5'-most EST	jC-atXLIB327402P1e08b1
Method	BLASTX
NCBI GI	g3377797
BLAST score	484

E value	2.0e-54
Match length	130
% identity	85
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	124826
Contig ID	15617_1.R1010
5'-most EST	jC-atXP113C105L6T7d1
Method	BLASTN
NCBI GI	g3510347
BLAST score	262
E value	1.0e-145
Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	124827
Contig ID	15620_1.R1010
5'-most EST	g2757319
Method	BLASTX
NCBI GI	g1903364
BLAST score	170
E value	1.0e-11
Match length	120
% identity	33
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	124828
Contig ID	15623_1.R1010
5'-most EST	jC-atXLIB327423P1f01b1
Method	BLASTX
NCBI GI	g3702332
BLAST score	296
E value	2.0e-26
Match length	152
% identity	40
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	124829
Contig ID	15625_1.R1010
5'-most EST	g2749616
Method	BLASTN
NCBI GI	g3522932
BLAST score	390
E value	0.0e+00
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124830

Contig ID	15627_1.R1010
5'-most EST	jC-atXLIB327409P1d10b1
Method	BLASTX
NCBI GI	g2811026
BLAST score	408
E value	1.0e-39
Match length	83
% identity	96
NCBI Description	TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi_2347204 (AC002338) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]

Seq. No.	124831
Contig ID	15636_1.R1010
5'-most EST	jC-alXLIB327435P4e06b1
Method	BLASTN
NCBI GI	g4662609
BLAST score	166
E value	6.0e-88
Match length	636
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	124832
Contig ID	15643_1.R1010
5'-most EST	g937246

Seq. No.	124833
Contig ID	15645_1.R1010
5'-most EST	jC-atXLIB327407P3b09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	70
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124834
Contig ID	15652_1.R1010
5'-most EST	LIB3177-033-P1-K2-A2
Method	BLASTN
NCBI GI	g3337347
BLAST score	49
E value	1.0e-18
Match length	219
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124835
Contig ID	15653_1.R1010
5'-most EST	g2749332
Method	BLASTX

NCBI GI	g3738285
BLAST score	73
E value	1.0e-23
Match length	62
% identity	95
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	124836
Contig ID	15653_2.R1010
5'-most EST	LIB25-101-Q1-E1-H1
Method	BLASTX
NCBI GI	g3738285
BLAST score	720
E value	2.0e-76
Match length	140
% identity	100
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	124837
Contig ID	15657_1.R1010
5'-most EST	jC-atXP96C248B9T7b1
Method	BLASTN
NCBI GI	g2760172
BLAST score	465
E value	0.0e+00
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	124838
Contig ID	15660_1.R1010
5'-most EST	LIB23-059-Q1-E1-B3

Seq. No.	124839
Contig ID	15664_1.R1010
5'-most EST	LIB3175-062-P1-K1-H2
Method	BLASTX
NCBI GI	g2191135
BLAST score	58
E value	4.0e-11
Match length	87
% identity	44
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	124840
Contig ID	15667_1.R1010
5'-most EST	jC-atXLIB327408P2a11b1
Method	BLASTX
NCBI GI	g1170606
BLAST score	429
E value	4.0e-42
Match length	130
% identity	67
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),

chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	124841
Contig ID	15669_1.R1010
5'-most EST	g935132
Method	BLASTX
NCBI GI	g1707016
BLAST score	210
E value	3.0e-16
Match length	137
% identity	41
NCBI Description	(U78721) cadmium-induced protein isolog [Arabidopsis thaliana]

Seq. No.	124842
Contig ID	15670_1.R1010
5'-most EST	jC-atXLIB327423P1g03a1
Method	BLASTN
NCBI GI	g4559375
BLAST score	207
E value	1.0e-112
Match length	314
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	124843
Contig ID	15670_2.R1010
5'-most EST	jC-atXLIB327427P1d03b1
Method	BLASTN
NCBI GI	g4584531
BLAST score	272
E value	1.0e-151
Match length	276
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	124844
Contig ID	15670_3.R1010
5'-most EST	jC-atXLIB327403P3b06a2
Method	BLASTX
NCBI GI	g3250693
BLAST score	491
E value	2.0e-49
Match length	94
% identity	99
NCBI Description	(AL024486) lectin like protein [Arabidopsis thaliana]

Seq. No.	124845
Contig ID	15670_5.R1010
5'-most EST	LIB35-008-Q1-E1-E1

Method	BLASTX
NCBI GI	g131372
BLAST score	161
E value	8.0e-11
Match length	34
% identity	100
NCBI Description	PHOTOSYSTEM II REACTION CENTRE M PROTEIN >gi_72719_pir__F2RZM photosystem II protein psbM - rice chloroplast >gi_11969_emb_CAA33984_ (X15901) PSII low MW protein [Oryza sativa] >gi_2924261_emb_CAA77413_ (Z00044) PSII M-protein [Nicotiana tabacum] >gi_226687_prf__1603356M photosystem II low MW protein [Oryza sativa]

Seq. No.	124846
Contig ID	15670_6.R1010
5'-most EST	LIB3234-060-P1-K1-C8
Method	BLASTN
NCBI GI	g2924257
BLAST score	54
E value	4.0e-21
Match length	205
% identity	93
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	124847
Contig ID	15670_7.R1010
5'-most EST	jC-atXmonuni26Ch05b1
Method	BLASTX
NCBI GI	g131372
BLAST score	161
E value	6.0e-11
Match length	34
% identity	100
NCBI Description	PHOTOSYSTEM II REACTION CENTRE M PROTEIN >gi_72719_pir__F2RZM photosystem II protein psbM - rice chloroplast >gi_11969_emb_CAA33984_ (X15901) PSII low MW protein [Oryza sativa] >gi_2924261_emb_CAA77413_ (Z00044) PSII M-protein [Nicotiana tabacum] >gi_226687_prf__1603356M photosystem II low MW protein [Oryza sativa]

Seq. No.	124848
Contig ID	15670_9.R1010
5'-most EST	jC-alXLIB327435P2g03a1
Method	BLASTX
NCBI GI	g3250693
BLAST score	328
E value	3.0e-30
Match length	63
% identity	100
NCBI Description	(AL024486) lectin like protein [Arabidopsis thaliana]

Seq. No.	124849
Contig ID	15670_13.R1010
5'-most EST	jC-atXLIB327402P2a04a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52

E value	4.0e-20
Match length	63
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	124850
Contig ID	15670_14.R1010
5'-most EST	jC-atXLIB327426P4f05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	124851
Contig ID	15670_15.R1010
5'-most EST	jC-atXLIB327421P1f11b1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	124852
Contig ID	15678_1.R1010
5'-most EST	LIB23-059-Q1-E1-D2
Method	BLASTX
NCBI GI	g3367517
BLAST score	857
E value	3.0e-92
Match length	171
% identity	94
NCBI Description	(AC004392) Similar to F4I1.26 putative beta-glucosidase gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene. [Arabidopsis thaliana]

Seq. No.	124853
Contig ID	15680_1.R1010
5'-most EST	LIB23-072-Q1-E1-G2
Method	BLASTX
NCBI GI	g2498887
BLAST score	191
E value	6.0e-14
Match length	115
% identity	37
NCBI Description	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) >gi_999036_bbs_164548 (S77162) steroid 5 alpha-reductase type 1 isoenzyme, SR type 1 [Cynomolgus monkeys, prostate, Peptide, 263 aa]

[Macaca fascicularis]

Seq. No.	124854
Contig ID	15680_2.R1010
5'-most EST	g2758654

Seq. No.	124855
Contig ID	15682_1.R1010
5'-most EST	g937975

Seq. No.	124856
Contig ID	15684_1.R1010
5'-most EST	LIB3175-056-P1-K1-G10

Seq. No.	124857
Contig ID	15689_1.R1010
5'-most EST	LIB23-059-Q1-E1-E8
Method	BLASTN
NCBI GI	g2828183
BLAST score	301
E value	1.0e-168
Match length	748
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	124858
Contig ID	15689_2.R1010
5'-most EST	jC-atXP112C130F5T7a1
Method	BLASTN
NCBI GI	g2828183
BLAST score	276
E value	1.0e-153
Match length	489
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	124859
Contig ID	15689_3.R1010
5'-most EST	jC-atXLIB327426P3h09b1
Method	BLASTN
NCBI GI	g2828183
BLAST score	66
E value	1.0e-28
Match length	189
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	124860
Contig ID	15692_1.R1010
5'-most EST	LIB3177-073-P1-K1-D9

Seq. No.	124861
Contig ID	15706_1.R1010
5'-most EST	LIB23-059-Q1-E1-G3

Method	BLASTN
NCBI GI	g3355463
BLAST score	528
E value	0.0e+00
Match length	592
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124862
Contig ID	15709_1.R1010
5'-most EST	LIB3176-096-P1-K1-A11
Method	BLASTN
NCBI GI	g3128136
BLAST score	243
E value	1.0e-134
Match length	275
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	124863
Contig ID	15710_1.R1010
5'-most EST	jC-atXP14C106C5T7d1
Method	BLASTN
NCBI GI	g3046856
BLAST score	180
E value	2.0e-96
Match length	531
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	124864
Contig ID	15715_1.R1010
5'-most EST	jC-atXL1029Q1B1G08a1

Seq. No.	124865
Contig ID	15715_2.R1010
5'-most EST	g906836
Method	BLASTN
NCBI GI	g3869075
BLAST score	35
E value	9.0e-10
Match length	93
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	124866
Contig ID	15718_1.R1010
5'-most EST	jC-atXLIB327417P3b11b1
Method	BLASTN
NCBI GI	g3193311
BLAST score	280
E value	1.0e-156
Match length	761

% identity	98
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	124867
Contig ID	15720_1.R1010
5'-most EST	LIB23-059-Q1-E1-H7
Method	BLASTX
NCBI GI	g4455156
BLAST score	460
E value	4.0e-46
Match length	90
% identity	99
NCBI Description	(AL021712) CDP-diacylglycerol synthetase-like protein [Arabidopsis thaliana]

Seq. No.	124868
Contig ID	15735_1.R1010
5'-most EST	jC-atXLIB327424P1f11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	124869
Contig ID	15741_1.R1010
5'-most EST	LIB24-064-Q1-E1-A5
Method	BLASTX
NCBI GI	g730864
BLAST score	179
E value	6.0e-13
Match length	147
% identity	31
NCBI Description	SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN SPX19) >gi_2117442_pir__S50729 sporulation protein SPS19 - yeast (Saccharomyces cerevisiae) >gi_600063_emb_CAA55506_ (X78898) N1362 [Saccharomyces cerevisiae] >gi_1302205_emb_CAA96103_ (Z71479) ORF YNL202w [Saccharomyces cerevisiae]

Seq. No.	124870
Contig ID	15742_1.R1010
5'-most EST	LIB23-060-Q1-E1-B9
Method	BLASTN
NCBI GI	g4539448
BLAST score	402
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	124871
Contig ID	15746_1.R1010

5'-most EST	LIB3176-051-P1-K1-G1
Seq. No.	124872
Contig ID	15747_1.R1010
5'-most EST	jC-atXP17C110D15T7d3
Method	BLASTX
NCBI GI	g3831439
BLAST score	123
E value	3.0e-36
Match length	108
% identity	76
NCBI Description	(AC005819) putative cytochrome b5 [Arabidopsis thaliana] >gi_4415945_gb_AAD20175_ (AC006418) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.	124873
Contig ID	15747_2.R1010
5'-most EST	jC-atXLIB327421P3f06b1
Method	BLASTX
NCBI GI	g3831439
BLAST score	553
E value	1.0e-56
Match length	117
% identity	88
NCBI Description	(AC005819) putative cytochrome b5 [Arabidopsis thaliana] >gi_4415945_gb_AAD20175_ (AC006418) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.	124874
Contig ID	15747_4.R1010
5'-most EST	LIB23-073-Q1-E1-G6
Method	BLASTX
NCBI GI	g3831439
BLAST score	391
E value	5.0e-38
Match length	72
% identity	100
NCBI Description	(AC005819) putative cytochrome b5 [Arabidopsis thaliana] >gi_4415945_gb_AAD20175_ (AC006418) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.	124875
Contig ID	15754_1.R1010
5'-most EST	LIB23-060-Q1-E1-D10
Seq. No.	124876
Contig ID	15760_1.R1010
5'-most EST	jC-atXLIB327423P2d07b1
Method	BLASTX
NCBI GI	g4056469
BLAST score	934
E value	1.0e-101
Match length	180
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,

gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	124877
Contig ID	15760_2.R1010
5'-most EST	jC-atXP102CE2G12T7034d1
Method	BLASTX
NCBI GI	g4056469
BLAST score	524
E value	2.0e-63
Match length	149
% identity	86
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	124878
Contig ID	15771_1.R1010
5'-most EST	g2758794
Method	BLASTN
NCBI GI	g3510339
BLAST score	254
E value	1.0e-140
Match length	692
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	124879
Contig ID	15771_2.R1010
5'-most EST	jC-atXLIB327405P4c06a1
Method	BLASTN
NCBI GI	g3510339
BLAST score	299
E value	1.0e-167
Match length	473
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	124880
Contig ID	15772_1.R1010
5'-most EST	LIB23-060-Q1-E1-E9
Method	BLASTN
NCBI GI	g3176694
BLAST score	272
E value	1.0e-151
Match length	409
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124881
Contig ID	15774_1.R1010
5'-most EST	jC-atXLIB327409P1a11b1

Method	BLASTX
NCBI GI	g4835244
BLAST score	482
E value	1.0e-83
Match length	179
% identity	90
NCBI Description	(AL049862) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	124882
Contig ID	15777_1.R1010
5'-most EST	jC-atXLIB327420P4h11b1
Method	BLASTN
NCBI GI	g3184270
BLAST score	165
E value	1.0e-87
Match length	458
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124883
Contig ID	15777_2.R1010
5'-most EST	jC-atXLIB327421P3d03b1
Method	BLASTN
NCBI GI	g3184270
BLAST score	425
E value	0.0e+00
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124884
Contig ID	15777_3.R1010
5'-most EST	LIB24-032-Q1-E1-H3
Method	BLASTN
NCBI GI	g3184270
BLAST score	202
E value	1.0e-110
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124885
Contig ID	15778_1.R1010
5'-most EST	LIB23-060-Q1-E1-F4
Method	BLASTN
NCBI GI	g2924652
BLAST score	255
E value	1.0e-141
Match length	287
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	124886
Contig ID	15781_1.R1010
5'-most EST	jC-atXLIB327426P1f02b1
Method	BLASTN
NCBI GI	g531828
BLAST score	38
E value	1.0e-11
Match length	130
% identity	87
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	124887
Contig ID	15785_1.R1010
5'-most EST	LIB3168-068-P1-K1-H4
Method	BLASTX
NCBI GI	g4455351
BLAST score	354
E value	1.0e-33
Match length	118
% identity	61
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	124888
Contig ID	15787_1.R1010
5'-most EST	jC-atXP100C251P15T7b1
Method	BLASTN
NCBI GI	g4468801
BLAST score	250
E value	1.0e-138
Match length	497
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	124889
Contig ID	15787_4.R1010
5'-most EST	jC-atXLIB327424P3c12b1
Method	BLASTN
NCBI GI	g4468801
BLAST score	231
E value	1.0e-127
Match length	464
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	124890
Contig ID	15797_1.R1010
5'-most EST	LIB3168-044-P1-K1-A12
Method	BLASTN
NCBI GI	g4757411
BLAST score	293
E value	1.0e-164
Match length	390
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	124891
Contig ID	15797_2.R1010
5'-most EST	jC-atXLIB327403P3g05b2
Method	BLASTX
NCBI GI	g2244806
BLAST score	424
E value	1.0e-41
Match length	131
% identity	66
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124892
Contig ID	15803_1.R1010
5'-most EST	LIB23-060-Q1-E1-H8
Method	BLASTX
NCBI GI	g3176707
BLAST score	336
E value	2.0e-31
Match length	108
% identity	60
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	124893
Contig ID	15805_1.R1010
5'-most EST	LIB23-074-Q1-E1-A6
Method	BLASTN
NCBI GI	g4522002
BLAST score	256
E value	1.0e-142
Match length	522
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T23K3 genomic sequence, complete sequence

Seq. No.	124894
Contig ID	15807_1.R1010
5'-most EST	LIB25-105-Q1-E1-D6
Method	BLASTX
NCBI GI	g3914015
BLAST score	325
E value	3.0e-30
Match length	135
% identity	50
NCBI Description	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) >gi_1001661_dbj_BAA10395_ (D64002) transcription-repair coupling factor [Synechocystis sp.]

Seq. No.	124895
Contig ID	15812_1.R1010
5'-most EST	LIB23-061-Q1-E1-A5
Method	BLASTN
NCBI GI	g3449314
BLAST score	491
E value	0.0e+00
Match length	495

% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]

Seq. No.	124896
Contig ID	15820_1.R1010
5'-most EST	g315502
Method	BLASTX
NCBI GI	g3096939
BLAST score	543
E value	2.0e-55
Match length	117
% identity	88
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	124897
Contig ID	15820_2.R1010
5'-most EST	g905770
Method	BLASTX
NCBI GI	g3096939
BLAST score	394
E value	4.0e-38
Match length	86
% identity	84
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	124898
Contig ID	15828_1.R1010
5'-most EST	g501966
Method	BLASTX
NCBI GI	g4206787
BLAST score	387
E value	3.0e-37
Match length	155
% identity	55
NCBI Description	(AF112863) syntaxin-related protein Nt-syr1 [Nicotiana tabacum]

Seq. No.	124899
Contig ID	15835_1.R1010
5'-most EST	LIB35-040-Q1-E1-G8

Seq. No.	124900
Contig ID	15836_1.R1010
5'-most EST	jC-atXP10C96L15T7d1
Method	BLASTX
NCBI GI	g3935167
BLAST score	644
E value	2.0e-67
Match length	122
% identity	100
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No.	124901
Contig ID	15842_1.R1010
5'-most EST	jC-atXLIB327403P3d09b2
Method	BLASTN

NCBI GI	g4539331
BLAST score	386
E value	0.0e+00
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	124902
Contig ID	15844_1.R1010
5'-most EST	jC-atXLIB327422P2e11b2
Method	BLASTN
NCBI GI	g4468801
BLAST score	568
E value	0.0e+00
Match length	820
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	124903
Contig ID	15848_1.R1010
5'-most EST	LIB23-061-Q1-E1-D5
Method	BLASTX
NCBI GI	g3582340
BLAST score	317
E value	6.0e-29
Match length	134
% identity	52
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	124904
Contig ID	15856_1.R1010
5'-most EST	jC-alXLIB327434P3h05b1
Method	BLASTX
NCBI GI	g3894190
BLAST score	793
E value	1.0e-84
Match length	221
% identity	70
NCBI Description	(AC005662) putative RNA polymerase [Arabidopsis thaliana]

Seq. No.	124905
Contig ID	15859_1.R1010
5'-most EST	LIB3177-056-P1-K1-H12
Method	BLASTX
NCBI GI	g1617270
BLAST score	704
E value	1.0e-74
Match length	135
% identity	93
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	124906
Contig ID	15860_1.R1010
5'-most EST	jC-atXLIB327408P2h11b1
Method	BLASTX

NCBI GI	g4455274
BLAST score	585
E value	4.0e-60
Match length	295
% identity	71
NCBI Description	(AL035527) spliceosome associated protein-like [Arabidopsis thaliana]

Seq. No.	124907
Contig ID	15866_1.R1010
5'-most EST	g671765
Method	BLASTX
NCBI GI	g1922246
BLAST score	400
E value	3.0e-43
Match length	97
% identity	98
NCBI Description	(Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No.	124908
Contig ID	15867_1.R1010
5'-most EST	LIB24-006-Q1-E1-E6
Method	BLASTX
NCBI GI	g2651313
BLAST score	517
E value	1.0e-52
Match length	115
% identity	62
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124909
Contig ID	15869_1.R1010
5'-most EST	LIB23-061-Q1-E1-F4
Method	BLASTN
NCBI GI	g4159706
BLAST score	250
E value	1.0e-138
Match length	284
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	124910
Contig ID	15871_1.R1010
5'-most EST	jC-atXLIB327431P2b09a1
Method	BLASTN
NCBI GI	g4417264
BLAST score	198
E value	1.0e-107
Match length	544
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124911
Contig ID	15875_1.R1010
5'-most EST	jC-atXLIB327431P1f04a1

Method	BLASTX
NCBI GI	g4337195
BLAST score	627
E value	3.0e-65
Match length	197
% identity	68
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	124912
Contig ID	15876_1.R1010
5'-most EST	LIB23-061-Q1-E1-G10

Seq. No.	124913
Contig ID	15878_1.R1010
5'-most EST	LIB23-061-Q1-E1-G12
Method	BLASTX
NCBI GI	g2435395
BLAST score	586
E value	2.0e-68
Match length	141
% identity	89
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	124914
Contig ID	15886_1.R1010
5'-most EST	jC-atXLIB327407P3b08b1
Method	BLASTX
NCBI GI	g4454014
BLAST score	267
E value	3.0e-23
Match length	88
% identity	56
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	124915
Contig ID	15893_1.R1010
5'-most EST	jC-atX22008Q1E1E08b1

Seq. No.	124916
Contig ID	15904_1.R1010
5'-most EST	LIB23-062-Q1-E1-G12
Method	BLASTX
NCBI GI	g4584527
BLAST score	258
E value	3.0e-22
Match length	113
% identity	46
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	124917
Contig ID	15906_1.R1010
5'-most EST	LIB3175-027-P1-K1-A2
Method	BLASTX
NCBI GI	g2226202
BLAST score	173
E value	3.0e-12
Match length	102

% identity	42
NCBI Description	(Y14082) hypothetical protein [Bacillus subtilis] >gi_2633281_emb_CAB12785_ (Z99109) similar to amino acid transporter [Bacillus subtilis]

Seq. No.	124918
Contig ID	15907_1.R1010
5'-most EST	jC-atXLIB327419P3a09b2
Method	BLASTX
NCBI GI	g4583153
BLAST score	375
E value	1.0e-35
Match length	138
% identity	54
NCBI Description	(AF108211) cytosolic inorganic pyrophosphatase [Homo sapiens]

Seq. No.	124919
Contig ID	15914_1.R1010
5'-most EST	g2762774
Method	BLASTX
NCBI GI	g3283893
BLAST score	152
E value	3.0e-10
Match length	53
% identity	53
NCBI Description	(AF070626) unknown [Homo sapiens]

Seq. No.	124920
Contig ID	15928_1.R1010
5'-most EST	LIB23-062-Q1-E1-D4

Seq. No.	124921
Contig ID	15929_1.R1010
5'-most EST	LIB3175-064-P1-K1-G10
Method	BLASTX
NCBI GI	g1651915
BLAST score	187
E value	2.0e-13
Match length	64
% identity	59
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	124922
Contig ID	15932_1.R1010
5'-most EST	LIB3168-011-P1-K1-H11
Method	BLASTN
NCBI GI	g2564045
BLAST score	145
E value	9.0e-76
Match length	387
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	124923
Contig ID	15934_1.R1010

5'-most EST	LIB3168-004-P1-K1-G3
Method	BLASTN
NCBI GI	g2656028
BLAST score	410
E value	0.0e+00
Match length	668
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	124924
Contig ID	15935_1.R1010
5'-most EST	jC-atXLIB327437P3g12b3
Method	BLASTN
NCBI GI	g2564046
BLAST score	481
E value	0.0e+00
Match length	497
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	124925
Contig ID	15936_1.R1010
5'-most EST	g2048206
Method	BLASTN
NCBI GI	g4733953
BLAST score	267
E value	1.0e-148
Match length	462
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	124926
Contig ID	15937_1.R1010
5'-most EST	jC-atXP12C99H22T7d2
Method	BLASTX
NCBI GI	g3738306
BLAST score	222
E value	9.0e-18
Match length	138
% identity	36
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	124927
Contig ID	15938_1.R1010
5'-most EST	LIB3234-097-P1-K1-E6
Method	BLASTX
NCBI GI	g4165025
BLAST score	233
E value	3.0e-19
Match length	110
% identity	41
NCBI Description	(AF043611) zinc-finger protein MCG4 [Homo sapiens]

Seq. No. 124928

Contig ID	15946_1.R1010
5'-most EST	jC-atXP102CE2H2T7b1
Method	BLASTX
NCBI GI	g2827139
BLAST score	1060
E value	1.0e-116
Match length	203
% identity	100
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	124929
Contig ID	15946_2.R1010
5'-most EST	g2413967
Method	BLASTN
NCBI GI	g2827138
BLAST score	429
E value	0.0e+00
Match length	519
% identity	97
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit (RSW1) gene, complete cds

Seq. No.	124930
Contig ID	15946_3.R1010
5'-most EST	g1520588
Method	BLASTN
NCBI GI	g2827138
BLAST score	399
E value	0.0e+00
Match length	434
% identity	98
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit (RSW1) gene, complete cds

Seq. No.	124931
Contig ID	15946_4.R1010
5'-most EST	jC-atXLIB327402P3b09a1
Method	BLASTN
NCBI GI	g4049332
BLAST score	258
E value	1.0e-143
Match length	397
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	124932
Contig ID	15951_1.R1010
5'-most EST	LIB23-072-Q1-E1-E7
Method	BLASTX
NCBI GI	g4049353
BLAST score	502
E value	6.0e-51
Match length	142

% identity	60
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	124933
Contig ID	15954_1.R1010
5'-most EST	g1216730
Method	BLASTX
NCBI GI	g3033397
BLAST score	706
E value	1.0e-74
Match length	138
% identity	97
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	124934
Contig ID	15956_1.R1010
5'-most EST	jC-atXP86CG10B11T7d2
Method	BLASTX
NCBI GI	g4163997
BLAST score	1299
E value	1.0e-144
Match length	229
% identity	100
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	124935
Contig ID	15956_2.R1010
5'-most EST	LIB24-090-Q1-E1-C8
Method	BLASTX
NCBI GI	g4163997
BLAST score	1109
E value	1.0e-122
Match length	205
% identity	100
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	124936
Contig ID	15980_1.R1010
5'-most EST	LIB23-063-Q1-E1-A6
Method	BLASTX
NCBI GI	g549010
BLAST score	438
E value	2.0e-43
Match length	96
% identity	92
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	124937
Contig ID	16001_1.R1010
5'-most EST	g2047766
Method	BLASTX
NCBI GI	g4376650
BLAST score	363
E value	2.0e-34
Match length	99
% identity	67
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	124938
Contig ID	16001_2.R1010
5'-most EST	g406842
Method	BLASTX
NCBI GI	g4376650
BLAST score	392
E value	2.0e-37
Match length	195
% identity	43
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	124939
Contig ID	16005_1.R1010
5'-most EST	jC-atX24063Q1E1C10b1

Seq. No.	124940
Contig ID	16008_1.R1010
5'-most EST	jC-atXLIB327405P3b07b1
Method	BLASTX
NCBI GI	g116229
BLAST score	296
E value	1.0e-26
Match length	139
% identity	40
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR >gi_99676_pir__S20876 chaperonin hsp60 precursor - Arabidopsis thaliana >gi_16221_emb_CAA77646_ (Z11547) chaperonin hsp60 [Arabidopsis thaliana]

Seq. No.	124941
Contig ID	16009_1.R1010
5'-most EST	LIB23-063-Q1-E1-D5
Method	BLASTN
NCBI GI	g4757414
BLAST score	191
E value	1.0e-103
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	124942
Contig ID	16026_1.R1010
5'-most EST	jC-alXLIB327435P3d08b1
Method	BLASTN

NCBI GI	g3869068
BLAST score	484
E value	0.0e+00
Match length	607
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	124943
Contig ID	16041_1.R1010
5'-most EST	LIB3176-041-P1-K1-G7
Method	BLASTN
NCBI GI	g3687221
BLAST score	77
E value	3.0e-35
Match length	270
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124944
Contig ID	16046_1.R1010
5'-most EST	jC-atXLIB327408P4c09b1
Method	BLASTX
NCBI GI	g2408068
BLAST score	454
E value	5.0e-45
Match length	170
% identity	46
NCBI Description	(Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	124945
Contig ID	16051_1.R1010
5'-most EST	LIB25-063-Q1-E1-D9

Seq. No.	124946
Contig ID	16058_1.R1010
5'-most EST	jC-atXP98CH2G6T7084d1
Method	BLASTX
NCBI GI	g2827139
BLAST score	1147
E value	1.0e-126
Match length	229
% identity	93
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	124947
Contig ID	16064_1.R1010
5'-most EST	g2757606
Method	BLASTN
NCBI GI	g4544381
BLAST score	339
E value	0.0e+00
Match length	436

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	124948
Contig ID	16065_1.R1010
5'-most EST	jC-atXLIB327417P1h04b1
Method	BLASTX
NCBI GI	g4006854
BLAST score	846
E value	6.0e-91
Match length	192
% identity	88
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	124949
Contig ID	16065_2.R1010
5'-most EST	jC-atXLIB327418P2f12b2
Method	BLASTN
NCBI GI	g4376087
BLAST score	211
E value	1.0e-115
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	124950
Contig ID	16069_1.R1010
5'-most EST	ARABL1-08-Q1-B1-A8
Method	BLASTX
NCBI GI	g4415913
BLAST score	277
E value	2.0e-24
Match length	105
% identity	58
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	124951
Contig ID	16080_1.R1010
5'-most EST	g1216943
Method	BLASTN
NCBI GI	g2833627
BLAST score	417
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	124952
Contig ID	16085_1.R1010
5'-most EST	LIB3176-017-P1-K1-G11
Method	BLASTX
NCBI GI	g2245131
BLAST score	328
E value	4.0e-30

Match length	170
% identity	46
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124953
Contig ID	16094_1.R1010
5'-most EST	LIB3177-046-P1-K2-H2
Method	BLASTX
NCBI GI	g4490329
BLAST score	455
E value	2.0e-45
Match length	148
% identity	62
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	124954
Contig ID	16101_1.R1010
5'-most EST	jC-atXLIB327409P3c05b1
Method	BLASTX
NCBI GI	g4388726
BLAST score	703
E value	2.0e-74
Match length	132
% identity	100
NCBI Description	(AC006413) putative 12-oxophytodienoate-10,11-reductase [Arabidopsis thaliana]

Seq. No.	124955
Contig ID	16106_1.R1010
5'-most EST	LIB23-065-Q1-E1-D1
Method	BLASTX
NCBI GI	g3139079
BLAST score	278
E value	2.0e-24
Match length	117
% identity	56
NCBI Description	(AF062537) cullin 3 [Homo sapiens]

Seq. No.	124956
Contig ID	16107_1.R1010
5'-most EST	LIB23-065-Q1-E1-D10
Method	BLASTN
NCBI GI	g4589429
BLAST score	368
E value	0.0e+00
Match length	372
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJM18, complete sequence

Seq. No.	124957
Contig ID	16111_1.R1010
5'-most EST	LIB24-009-Q1-E1-F1

Seq. No.	124958
Contig ID	16113_1.R1010
5'-most EST	LIB23-065-Q1-E1-D6

Seq. No.	124959
Contig ID	16121_1.R1010
5'-most EST	LIB3177-076-P1-K1-D1
Method	BLASTX
NCBI GI	g2829896
BLAST score	278
E value	2.0e-24
Match length	108
% identity	52
NCBI Description	(AC002311) highly similar to auxin-regulated protein GH3, gp_X60033_18591 [Arabidopsis thaliana]

Seq. No.	124960
Contig ID	16121_2.R1010
5'-most EST	LIB23-065-Q1-E1-E2
Method	BLASTX
NCBI GI	g2829896
BLAST score	123
E value	2.0e-13
Match length	75
% identity	59
NCBI Description	(AC002311) highly similar to auxin-regulated protein GH3, gp_X60033_18591 [Arabidopsis thaliana]

Seq. No.	124961
Contig ID	16126_1.R1010
5'-most EST	jC-atXP92C247M5T7050d1
Method	BLASTX
NCBI GI	g3522957
BLAST score	798
E value	3.0e-85
Match length	168
% identity	93
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	124962
Contig ID	16126_3.R1010
5'-most EST	jC-atXP38C158I21T7d1
Method	BLASTN
NCBI GI	g3522932
BLAST score	258
E value	1.0e-143
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	124963
Contig ID	16129_1.R1010
5'-most EST	jC-atXP74C223P18T7076d1
Method	BLASTN
NCBI GI	g4757678
BLAST score	501
E value	0.0e+00
Match length	976
% identity	100

NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	124964
Contig ID	16129_2.R1010
5'-most EST	jC-atXLIB327416P1h08b1
Method	BLASTN
NCBI GI	g4757678
BLAST score	381
E value	0.0e+00
Match length	468
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	124965
Contig ID	16129_4.R1010
5'-most EST	jC-atXLIB327405P2e07b2
Method	BLASTN
NCBI GI	g4757678
BLAST score	293
E value	1.0e-164
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	124966
Contig ID	16140_1.R1010
5'-most EST	jC-atXP19C111O4T7020a1
Method	BLASTX
NCBI GI	g4680192
BLAST score	317
E value	6.0e-29
Match length	89
% identity	70
NCBI Description	(AF111710) hypothetical protein [Oryza sativa subsp. indica]

Seq. No.	124967
Contig ID	16141_1.R1010
5'-most EST	jC-atXLIB327415P2e06b2
Method	BLASTN
NCBI GI	g4580365
BLAST score	215
E value	1.0e-117
Match length	452
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	124968
Contig ID	16146_1.R1010
5'-most EST	LIB25-082-Q1-E1-H5
Method	BLASTN
NCBI GI	g3264774
BLAST score	365

E value	0.0e+00
Match length	428
% identity	50
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	124969
Contig ID	16154_1.R1010
5'-most EST	g2733634
Method	BLASTN
NCBI GI	g4220641
BLAST score	235
E value	1.0e-129
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	124970
Contig ID	16161_1.R1010
5'-most EST	jC-atXLIB327417P1g03a1
Method	BLASTX
NCBI GI	g1710401
BLAST score	726
E value	7.0e-77
Match length	160
% identity	87
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	124971
Contig ID	16161_2.R1010
5'-most EST	g957462
Method	BLASTX
NCBI GI	g1710401
BLAST score	1051
E value	1.0e-115
Match length	244
% identity	80
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	124972
Contig ID	16161_3.R1010
5'-most EST	LIB3175-066-P1-K1-A3
Method	BLASTX
NCBI GI	g1710401
BLAST score	546
E value	8.0e-56
Match length	164
% identity	68
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

	>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]
Seq. No.	124973
Contig ID	16161_4.R1010
5'-most EST	jC-atXP54C186F14T7023a1
Method	BLASTX
NCBI GI	g1710401
BLAST score	518
E value	2.0e-52
Match length	121
% identity	82
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]
Seq. No.	124974
Contig ID	16163_1.R1010
5'-most EST	jC-atXLIB327428P4c05a2
Method	BLASTN
NCBI GI	g2264321
BLAST score	453
E value	0.0e+00
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.	124975
Contig ID	16164_1.R1010
5'-most EST	LIB3176-118-P2-K1-H9
Method	BLASTX
NCBI GI	g2832625
BLAST score	579
E value	8.0e-60
Match length	128
% identity	86
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	124976
Contig ID	16166_1.R1010
5'-most EST	LIB23-070-Q1-E1-A12
Method	BLASTX
NCBI GI	g3776572
BLAST score	1240
E value	1.0e-137
Match length	285
% identity	88
NCBI Description	(AC005388) ESTs gb_R65052, gb_AA712146, gb_H76533, gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383, gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis thaliana]
Seq. No.	124977
Contig ID	16166_2.R1010
5'-most EST	LIB3177-016-P1-K2-B2

Method	BLASTN
NCBI GI	g3659491
BLAST score	334
E value	0.0e+00
Match length	411
% identity	99
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	124978
Contig ID	16174_1.R1010
5'-most EST	LIB24-096-Q1-E1-H3

Seq. No.	124979
Contig ID	16179_1.R1010
5'-most EST	LIB3176-114-P2-K1-B8
Method	BLASTX
NCBI GI	g4049354
BLAST score	629
E value	1.0e-65
Match length	166
% identity	87
NCBI Description	(AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No.	124980
Contig ID	16185_1.R1010
5'-most EST	LIB23-066-Q1-E1-B9
Method	BLASTX
NCBI GI	g4455323
BLAST score	910
E value	3.0e-98
Match length	292
% identity	66
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	124981
Contig ID	16186_1.R1010
5'-most EST	LIB23-066-Q1-E1-C1
Method	BLASTN
NCBI GI	g4733953
BLAST score	165
E value	1.0e-87
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	124982
Contig ID	16187_1.R1010
5'-most EST	LIB25-110-Q1-E1-B5
Method	BLASTX
NCBI GI	g3608147
BLAST score	573
E value	4.0e-59
Match length	163

% identity	52
NCBI Description	(AC005314) putative chloroplast 31 kDa ribonucleoprotein precursor [Arabidopsis thaliana]

Seq. No.	124983
Contig ID	16188_1.R1010
5'-most EST	LIB24-089-Q1-E1-A9
Method	BLASTN
NCBI GI	g4159705
BLAST score	80
E value	9.0e-37
Match length	287
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	124984
Contig ID	16197_1.R1010
5'-most EST	LIB23-066-Q1-E1-F3
Method	BLASTX
NCBI GI	g1076758
BLAST score	430
E value	1.0e-42
Match length	118
% identity	69
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	124985
Contig ID	16207_1.R1010
5'-most EST	jC-alXLIB327435P2b06a1
Method	BLASTX
NCBI GI	g729477
BLAST score	500
E value	2.0e-50
Match length	105
% identity	88
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi_167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No.	124986
Contig ID	16207_2.R1010
5'-most EST	jC-atXLIB327420P4f10b1
Method	BLASTX
NCBI GI	g3913651
BLAST score	984
E value	1.0e-107
Match length	279
% identity	67
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032)

ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	124987
Contig ID	16212_1.R1010
5'-most EST	LIB3176-037-P1-K1-F1
Method	BLASTX
NCBI GI	g3924606
BLAST score	635
E value	1.0e-66
Match length	135
% identity	34
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	124988
Contig ID	16215_1.R1010
5'-most EST	LIB3175-007-P1-K1-B6
Method	BLASTX
NCBI GI	g2618691
BLAST score	493
E value	2.0e-49
Match length	198
% identity	55
NCBI Description	(AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	124989
Contig ID	16226_1.R1010
5'-most EST	g558161
Method	BLASTX
NCBI GI	g2842484
BLAST score	461
E value	4.0e-46
Match length	122
% identity	68
NCBI Description	(AL021749) tyrosine transaminase-like protein [Arabidopsis thaliana]

Seq. No.	124990
Contig ID	16234_1.R1010
5'-most EST	LIB24-017-Q1-E1-G7
Method	BLASTX
NCBI GI	g2739389
BLAST score	469
E value	4.0e-47
Match length	124
% identity	75
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	124991
Contig ID	16243_1.R1010
5'-most EST	LIB3176-011-P1-K1-H6
Method	BLASTN
NCBI GI	g4539290
BLAST score	381
E value	0.0e+00
Match length	438
% identity	98

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	124992
Contig ID	16246_1.R1010
5'-most EST	LIB23-066-Q1-E1-H9
Method	BLASTX
NCBI GI	g4768998
BLAST score	403
E value	4.0e-39
Match length	129
% identity	67
NCBI Description	(AF140499) chloroplast envelope calcium ATPase precursor [Oryza sativa]

Seq. No.	124993
Contig ID	16249_1.R1010
5'-most EST	LIB25-097-Q1-E1-B6
Method	BLASTN
NCBI GI	g2191126
BLAST score	281
E value	1.0e-157
Match length	323
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	124994
Contig ID	16252_1.R1010
5'-most EST	jC-atXLIB327409P3d11b1
Method	BLASTX
NCBI GI	g3834306
BLAST score	415
E value	3.0e-40
Match length	160
% identity	60
NCBI Description	(AC005679) EST gb_R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No.	124995
Contig ID	16263_1.R1010
5'-most EST	jC-alXLIB327436P4f09b1
Method	BLASTX
NCBI GI	g4191785
BLAST score	924
E value	1.0e-100
Match length	241
% identity	72
NCBI Description	(AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No.	124996
Contig ID	16265_1.R1010
5'-most EST	LIB25-109-Q1-E1-B2
Method	BLASTN
NCBI GI	g4220634
BLAST score	305
E value	1.0e-171
Match length	364

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9H21, complete sequence [Arabidopsis thaliana]

Seq. No.	124997
Contig ID	16267_1.R1010
5'-most EST	LIB24-027-Q1-E1-H12
Method	BLASTX
NCBI GI	g3953458
BLAST score	658
E value	5.0e-69
Match length	196
% identity	73
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	124998
Contig ID	16270_1.R1010
5'-most EST	jC-atXP92CH3G8T7078d1

Seq. No.	124999
Contig ID	16271_1.R1010
5'-most EST	LIB3234-076-P1-K1-C12
Method	BLASTX
NCBI GI	g4587550
BLAST score	214
E value	3.0e-17
Match length	78
% identity	58
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	125000
Contig ID	16274_1.R1010
5'-most EST	jC-atXLIB327405P2g01b2
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	56
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125001
Contig ID	16274_2.R1010
5'-most EST	jC-atXmonuni26Cg08a1

Seq. No.	125002
Contig ID	16297_1.R1010
5'-most EST	jC-atXLIB327408P2c11b1
Method	BLASTX
NCBI GI	g3236240
BLAST score	482
E value	3.0e-48
Match length	143
% identity	69
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	125003
Contig ID	16300_1.R1010
5'-most EST	jC-atXP115C116A22T7063d1
Method	BLASTX
NCBI GI	g2660677
BLAST score	1141
E value	1.0e-131
Match length	237
% identity	94
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	125004
Contig ID	16300_2.R1010
5'-most EST	jC-atXLIB327422P3d07b2
Method	BLASTN
NCBI GI	g3449315
BLAST score	151
E value	3.0e-79
Match length	352
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	125005
Contig ID	16303_1.R1010
5'-most EST	LIB23-067-Q1-E1-F6

Seq. No.	125006
Contig ID	16306_1.R1010
5'-most EST	LIB3175-080-P1-K1-B2

Seq. No.	125007
Contig ID	16307_1.R1010
5'-most EST	LIB24-078-Q1-E1-F1
Method	BLASTX
NCBI GI	g4105798
BLAST score	389
E value	1.0e-37
Match length	84
% identity	71
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	125008
Contig ID	16307_2.R1010
5'-most EST	LIB23-067-Q1-E1-G10
Method	BLASTX
NCBI GI	g4105798
BLAST score	731
E value	1.0e-77
Match length	158
% identity	72
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	125009
Contig ID	16308_1.R1010
5'-most EST	jC-atXLIB327407P1h08b2
Method	BLASTX

NCBI GI	g3063637
BLAST score	320
E value	2.0e-29
Match length	89
% identity	65
NCBI Description	(AF056204) thioesterase homolog [Gossypium hirsutum]

Seq. No.	125010
Contig ID	16313_1.R1010
5'-most EST	jC-atXLIB327406P1b06b1
Method	BLASTN
NCBI GI	g2842474
BLAST score	175
E value	1.0e-93
Match length	375
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	125011
Contig ID	16320_1.R1010
5'-most EST	LIB23-067-Q1-E1-H5
Method	BLASTN
NCBI GI	g2656029
BLAST score	236
E value	1.0e-130
Match length	321
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	125012
Contig ID	16335_1.R1010
5'-most EST	LIB3176-021-P1-K1-E12
Method	BLASTX
NCBI GI	g3319355
BLAST score	1348
E value	1.0e-166
Match length	328
% identity	92
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No.	125013
Contig ID	16335_4.R1010
5'-most EST	g2748936
Method	BLASTN
NCBI GI	g3319339
BLAST score	382
E value	0.0e+00
Match length	438
% identity	96
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	125014
Contig ID	16339_1.R1010
5'-most EST	LIB23-068-Q1-E1-B3

Seq. No.	125015
Contig ID	16344_1.R1010
5'-most EST	jC-atXLIB327438P3g12a2
Method	BLASTN
NCBI GI	g4538972
BLAST score	106
E value	2.0e-52
Match length	445
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M11 (ESSA project)

Seq. No.	125016
Contig ID	16351_1.R1010
5'-most EST	LIB23-068-Q1-E1-C8
Method	BLASTX
NCBI GI	g349379
BLAST score	478
E value	5.0e-48
Match length	160
% identity	67
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	125017
Contig ID	16352_1.R1010
5'-most EST	LIB23-068-Q1-E1-C9
Method	BLASTX
NCBI GI	g2252631
BLAST score	231
E value	4.0e-19
Match length	135
% identity	45
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125018
Contig ID	16353_1.R1010
5'-most EST	g3719178
Method	BLASTN
NCBI GI	g3702728
BLAST score	310
E value	1.0e-174
Match length	810
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	125019
Contig ID	16354_1.R1010
5'-most EST	jC-atXLIB327415P4e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	125020
Contig ID	16356_1.R1010
5'-most EST	jC-atXLIB327420P4e11b1
Method	BLASTX
NCBI GI	g4587686
BLAST score	585
E value	5.0e-63
Match length	143
% identity	88
NCBI Description	(AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	125021
Contig ID	16357_1.R1010
5'-most EST	LIB23-068-Q1-E1-D4
Method	BLASTN
NCBI GI	g3128135
BLAST score	443
E value	0.0e+00
Match length	477
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	125022
Contig ID	16358_2.R1010
5'-most EST	g2749069
Method	BLASTX
NCBI GI	g3413705
BLAST score	422
E value	3.0e-41
Match length	92
% identity	84
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	125023
Contig ID	16358_3.R1010
5'-most EST	g2758558
Method	BLASTX
NCBI GI	g3413705
BLAST score	1004
E value	1.0e-109
Match length	208
% identity	93
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	125024
Contig ID	16367_1.R1010
5'-most EST	LIB24-065-Q1-E1-C5
Method	BLASTX
NCBI GI	g1652323
BLAST score	187
E value	2.0e-13
Match length	151

% identity	42
NCBI Description	(D90904) fibrillin [Synechocystis sp.]

Seq. No.	125025
Contig ID	16376_1.R1010
5'-most EST	LIB23-068-Q1-E1-F5
Method	BLASTN
NCBI GI	g2213606
BLAST score	478
E value	0.0e+00
Match length	486
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	125026
Contig ID	16380_1.R1010
5'-most EST	LIB23-068-Q1-E1-F9
Method	BLASTX
NCBI GI	g1531758
BLAST score	395
E value	3.0e-38
Match length	96
% identity	76
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	125027
Contig ID	16381_1.R1010
5'-most EST	jC-alXLIB327436P4a12b1
Method	BLASTN
NCBI GI	g2760167
BLAST score	365
E value	0.0e+00
Match length	950
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	125028
Contig ID	16381_2.R1010
5'-most EST	jC-alXLIB327435P2h11a1
Method	BLASTN
NCBI GI	g2760167
BLAST score	255
E value	1.0e-141
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	125029
Contig ID	16385_1.R1010
5'-most EST	LIB23-068-Q1-E1-G6
Method	BLASTX
NCBI GI	g4469012
BLAST score	291

E value	6.0e-26
Match length	61
% identity	92
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125030
Contig ID	16391_1.R1010
5'-most EST	jC-alXLIB327434P3d03b1
Method	BLASTX
NCBI GI	g2983147
BLAST score	259
E value	5.0e-22
Match length	122
% identity	44
NCBI Description	(AE000692) hypothetical protein [Aquifex aeolicus]

Seq. No.	125031
Contig ID	16391_2.R1010
5'-most EST	jC-atXLIB327420P3c01b1
Method	BLASTN
NCBI GI	g4220640
BLAST score	152
E value	7.0e-80
Match length	359
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	125032
Contig ID	16393_1.R1010
5'-most EST	jC-atXLIB327427P4a10b2

Seq. No.	125033
Contig ID	16401_1.R1010
5'-most EST	jC-atXP122C120H15T7021a1
Method	BLASTX
NCBI GI	g2252857
BLAST score	355
E value	2.0e-33
Match length	112
% identity	70
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	125034
Contig ID	16401_2.R1010
5'-most EST	LIB3176-018-P1-K1-F3
Method	BLASTX
NCBI GI	g2252857
BLAST score	352
E value	4.0e-33
Match length	111
% identity	68
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	125035

Contig ID	16401_3.R1010
5'-most EST	g2747448
Method	BLASTX
NCBI GI	g2252857
BLAST score	232
E value	6.0e-19
Match length	81
% identity	60
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	125036
Contig ID	16406_1.R1010
5'-most EST	LIB3175-018-P1-K1-G3
Method	BLASTX
NCBI GI	g1304227
BLAST score	315
E value	1.0e-28
Match length	119
% identity	48
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	125037
Contig ID	16406_2.R1010
5'-most EST	jC-atXLIB327422P3d11b2
Method	BLASTX
NCBI GI	g1304227
BLAST score	748
E value	3.0e-79
Match length	285
% identity	50
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	125038
Contig ID	16413_1.R1010
5'-most EST	LIB25-060-Q1-E1-F2
Method	BLASTN
NCBI GI	g4757388
BLAST score	192
E value	1.0e-104
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	125039
Contig ID	16422_1.R1010
5'-most EST	jC-atXLIB327419P3b08b2
Method	BLASTN
NCBI GI	g4159707
BLAST score	464
E value	0.0e+00
Match length	785

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	125040
Contig ID	16432_1.R1010
5'-most EST	jC-atXLIB327424P1e05b2
Method	BLASTN
NCBI GI	g2564046
BLAST score	301
E value	1.0e-168
Match length	313
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	125041
Contig ID	16436_1.R1010
5'-most EST	g755107
Method	BLASTX
NCBI GI	g3342552
BLAST score	232
E value	6.0e-19
Match length	90
% identity	53
NCBI Description	(AF076979) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	125042
Contig ID	16438_1.R1010
5'-most EST	jC-atXLIB327425P1e06b1
Method	BLASTN
NCBI GI	g2760169
BLAST score	304
E value	1.0e-170
Match length	1032
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	125043
Contig ID	16442_1.R1010
5'-most EST	jC-atX24102Q1E1H04a2
Method	BLASTX
NCBI GI	g4455192
BLAST score	387
E value	2.0e-37
Match length	98
% identity	74
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	125044
Contig ID	16448_1.R1010
5'-most EST	jC-atXLIB327431P1c11a1
Method	BLASTX
NCBI GI	g4218121
BLAST score	588

E value	9.0e-61
Match length	172
% identity	67
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	125045
Contig ID	16454_1.R1010
5'-most EST	jC-atXLIB327421P4e04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125046
Contig ID	16455_1.R1010
5'-most EST	LIB23-069-Q1-E1-F5
Method	BLASTN
NCBI GI	g3172156
BLAST score	301
E value	1.0e-168
Match length	669
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125047
Contig ID	16466_1.R1010
5'-most EST	LIB3168-089-P1-K1-A5
Method	BLASTX
NCBI GI	g1117780
BLAST score	245
E value	1.0e-20
Match length	147
% identity	37
NCBI Description	(D49367) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]

Seq. No.	125048
Contig ID	16472_1.R1010
5'-most EST	g2759453
Method	BLASTN
NCBI GI	g4063735
BLAST score	440
E value	0.0e+00
Match length	522
% identity	97
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	125049
Contig ID	16473_1.R1010
5'-most EST	g2758479
Method	BLASTX

NCBI GI	g2642441
BLAST score	758
E value	1.0e-160
Match length	469
% identity	58
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	125050
Contig ID	16483_1.R1010
5'-most EST	jC-atXLIB327407P1e11b2

Seq. No.	125051
Contig ID	16485_1.R1010
5'-most EST	jC-atXLIB327430P4e09b1
Method	BLASTN
NCBI GI	g4589434
BLAST score	437
E value	0.0e+00
Match length	533
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	125052
Contig ID	16487_1.R1010
5'-most EST	jC-atXP91CH1E9T7b1
Method	BLASTX
NCBI GI	g4455359
BLAST score	385
E value	3.0e-42
Match length	158
% identity	65
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	125053
Contig ID	16494_1.R1010
5'-most EST	LIB23-070-Q1-E1-B7
Method	BLASTN
NCBI GI	g3510336
BLAST score	33
E value	8.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	125054
Contig ID	16495_1.R1010
5'-most EST	LIB3168-076-P1-K1-C6
Method	BLASTX
NCBI GI	g2622714
BLAST score	329
E value	2.0e-30
Match length	136
% identity	46
NCBI Description	(AE000918) phosphonopyruvate decarboxylase [Methanobacterium thermoautotrophicum]

Seq. No.	125055
Contig ID	16504_1.R1010
5'-most EST	g957863

Seq. No.	125056
Contig ID	16516_1.R1010
5'-most EST	jC-atXLIB327402P1h03b1
Method	BLASTX
NCBI GI	g2342674
BLAST score	1100
E value	1.0e-120
Match length	299
% identity	78
NCBI Description	(AC000106) Similar to ATP-dependent Clp protease (gb_D90915). EST gb_N65461 comes from this gene. [Arabidopsis thaliana]

Seq. No.	125057
Contig ID	16517_1.R1010
5'-most EST	jC-atXLIB327419P2d03b2
Method	BLASTN
NCBI GI	g2828182
BLAST score	214
E value	1.0e-117
Match length	460
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	125058
Contig ID	16518_1.R1010
5'-most EST	g3450236
Method	BLASTX
NCBI GI	g3249096
BLAST score	239
E value	7.0e-20
Match length	49
% identity	92
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	125059
Contig ID	16518_2.R1010
5'-most EST	LIB3234-094-P1-K1-C6
Method	BLASTX
NCBI GI	g3249096
BLAST score	103
E value	1.0e-03
Match length	195
% identity	23
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	125060
Contig ID	16522_1.R1010
5'-most EST	jC-atXLIB327422P2g02b2
Method	BLASTX
NCBI GI	g4678261
BLAST score	1000
E value	1.0e-109
Match length	233
% identity	88
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	125061
Contig ID	16522_2.R1010
5'-most EST	LIB23-070-Q1-E1-E7
Method	BLASTX
NCBI GI	g4678261
BLAST score	67
E value	4.0e-57
Match length	138
% identity	91
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	125062
Contig ID	16523_1.R1010
5'-most EST	LIB23-070-Q1-E1-E8

Seq. No.	125063
Contig ID	16526_1.R1010
5'-most EST	LIB3176-084-P1-K1-C5
Method	BLASTX
NCBI GI	g3367522
BLAST score	270
E value	1.0e-23
Match length	89
% identity	63
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	125064
Contig ID	16529_1.R1010
5'-most EST	jC-atXLIB327418P2c03b2
Method	BLASTX
NCBI GI	g4490329
BLAST score	709
E value	3.0e-77
Match length	164
% identity	88
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	125065
Contig ID	16530_1.R1010
5'-most EST	jC-alXLIB327434P1b11b1
Method	BLASTX
NCBI GI	g2979559

BLAST score	310
E value	6.0e-28
Match length	97
% identity	63
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	125066
Contig ID	16540_1.R1010
5'-most EST	jC-atXP79C239H2T7b1

Seq. No.	125067
Contig ID	16543_1.R1010
5'-most EST	jC-atXLIB327408P3d02b1
Method	BLASTX
NCBI GI	g2654208
BLAST score	744
E value	2.0e-83
Match length	225
% identity	75
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	125068
Contig ID	16549_1.R1010
5'-most EST	LIB23-070-Q1-E1-H7

Seq. No.	125069
Contig ID	16561_1.R1010
5'-most EST	g2748741
Method	BLASTX
NCBI GI	g3033398
BLAST score	617
E value	4.0e-64
Match length	127
% identity	97
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	125070
Contig ID	16564_1.R1010
5'-most EST	LIB23-071-Q1-E1-B7
Method	BLASTX
NCBI GI	g1841540
BLAST score	433
E value	7.0e-43
Match length	128
% identity	64
NCBI Description	(U87317) ATP citrate lyase [Drosophila melanogaster]

Seq. No.	125071
Contig ID	16565_1.R1010
5'-most EST	LIB23-071-Q1-E1-B8

Seq. No.	125072
Contig ID	16578_1.R1010

5'-most EST	jC-atXP108C180P11T7062d1
Method	BLASTX
NCBI GI	g3860257
BLAST score	414
E value	3.0e-40
Match length	166
% identity	52
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125073
Contig ID	16581_1.R1010
5'-most EST	ARABL1-045-Q1-B1-H8
Method	BLASTX
NCBI GI	g4455155
BLAST score	575
E value	1.0e-59
Match length	119
% identity	93
NCBI Description	(AL022023) EF-1 alpha-like protein (fragment) [Arabidopsis thaliana]

Seq. No.	125074
Contig ID	16584_1.R1010
5'-most EST	LIB23-071-Q1-E1-D8
Method	BLASTX
NCBI GI	g4584358
BLAST score	268
E value	1.0e-23
Match length	66
% identity	83
NCBI Description	(AC006420) unknown protein [Arabidopsis thaliana]

Seq. No.	125075
Contig ID	16588_1.R1010
5'-most EST	LIB25-060-Q1-E1-F7
Method	BLASTX
NCBI GI	g3687251
BLAST score	718
E value	6.0e-76
Match length	143
% identity	100
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	125076
Contig ID	16588_2.R1010
5'-most EST	jC-atXP102CE2H7T7090d1
Method	BLASTN
NCBI GI	g3687221
BLAST score	160
E value	2.0e-84
Match length	454
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125077
Contig ID	16590_1.R1010

5'-most EST	g2762188
Method	BLASTX
NCBI GI	g3164140
BLAST score	689
E value	6.0e-77
Match length	261
% identity	57
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	125078
Contig ID	16596_1.R1010
5'-most EST	jC-atXLIB327417P4b02b1
Method	BLASTN
NCBI GI	g4757662
BLAST score	352
E value	0.0e+00
Match length	465
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	125079
Contig ID	16599_1.R1010
5'-most EST	LIB35-040-Q1-E1-D10
Method	BLASTX
NCBI GI	g3859599
BLAST score	746
E value	2.0e-79
Match length	154
% identity	88
NCBI Description	(AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]

Seq. No.	125080
Contig ID	16603_1.R1010
5'-most EST	jC-atX24004Q1E1A06b1
Method	BLASTX
NCBI GI	g1399380
BLAST score	647
E value	8.0e-68
Match length	138
% identity	85
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	125081
Contig ID	16607_1.R1010
5'-most EST	jC-alXLIB327434P4e10b1

Seq. No.	125082
Contig ID	16612_1.R1010
5'-most EST	LIB35-030-Q1-E1-H3

Seq. No.	125083
Contig ID	16614_1.R1010
5'-most EST	g931169

Seq. No.	125084
Contig ID	16620_1.R1010
5'-most EST	jC-atXP82C240P12T7b1
Method	BLASTX
NCBI GI	g1523796
BLAST score	618
E value	3.0e-64
Match length	174
% identity	67
NCBI Description	(X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	125085
Contig ID	16628_1.R1010
5'-most EST	LIB3175-048-P1-K1-B9
Method	BLASTX
NCBI GI	g2982243
BLAST score	175
E value	4.0e-12
Match length	146
% identity	32
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	125086
Contig ID	16628_2.R1010
5'-most EST	g937630

Seq. No.	125087
Contig ID	16630_1.R1010
5'-most EST	LIB23-072-Q1-E1-A7
Method	BLASTN
NCBI GI	g2815519
BLAST score	453
E value	0.0e+00
Match length	461
% identity	100
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	125088
Contig ID	16632_1.R1010
5'-most EST	LIB24-007-Q1-E1-D9
Method	BLASTN
NCBI GI	g4589415
BLAST score	161
E value	3.0e-85
Match length	353
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	125089
Contig ID	16633_1.R1010
5'-most EST	LIB23-072-Q1-E1-B1
Method	BLASTX
NCBI GI	g2995366
BLAST score	292

E value	6.0e-26
Match length	173
% identity	37
NCBI Description	(AL022245) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	125090
Contig ID	16638_1.R1010
5'-most EST	jC-atXLIB327421P3a11b1
Method	BLASTX
NCBI GI	g4505721
BLAST score	142
E value	1.0e-08
Match length	129
% identity	32
NCBI Description	peroxisomal biogenesis factor 12 >gi_3024371_sp_O00623_PEXC_HUMAN PEROXIN-12 >gi_1938367 (U91521) peroxin 12 [Homo sapiens] >gi_1938369 (U91522) peroxin 12 [Homo sapiens] >gi_3308973_dbj_BAA31559_ (AB004546) peroxisome assembly factor-3 (PAF-3) [Homo sapiens]

Seq. No.	125091
Contig ID	16640_1.R1010
5'-most EST	LIB23-072-Q1-E1-B5
Method	BLASTX
NCBI GI	g4580392
BLAST score	452
E value	3.0e-45
Match length	112
% identity	88
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125092
Contig ID	16646_1.R1010
5'-most EST	jC-alXLIB327436P2d03b1
Method	BLASTX
NCBI GI	g1708972
BLAST score	266
E value	4.0e-23
Match length	121
% identity	50
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR (HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi_1262279 (U51562) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina] >gi_2343181 (AF013161) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina]

Seq. No.	125093
Contig ID	16653_1.R1010
5'-most EST	LIB23-072-Q1-E1-C9
Method	BLASTX
NCBI GI	g3287864
BLAST score	87
E value	2.0e-43
Match length	85

% identity	99
NCBI Description	PUTATIVE TRYPSIN INHIBITOR ATTI-2 PRECURSOR

Seq. No.	125094
Contig ID	16654_1.R1010
5'-most EST	LIB23-072-Q1-E1-D1
Method	BLASTX
NCBI GI	g3935181
BLAST score	921
E value	1.0e-99
Match length	175
% identity	97
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	125095
Contig ID	16659_1.R1010
5'-most EST	jC-atXP82CG2E12T7b1
Method	BLASTX
NCBI GI	g4206122
BLAST score	154
E value	8.0e-10
Match length	64
% identity	55
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	125096
Contig ID	16662_1.R1010
5'-most EST	LIB23-072-Q1-E1-D6
Method	BLASTN
NCBI GI	g4191771
BLAST score	449
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125097
Contig ID	16685_1.R1010
5'-most EST	LIB35-028-Q1-E1-A4
Method	BLASTN
NCBI GI	g4713943
BLAST score	156
E value	5.0e-82
Match length	407
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	125098
Contig ID	16694_1.R1010
5'-most EST	g2764051
Method	BLASTN
NCBI GI	g4335744
BLAST score	102
E value	4.0e-50

Match length	329
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125099
Contig ID	16695_1.R1010
5'-most EST	jC-atXLIB327408P4c07b1
Method	BLASTN
NCBI GI	g3402695
BLAST score	167
E value	9.0e-89
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125100
Contig ID	16695_2.R1010
5'-most EST	LIB3168-051-P1-K1-A8
Method	BLASTN
NCBI GI	g3402695
BLAST score	342
E value	0.0e+00
Match length	398
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125101
Contig ID	16698_1.R1010
5'-most EST	jC-atXLIB327408P4e01b1
Method	BLASTX
NCBI GI	g3786017
BLAST score	587
E value	1.0e-60
Match length	115
% identity	100
NCBI Description	(AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No.	125102
Contig ID	16703_1.R1010
5'-most EST	jC-atXLIB327416P1h11b1

Seq. No.	125103
Contig ID	16704_1.R1010
5'-most EST	LIB23-072-Q1-E1-H7
Method	BLASTX
NCBI GI	g114339
BLAST score	509
E value	1.0e-51
Match length	123
% identity	80
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625

(J04737) ATPase [Arabidopsis thaliana]

Seq. No.	125104
Contig ID	16709_1.R1010
5'-most EST	jC-atXLIB327416P1d08b1
Method	BLASTX
NCBI GI	g4587595
BLAST score	288
E value	1.0e-25
Match length	99
% identity	53
NCBI Description	(AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	125105
Contig ID	16730_1.R1010
5'-most EST	LIB25-104-Q1-E1-E8
Method	BLASTN
NCBI GI	g2760316
BLAST score	139
E value	3.0e-72
Match length	376
% identity	98
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	125106
Contig ID	16731_1.R1010
5'-most EST	jC-atXLIB327408P1g04b1
Method	BLASTX
NCBI GI	g2529683
BLAST score	811
E value	1.0e-86
Match length	215
% identity	76
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	125107
Contig ID	16745_1.R1010
5'-most EST	jC-atXLIB327419P4b02b1

Seq. No.	125108
Contig ID	16748_1.R1010
5'-most EST	LIB23-073-Q1-E1-E6
Method	BLASTX
NCBI GI	g1495259
BLAST score	211
E value	9.0e-17
Match length	81
% identity	52
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	125109
Contig ID	16752_1.R1010
5'-most EST	jC-atXLIB327422P1c10b1
Method	BLASTX
NCBI GI	g2088651

BLAST score	157
E value	3.0e-17
Match length	201
% identity	36
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	125110
Contig ID	16756_1.R1010
5'-most EST	LIB23-073-Q1-E1-F2
Method	BLASTX
NCBI GI	g3805845
BLAST score	1358
E value	1.0e-151
Match length	273
% identity	95
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	125111
Contig ID	16763_1.R1010
5'-most EST	LIB3234-015-P1-K1-H4
Method	BLASTX
NCBI GI	g4335749
BLAST score	1205
E value	1.0e-133
Match length	232
% identity	100
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	125112
Contig ID	16792_1.R1010
5'-most EST	LIB3177-013-P1-K2-D3
Method	BLASTX
NCBI GI	g4539335
BLAST score	685
E value	7.0e-72
Match length	328
% identity	42
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	125113
Contig ID	16804_1.R1010
5'-most EST	LIB24-058-Q1-E1-C9
Method	BLASTN
NCBI GI	g2351063
BLAST score	222
E value	1.0e-121
Match length	378
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	125114
Contig ID	16808_1.R1010
5'-most EST	jC-alXLIB327436P3b05b1
Method	BLASTX
NCBI GI	g4544393

BLAST score	88
E value	4.0e-34
Match length	102
% identity	78
NCBI Description	(AC007047) putative ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	125115
Contig ID	16812_1.R1010
5'-most EST	LIB23-074-Q1-E1-D3
Method	BLASTN
NCBI GI	g16473
BLAST score	385
E value	0.0e+00
Match length	396
% identity	51
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No.	125116
Contig ID	16817_1.R1010
5'-most EST	LIB3176-091-P1-K1-B11
Method	BLASTN
NCBI GI	g2664199
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Arabidopsis thaliana GTL2 gene

Seq. No.	125117
Contig ID	16823_1.R1010
5'-most EST	LIB23-074-Q1-E1-E5
Method	BLASTN
NCBI GI	g3869075
BLAST score	364
E value	0.0e+00
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	125118
Contig ID	16827_1.R1010
5'-most EST	LIB24-097-Q1-E1-C7
Method	BLASTN
NCBI GI	g2760169
BLAST score	341
E value	0.0e+00
Match length	408
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	125119
Contig ID	16832_1.R1010
5'-most EST	jC-atXP13C104N18T7d2
Method	BLASTN

NCBI GI	g3241924
BLAST score	250
E value	1.0e-138
Match length	492
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	125120
Contig ID	16842_1.R1010
5'-most EST	LIB23-074-Q1-E1-G4
Method	BLASTX
NCBI GI	g2780225
BLAST score	348
E value	7.0e-33
Match length	111
% identity	59
NCBI Description	(AJ223281) alpha-hydroxynitrile lyase [Manihot esculenta]

Seq. No.	125121
Contig ID	16864_1.R1010
5'-most EST	LIB23-075-Q1-E1-E9
Method	BLASTN
NCBI GI	g2696018
BLAST score	424
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	125122
Contig ID	16868_1.R1010
5'-most EST	LIB23-075-Q1-E1-F9
Method	BLASTN
NCBI GI	g4415928
BLAST score	251
E value	1.0e-139
Match length	492
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125123
Contig ID	16876_2.R1010
5'-most EST	jC-atXLIB327430P1f03b1
Method	BLASTN
NCBI GI	g3128138
BLAST score	289
E value	1.0e-161
Match length	658
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	125124
Contig ID	16877_1.R1010

5'-most EST	jC-atXLIB327421P4c10b1
Method	BLASTX
NCBI GI	g4415916
BLAST score	194
E value	3.0e-48
Match length	281
% identity	39
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	125125
Contig ID	16877_2.R1010
5'-most EST	jC-atXLIB327405P3h10b1
Method	BLASTX
NCBI GI	g4415916
BLAST score	294
E value	3.0e-26
Match length	121
% identity	48
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	125126
Contig ID	16877_3.R1010
5'-most EST	jC-atXLIB327420P3g10b1
Method	BLASTX
NCBI GI	g4567229
BLAST score	370
E value	5.0e-35
Match length	154
% identity	44
NCBI Description	(AC007119) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	125127
Contig ID	16880_1.R1010
5'-most EST	jC-atXLIB327423P4b11b1
Method	BLASTX
NCBI GI	g3876095
BLAST score	190
E value	3.0e-14
Match length	146
% identity	34
NCBI Description	(Z75537) Similarity to Yeast ATP-dependent transporter (SW:YEM6_YEAST); cDNA EST EMBL:C09155 comes from this gene; cDNA EST yk259a9.3 comes from this gene; cDNA EST yk259a9.5 comes from this gene; cDNA EST yk453c2.3 comes from

Seq. No.	125128
Contig ID	16883_1.R1010
5'-most EST	jC-atXLIB327423P4b05b1
Method	BLASTN
NCBI GI	g4585952
BLAST score	34
E value	2.0e-09
Match length	113
% identity	89

NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence
Seq. No.	125129
Contig ID	16884_1.R1010
5'-most EST	LIB3175-070-P1-K-A1
Method	BLASTX
NCBI GI	g1732411
BLAST score	545
E value	2.0e-55
Match length	261
% identity	45
NCBI Description	(U47924) isopeptidase T [Homo sapiens]
Seq. No.	125130
Contig ID	16885_1.R1010
5'-most EST	LIB3175-041-P1-K1-B7
Method	BLASTX
NCBI GI	g629669
BLAST score	157
E value	2.0e-10
Match length	139
% identity	30
NCBI Description	hypothetical protein - tomato
Seq. No.	125131
Contig ID	16886_1.R1010
5'-most EST	jC-atXLIB327423P3b06b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	167
E value	2.0e-13
Match length	83
% identity	55
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.	125132
Contig ID	16887_1.R1010
5'-most EST	jC-atXP79C231H9T7b1
Method	BLASTX
NCBI GI	g2088653
BLAST score	762
E value	4.0e-81
Match length	149
% identity	100
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]
Seq. No.	125133
Contig ID	16887_2.R1010
5'-most EST	jC-atXLIB327423P3b12b1
Method	BLASTX
NCBI GI	g2088653
BLAST score	811
E value	8.0e-87
Match length	173
% identity	92

NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]
Seq. No.	125134
Contig ID	16889_1.R1010
5'-most EST	jC-atXLIB327423P1c02b1
Method	BLASTN
NCBI GI	g4220644
BLAST score	530
E value	0.0e+00
Match length	1191
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.	125135
Contig ID	16889_2.R1010
5'-most EST	LIB35-020-Q1-E1-F12
Method	BLASTN
NCBI GI	g4220644
BLAST score	372
E value	0.0e+00
Match length	445
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.	125136
Contig ID	16891_1.R1010
5'-most EST	LIB3175-033-P1-K1-H4
Method	BLASTX
NCBI GI	g4263777
BLAST score	53
E value	3.0e-71
Match length	164
% identity	83
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]
Seq. No.	125137
Contig ID	16892_1.R1010
5'-most EST	LIB24-001-Q1-E1-B3
Method	BLASTX
NCBI GI	g3004551
BLAST score	255
E value	2.0e-21
Match length	86
% identity	58
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.	125138
Contig ID	16900_1.R1010
5'-most EST	jC-atXLIB327423P1c10b1
Method	BLASTX
NCBI GI	g4581141
BLAST score	479

E value	8.0e-48
Match length	125
% identity	86
NCBI Description	(AC006919) unknown protein [Arabidopsis thaliana]

Seq. No.	125139
Contig ID	16900_2.R1010
5'-most EST	jC-atXLIB327423P1c10a1
Method	BLASTX
NCBI GI	g4581141
BLAST score	331
E value	2.0e-30
Match length	83
% identity	90
NCBI Description	(AC006919) unknown protein [Arabidopsis thaliana]

Seq. No.	125140
Contig ID	16903_1.R1010
5'-most EST	LIB24-014-Q1-E1-B8
Method	BLASTN
NCBI GI	g2760168
BLAST score	469
E value	0.0e+00
Match length	523
% identity	67
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	125141
Contig ID	16906_1.R1010
5'-most EST	g935663
Method	BLASTX
NCBI GI	g2244772
BLAST score	746
E value	3.0e-88
Match length	176
% identity	98
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	125142
Contig ID	16909_1.R1010
5'-most EST	LIB25-112-Q1-E1-C8
Method	BLASTX
NCBI GI	g4510399
BLAST score	377
E value	3.0e-36
Match length	65
% identity	100
NCBI Description	(AC006587) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	125143
Contig ID	16912_1.R1010
5'-most EST	LIB24-130-Q1-E1-H5
Method	BLASTN
NCBI GI	g3702729
BLAST score	314

E value	1.0e-176
Match length	360
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A11, complete sequence [Arabidopsis thaliana]

Seq. No.	125144
Contig ID	16916_1.R1010
5'-most EST	LIB24-001-Q1-E1-D7
Method	BLASTX
NCBI GI	g3763926
BLAST score	309
E value	3.0e-28
Match length	116
% identity	56
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	125145
Contig ID	16918_1.R1010
5'-most EST	LIB24-001-Q1-E1-D9

Seq. No.	125146
Contig ID	16924_1.R1010
5'-most EST	g507052
Method	BLASTX
NCBI GI	g1172657
BLAST score	723
E value	1.0e-76
Match length	183
% identity	68
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_1363577_pir__S58551 photosystem I protein A2 - maize chloroplast >gi_902221_emb_CAA60285_ (X86563) PSI P700 apoprotein A2 [Zea mays]

Seq. No.	125147
Contig ID	16928_1.R1010
5'-most EST	jC-atXLIB327419P2e01b2
Method	BLASTX
NCBI GI	g3062791
BLAST score	325
E value	5.0e-30
Match length	84
% identity	73
NCBI Description	(AB010433) Lipid transfer protein [Brassica rapa]

Seq. No.	125148
Contig ID	16929_1.R1010
5'-most EST	LIB24-001-Q1-E1-F1
Method	BLASTX
NCBI GI	g4559322
BLAST score	86
E value	8.9e-02
Match length	241
% identity	65
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	125149
Contig ID	16931_1.R1010
5'-most EST	LIB24-001-Q1-E1-F11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	46
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	125150
Contig ID	16934_1.R1010
5'-most EST	jC-alXLIB327434P2d01b1
Method	BLASTX
NCBI GI	g2695931
BLAST score	358
E value	1.0e-33
Match length	91
% identity	73
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No.	125151
Contig ID	16936_1.R1010
5'-most EST	jC-alXLIB327434P1b12b1
Method	BLASTX
NCBI GI	g4678310
BLAST score	329
E value	3.0e-30
Match length	68
% identity	97
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	125152
Contig ID	16942_1.R1010
5'-most EST	LIB3177-075-P1-K1-H6
Method	BLASTX
NCBI GI	g2347192
BLAST score	626
E value	2.0e-65
Match length	139
% identity	55
NCBI Description	(AC002338) spliceosomal protein U2B isolog [Arabidopsis thaliana]

Seq. No.	125153
Contig ID	16943_1.R1010
5'-most EST	g17419
Method	BLASTX
NCBI GI	g4539307
BLAST score	294
E value	3.0e-26
Match length	120
% identity	53
NCBI Description	(AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	125154
Contig ID	16944_1.R1010
5'-most EST	LIB24-001-Q1-E1-G3
Method	BLASTN
NCBI GI	g3337347
BLAST score	458
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125155
Contig ID	16950_1.R1010
5'-most EST	jC-atXP123C117D14T7020d1
Method	BLASTN
NCBI GI	g2618599
BLAST score	271
E value	1.0e-150
Match length	718
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	125156
Contig ID	16951_1.R1010
5'-most EST	LIB3177-091-P1-K1-C2
Method	BLASTX
NCBI GI	g4584527
BLAST score	223
E value	3.0e-18
Match length	105
% identity	39
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	125157
Contig ID	16954_1.R1010
5'-most EST	jC-atXLIB327422P2e09b2
Method	BLASTX
NCBI GI	g543187
BLAST score	112
E value	5.0e-05
Match length	158
% identity	4
NCBI Description	ankyrin, erythrocyte - mouse >gi_311817_emb_CAA48801_ (X69063) erythroid ankyrin [Mus musculus]

Seq. No.	125158
Contig ID	16956_1.R1010
5'-most EST	jC-atXLIB327426P1f02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125159
Contig ID	16958_1.R1010
5'-most EST	jC-atXLIB327423P1d01b1
Method	BLASTN
NCBI GI	g3510336
BLAST score	634
E value	0.0e+00
Match length	727
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	125160
Contig ID	16960_1.R1010
5'-most EST	jC-atXLIB327423P1d02b1
Method	BLASTX
NCBI GI	g4835235
BLAST score	223
E value	9.0e-18
Match length	115
% identity	39
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	125161
Contig ID	16961_1.R1010
5'-most EST	jC-atX24001Q1E1H09b1

Seq. No.	125162
Contig ID	16962_1.R1010
5'-most EST	jC-atXLIB327423P4b08b1
Method	BLASTX
NCBI GI	g99809
BLAST score	609
E value	2.0e-63
Match length	144
% identity	78
NCBI Description	gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608) Bplo [Brassica napus]

Seq. No.	125163
Contig ID	16963_1.R1010
5'-most EST	jC-alX22084Q1E2C03a1
Method	BLASTX
NCBI GI	g3461842
BLAST score	215
E value	5.0e-17
Match length	145
% identity	37
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	125164
Contig ID	16964_1.R1010
5'-most EST	jC-atXLIB327423P4b09b1
Method	BLASTX
NCBI GI	g4099605

BLAST score	178
E value	8.0e-13
Match length	147
% identity	53
NCBI Description	(U88836) translational activator GCN1 [Homo sapiens]

Seq. No.	125165
Contig ID	16965_1.R1010
5'-most EST	jC-atXP65C208K18T7087d1
Method	BLASTX
NCBI GI	g3413700
BLAST score	725
E value	1.0e-76
Match length	180
% identity	82
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	125166
Contig ID	16968_1.R1010
5'-most EST	LIB25-016-Q1-E1-B3
Method	BLASTN
NCBI GI	g1871173
BLAST score	330
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	125167
Contig ID	16974_1.R1010
5'-most EST	jC-atX24050Q1E1F03b1
Method	BLASTN
NCBI GI	g3004543
BLAST score	261
E value	1.0e-145
Match length	475
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125168
Contig ID	16979_1.R1010
5'-most EST	jC-atXLIB327423P1c04b1
Method	BLASTX
NCBI GI	g3236248
BLAST score	1013
E value	1.0e-110
Match length	248
% identity	80
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	125169
Contig ID	16980_1.R1010
5'-most EST	LIB25-091-Q1-E1-A5
Method	BLASTX
NCBI GI	g4584535

BLAST score	379
E value	2.0e-36
Match length	160
% identity	50
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	125170
Contig ID	16981_1.R1010
5'-most EST	jC-atXLIB327423P1c01b1
Method	BLASTN
NCBI GI	g2264314
BLAST score	566
E value	0.0e+00
Match length	818
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	125171
Contig ID	16982_1.R1010
5'-most EST	LIB3177-089-P1-K1-E9
Method	BLASTN
NCBI GI	g4589434
BLAST score	160
E value	1.0e-84
Match length	304
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	125172
Contig ID	16990_1.R1010
5'-most EST	LIB3177-078-P1-K1-H2
Method	BLASTX
NCBI GI	g4584541
BLAST score	586
E value	1.0e-60
Match length	114
% identity	100
NCBI Description	(AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]

Seq. No.	125173
Contig ID	16991_1.R1010
5'-most EST	jC-atXLIB327423P1c11b1
Method	BLASTX
NCBI GI	g3695375
BLAST score	850
E value	1.0e-107
Match length	244
% identity	79
NCBI Description	(AF096370) contains similarity to the major intrinsic protein domain (Pfam: PF00230 MIP, E-value: 5.7e-111) [Arabidopsis thaliana]

Seq. No.	125174
Contig ID	16995_1.R1010

5'-most EST	LIB35-031-Q1-E1-A10
Method	BLASTX
NCBI GI	g4586101
BLAST score	176
E value	8.0e-30
Match length	69
% identity	99
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	125175
Contig ID	17000_1.R1010
5'-most EST	LIB25-101-Q1-E1-E12
Method	BLASTX
NCBI GI	g4455192
BLAST score	322
E value	5.0e-30
Match length	107
% identity	34
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	125176
Contig ID	17001_1.R1010
5'-most EST	jC-atXLIB327423P3c02b1
Method	BLASTX
NCBI GI	g549706
BLAST score	155
E value	4.0e-10
Match length	94
% identity	41
NCBI Description	KTI12 PROTEIN >gi_539197_pir__S37937 KTI12 protein - yeast (Saccharomyces cerevisiae) >gi_486185_emb_CAA81950_ (Z28110) ORF YKL110c [Saccharomyces cerevisiae] >gi_536816_emb_CAA54646_ (X77511) KTI12 [Saccharomyces cerevisiae]

Seq. No.	125177
Contig ID	17003_1.R1010
5'-most EST	jC-atXLIB327420P1a05b1
Method	BLASTX
NCBI GI	g1575296
BLAST score	669
E value	1.0e-147
Match length	266
% identity	100
NCBI Description	(U58919) beta-carotene hydroxylase [Arabidopsis thaliana]

Seq. No.	125178
Contig ID	17005_1.R1010
5'-most EST	jC-atXLIB327423P1c12b1
Method	BLASTX
NCBI GI	g4337187
BLAST score	516
E value	5.0e-52
Match length	159
% identity	58
NCBI Description	(AC006403) putative prolylcarboxypeptidase, 5' partial [Arabidopsis thaliana]

Seq. No.	125179
Contig ID	17005_2.R1010
5'-most EST	g2445967
Method	BLASTX
NCBI GI	g2827710
BLAST score	208
E value	4.0e-36
Match length	84
% identity	99
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	125180
Contig ID	17005_3.R1010
5'-most EST	jC-atXLIB327423P1c12a1
Method	BLASTX
NCBI GI	g2827710
BLAST score	137
E value	9.0e-33
Match length	85
% identity	100
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	125181
Contig ID	17009_1.R1010
5'-most EST	jC-atXLIB327422P1f09b1

Seq. No.	125182
Contig ID	17013_1.R1010
5'-most EST	jC-atXLIB327423P4c07b1
Method	BLASTX
NCBI GI	g4539435
BLAST score	399
E value	9.0e-39
Match length	112
% identity	71
NCBI Description	(AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	125183
Contig ID	17015_1.R1010
5'-most EST	LIB3176-030-P1-K1-D2
Method	BLASTX
NCBI GI	g1495251
BLAST score	267
E value	3.0e-23
Match length	147
% identity	42
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	125184
Contig ID	17017_1.R1010
5'-most EST	jC-atXLIB327423P4c05b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	44

E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	125185
Contig ID	17018_1.R1010
5'-most EST	jC-atXLIB327423P3c05b1
Method	BLASTX
NCBI GI	g2827704
BLAST score	524
E value	4.0e-65
Match length	144
% identity	87
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No.	125186
Contig ID	17024_1.R1010
5'-most EST	jC-atXLIB327423P3c07b1
Method	BLASTX
NCBI GI	g126947
BLAST score	186
E value	5.0e-27
Match length	120
% identity	56
NCBI Description	MEI2 PROTEIN >gi_68996_pir__COZPME mei2 protein - fission yeast (Schizosaccharomyces pombe) >gi_4991_emb_CAA30165_ (X07180) put. mei2 protein (AA 1 - 750) [Schizosaccharomyces pombe] >gi_2664237_emb_CAA15822.1_ (AL009227) mei2 protein. [Schizosaccharomyces pombe]

Seq. No.	125187
Contig ID	17028_1.R1010
5'-most EST	jC-alXLIB327436P1f10b1

Seq. No.	125188
Contig ID	17029_1.R1010
5'-most EST	LIB3176-004-P1-K1-G11
Method	BLASTX
NCBI GI	g2462748
BLAST score	622
E value	9.0e-65
Match length	122
% identity	99
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	125189
Contig ID	17030_1.R1010
5'-most EST	jC-atXLIB327423P3c12b1
Method	BLASTX
NCBI GI	g2642157
BLAST score	222
E value	2.0e-58
Match length	147
% identity	76

NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	125190
Contig ID	17037_1.R1010
5'-most EST	jC-atXLIB327423P4c11b1
Method	BLASTX
NCBI GI	g4056499
BLAST score	192
E value	2.0e-14
Match length	87
% identity	51
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	125191
Contig ID	17038_1.R1010
5'-most EST	jC-atXLIB327423P3c11b1
Method	BLASTX
NCBI GI	g4510387
BLAST score	577
E value	1.0e-59
Match length	115
% identity	95
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	125192
Contig ID	17040_1.R1010
5'-most EST	g1158509
Method	BLASTN
NCBI GI	g3402695
BLAST score	48
E value	1.0e-17
Match length	253
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125193
Contig ID	17047_1.R1010
5'-most EST	LIB24-002-Q1-E1-H8
Method	BLASTX
NCBI GI	g2760326
BLAST score	883
E value	3.0e-95
Match length	228
% identity	70
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	125194
Contig ID	17050_1.R1010
5'-most EST	LIB24-055-Q1-E1-H2
Method	BLASTN
NCBI GI	g3047100
BLAST score	251
E value	1.0e-139
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	125195
Contig ID	17051_1.R1010
5'-most EST	jC-atX24003Q1E1A11b1
Method	BLASTN
NCBI GI	g3928074
BLAST score	386
E value	0.0e+00
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125196
Contig ID	17052_1.R1010
5'-most EST	g935552
Method	BLASTX
NCBI GI	g2281088
BLAST score	786
E value	4.0e-84
Match length	155
% identity	95
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	125197
Contig ID	17053_1.R1010
5'-most EST	jC-atXLIB327409P4e03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125198
Contig ID	17059_1.R1010
5'-most EST	jC-atXLIB327406P4b01b2
Method	BLASTN
NCBI GI	g2191126
BLAST score	273
E value	1.0e-152
Match length	772
% identity	94
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	125199
Contig ID	17059_2.R1010
5'-most EST	g2048234
Method	BLASTN
NCBI GI	g2191126
BLAST score	449
E value	0.0e+00
Match length	548
% identity	98

NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	125200
Contig ID	17059_3.R1010
5'-most EST	jC-atXLIB327406P4b01a2
Method	BLASTN
NCBI GI	g2191126
BLAST score	321
E value	1.0e-180
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	125201
Contig ID	17060_1.R1010
5'-most EST	LIB24-003-Q1-E1-A9

Seq. No.	125202
Contig ID	17063_1.R1010
5'-most EST	jC-atXLIB327413P1f04b1
Method	BLASTX
NCBI GI	g1076813
BLAST score	234
E value	2.0e-19
Match length	132
% identity	48
NCBI Description	initiator-binding protein - maize

Seq. No.	125203
Contig ID	17065_1.R1010
5'-most EST	LIB24-003-Q1-E1-B2
Method	BLASTX
NCBI GI	g2950472
BLAST score	366
E value	2.0e-34
Match length	301
% identity	35
NCBI Description	(AL022070) putative autophagocytosis protein [Schizosaccharomyces pombe]

Seq. No.	125204
Contig ID	17065_2.R1010
5'-most EST	g906493
Method	BLASTN
NCBI GI	g3046847
BLAST score	225
E value	1.0e-123
Match length	813
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	125205
Contig ID	17065_5.R1010
5'-most EST	g3449791
Method	BLASTN
NCBI GI	g3046847

BLAST score	233
E value	1.0e-128
Match length	245
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	125206
Contig ID	17066_1.R1010
5'-most EST	jC-atXLIB327415P2f05b2
Method	BLASTX
NCBI GI	g1143381
BLAST score	799
E value	4.0e-85
Match length	321
% identity	51
NCBI Description	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]

Seq. No.	125207
Contig ID	17068_1.R1010
5'-most EST	LIB24-003-Q1-E1-B5
Method	BLASTX
NCBI GI	g3334441
BLAST score	88
E value	3.0e-02
Match length	168
% identity	19
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN T5I7.9 IN CHROMOSOME II >gi_2642161 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125208
Contig ID	17071_1.R1010
5'-most EST	jC-alXLIB327434P3b12b1
Method	BLASTX
NCBI GI	g3513744
BLAST score	252
E value	2.0e-21
Match length	123
% identity	44
NCBI Description	(AF080118) contains similarity to Medicago truncatula MtN3 (GB:Y08726) [Arabidopsis thaliana]

Seq. No.	125209
Contig ID	17074_1.R1010
5'-most EST	LIB24-003-Q1-E1-C12
Method	BLASTN
NCBI GI	g2264310
BLAST score	53
E value	8.0e-21
Match length	251
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	125210
Contig ID	17076_2.R1010

5'-most EST	LIB24-033-Q1-E1-H8
Method	BLASTN
NCBI GI	g4204173
BLAST score	291
E value	1.0e-162
Match length	529
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125211
Contig ID	17077_1.R1010
5'-most EST	jC-alX24004Q1E1C03b1
Method	BLASTN
NCBI GI	g2760173
BLAST score	52
E value	3.0e-20
Match length	148
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	125212
Contig ID	17080_1.R1010
5'-most EST	LIB24-003-Q1-E1-C7
Method	BLASTN
NCBI GI	g2244901
BLAST score	235
E value	1.0e-129
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	125213
Contig ID	17081_2.R1010
5'-most EST	jC-atXLIB327404P2d07b1
Method	BLASTX
NCBI GI	g2495179
BLAST score	1208
E value	1.0e-133
Match length	254
% identity	94
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	125214
Contig ID	17082_1.R1010
5'-most EST	g935577
Method	BLASTN
NCBI GI	g4519194

BLAST score	171
E value	3.0e-91
Match length	332
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	125215
Contig ID	17091_1.R1010
5'-most EST	jC-atXLIB327413P3f11b1
Method	BLASTX
NCBI GI	g2558654
BLAST score	288
E value	1.0e-25
Match length	149
% identity	41
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	125216
Contig ID	17096_1.R1010
5'-most EST	jC-atXLIB327413P2g01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125217
Contig ID	17096_2.R1010
5'-most EST	LIB25-030-Q1-E1-C7

Seq. No.	125218
Contig ID	17098_1.R1010
5'-most EST	LIB3175-001-Q1-K1-C5
Method	BLASTN
NCBI GI	g3046852
BLAST score	302
E value	1.0e-169
Match length	404
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	125219
Contig ID	17098_2.R1010
5'-most EST	jC-alX24003Q1E1E02b1
Method	BLASTN
NCBI GI	g3046852
BLAST score	425
E value	0.0e+00
Match length	473
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	125220
Contig ID	17100_1.R1010
5'-most EST	jC-atX24003Q1E1E05b1
Method	BLASTN
NCBI GI	g1297184
BLAST score	52
E value	3.0e-20
Match length	222
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, co

Seq. No.	125221
Contig ID	17101_1.R1010
5'-most EST	LIB24-003-Q1-E1-E6

Seq. No.	125222
Contig ID	17102_1.R1010
5'-most EST	jC-atXLIB327413P1g11b1
Method	BLASTX
NCBI GI	g4539460
BLAST score	190
E value	3.0e-14
Match length	155
% identity	4
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	125223
Contig ID	17109_1.R1010
5'-most EST	jC-atXLIB327413P1h03b1
Method	BLASTX
NCBI GI	g2499973
BLAST score	235
E value	2.0e-19
Match length	105
% identity	53
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	125224
Contig ID	17109_2.R1010
5'-most EST	jC-atXP1C66C10T7d1
Method	BLASTX
NCBI GI	g2499973
BLAST score	235
E value	2.0e-19
Match length	105
% identity	53
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	125225

Contig ID	17111_1.R1010
5'-most EST	jC-atXLIB327413P2h03b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	46
E value	1.0e-16
Match length	46
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	125226
Contig ID	17111_3.R1010
5'-most EST	jC-atX22085Q1E2B06b1
Method	BLASTX
NCBI GI	g3063706
BLAST score	658
E value	3.0e-69
Match length	130
% identity	95
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	125227
Contig ID	17113_1.R1010
5'-most EST	jC-atXLIB327413P4g11b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	1040
E value	1.0e-166
Match length	305
% identity	91
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	125228
Contig ID	17114_1.R1010
5'-most EST	jC-alX24003Q1E1F06b1
Method	BLASTN
NCBI GI	g4468801
BLAST score	242
E value	1.0e-133
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	125229
Contig ID	17116_1.R1010
5'-most EST	jC-atXLIB327419P3h01b2

Seq. No.	125230
Contig ID	17117_1.R1010
5'-most EST	jC-atXLIB327413P1h11b1

Seq. No.	125231
Contig ID	17120_1.R1010
5'-most EST	jC-atXLIB327413P4h03b1
Method	BLASTX

NCBI GI	g112785
BLAST score	377
E value	1.0e-35
Match length	180
% identity	41
NCBI Description	DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No.	125232
Contig ID	17124_1.R1010
5'-most EST	g2576751
Method	BLASTX
NCBI GI	g2443890
BLAST score	421
E value	4.0e-56
Match length	230
% identity	51
NCBI Description	(AC002294) similar to NAM (gp_X92205_1321924) and CUC2 (gp_AB002560_1944132) proteins [Arabidopsis thaliana]

Seq. No.	125233
Contig ID	17131_1.R1010
5'-most EST	jC-atXLIB327414P1a03b1
Method	BLASTX
NCBI GI	g1916290
BLAST score	220
E value	3.0e-17
Match length	105
% identity	41
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	125234
Contig ID	17131_2.R1010
5'-most EST	g2763059

Seq. No.	125235
Contig ID	17131_3.R1010
5'-most EST	g931321

Seq. No.	125236
Contig ID	17144_1.R1010
5'-most EST	LIB25-019-Q1-E1-H7
Method	BLASTN
NCBI GI	g3063690
BLAST score	46
E value	1.0e-16
Match length	150
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11

(ESSAII project)

Seq. No.	125237
Contig ID	17146_1.R1010
5'-most EST	jC-alXLIB327436P2b09b1
Method	BLASTX
NCBI GI	g2642433
BLAST score	470
E value	6.0e-47
Match length	169
% identity	37
NCBI Description	(AC002391) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	125238
Contig ID	17147_1.R1010
5'-most EST	jC-atXLIB327427P2b09b1
Method	BLASTX
NCBI GI	g2500376
BLAST score	481
E value	4.0e-48
Match length	95
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	125239
Contig ID	17148_1.R1010
5'-most EST	g937571
Method	BLASTX
NCBI GI	g4185135
BLAST score	932
E value	1.0e-100
Match length	314
% identity	77
NCBI Description	(AC005724) unknown protein [Arabidopsis thaliana]

Seq. No.	125240
Contig ID	17151_2.R1010
5'-most EST	jC-atXLIB327413P1f06b1
Method	BLASTX
NCBI GI	g2500543
BLAST score	231
E value	6.0e-19
Match length	124
% identity	38
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5 >gi_733602 (U23484) similar to S. cerevisiae pre-mRNA splicing factor RNA helicase PRP22 (SP:PR22_YEAST, P24384) and other DEAH subfamily members of the DEAD box family helicases [Caenorhabditis elegans]

Seq. No.	125241
Contig ID	17154_1.R1010
5'-most EST	LIB24-121-Q1-E1-B9

Seq. No.	125242

Contig ID	17156_1.R1010
5'-most EST	jC-atXLIB327413P2f03b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	125243
Contig ID	17159_1.R1010
5'-most EST	jC-alX24004Q1E1C01b1
Method	BLASTX
NCBI GI	g4539324
BLAST score	197
E value	4.0e-15
Match length	120
% identity	49
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	125244
Contig ID	17162_1.R1010
5'-most EST	LIB3234-055-P1-K1-E10
Method	BLASTX
NCBI GI	g3851553
BLAST score	115
E value	2.0e-05
Match length	106
% identity	11
NCBI Description	(AF083898) RNA-binding protein Nova-2 [Homo sapiens]

Seq. No.	125245
Contig ID	17169_1.R1010
5'-most EST	jC-atXLIB327413P1g02b1
Method	BLASTX
NCBI GI	g1709358
BLAST score	333
E value	6.0e-31
Match length	114
% identity	56
NCBI Description	NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859 nucleoside triphosphatase - garden pea >gi_2129890_pir__S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase [Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No.	125246
Contig ID	17172_1.R1010
5'-most EST	jC-atXLIB327413P2g03b1
Method	BLASTX
NCBI GI	g2213643
BLAST score	897
E value	1.0e-96

Match length	219
% identity	78
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	125247
Contig ID	17172_3.R1010
5'-most EST	LIB3234-055-P1-K1-C1
Method	BLASTX
NCBI GI	g498038
BLAST score	452
E value	4.0e-45
Match length	127
% identity	72
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	125248
Contig ID	17175_1.R1010
5'-most EST	jC-atXLIB327413P4f11b1
Method	BLASTX
NCBI GI	g4538905
BLAST score	629
E value	1.0e-65
Match length	122
% identity	100
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	125249
Contig ID	17176_1.R1010
5'-most EST	jC-atXLIB327413P4f12b1
Method	BLASTX
NCBI GI	g4263522
BLAST score	253
E value	1.0e-21
Match length	108
% identity	41
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125250
Contig ID	17177_1.R1010
5'-most EST	jC-atXLIB327413P3f12b1
Method	BLASTX
NCBI GI	g2947059
BLAST score	560
E value	1.0e-57
Match length	114
% identity	90
NCBI Description	(AC002521) similar to myb transforming protein [Arabidopsis thaliana]

Seq. No.	125251
Contig ID	17183_1.R1010
5'-most EST	jC-atXLIB327413P4g04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	54

% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125252
Contig ID	17183_2.R1010
5'-most EST	jC-atXLIB327413P4g04b1
Method	BLASTN
NCBI GI	g3243214
BLAST score	55
E value	6.0e-22
Match length	251
% identity	83
NCBI Description	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	125253
Contig ID	17183_4.R1010
5'-most EST	jC-atXL1042Q1E1G09a1
Method	BLASTN
NCBI GI	g3243214
BLAST score	42
E value	3.0e-14
Match length	130
% identity	84
NCBI Description	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	125254
Contig ID	17185_1.R1010
5'-most EST	LIB24-075-Q1-E1-B11
Method	BLASTN
NCBI GI	g4589421
BLAST score	358
E value	0.0e+00
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	125255
Contig ID	17189_2.R1010
5'-most EST	jC-atX24003Q1E1G11b1

Seq. No.	125256
Contig ID	17197_1.R1010
5'-most EST	jC-atXLIB327413P3g12b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	125257
Contig ID	17198_1.R1010
5'-most EST	LIB3176-084-P1-K1-H5

Method	BLASTX
NCBI GI	g4006880
BLAST score	203
E value	7.0e-16
Match length	59
% identity	71
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	125258
Contig ID	17206_1.R1010
5'-most EST	jC-atXLIB327413P2h11b1
Method	BLASTN
NCBI GI	g4587641
BLAST score	409
E value	0.0e+00
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	125259
Contig ID	17212_1.R1010
5'-most EST	jC-atXLIB327419P4b01b1
Method	BLASTN
NCBI GI	g3985934
BLAST score	217
E value	1.0e-118
Match length	340
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	125260
Contig ID	17213_1.R1010
5'-most EST	jC-atX22034Q1E2H01b1
Method	BLASTN
NCBI GI	g2584827
BLAST score	288
E value	1.0e-161
Match length	498
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125261
Contig ID	17214_1.R1010
5'-most EST	jC-atXLIB327414P1a02b1
Method	BLASTN
NCBI GI	g4006885
BLAST score	455
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No. 125262

Contig ID	17216_1.R1010
5'-most EST	jC-atXP19C111J24T7058a1
Method	BLASTX
NCBI GI	g3123264
BLAST score	561
E value	2.0e-57
Match length	128
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125263
Contig ID	17216_2.R1010
5'-most EST	jC-atXLIB327417P4d11b1
Method	BLASTX
NCBI GI	g3123264
BLAST score	96
E value	6.0e-03
Match length	163
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125264
Contig ID	17216_3.R1010
5'-most EST	g1520950
Method	BLASTX
NCBI GI	g3123264
BLAST score	82
E value	5.0e-19
Match length	87
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125265
Contig ID	17216_4.R1010
5'-most EST	LIB3176-069-P1-K1-E3
Method	BLASTX
NCBI GI	g3123264
BLAST score	504
E value	4.0e-51
Match length	122
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125266
Contig ID	17218_2.R1010
5'-most EST	LIB24-004-Q1-E1-H7
Method	BLASTX
NCBI GI	g4006865
BLAST score	616
E value	5.0e-64
Match length	167
% identity	69
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	125267
Contig ID	17221_1.R1010
5'-most EST	jC-alX25047Q1E1E05b1
Method	BLASTX
NCBI GI	g99809
BLAST score	921
E value	1.0e-100
Match length	180
% identity	93
NCBI Description	gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608) Bplo [Brassica napus]

Seq. No.	125268
Contig ID	17225_1.R1010
5'-most EST	jC-atXP69C219C2T7077d1
Method	BLASTN
NCBI GI	g2656026
BLAST score	110
E value	2.0e-54
Match length	434
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	125269
Contig ID	17225_2.R1010
5'-most EST	jC-atX25041Q1E1F09b1

Seq. No.	125270
Contig ID	17225_5.R1010
5'-most EST	jC-atXLIB327409P2e09b1

Seq. No.	125271
Contig ID	17225_6.R1010
5'-most EST	LIB24-122-Q1-E1-G11
Method	BLASTN
NCBI GI	g598848
BLAST score	43
E value	1.0e-14
Match length	63
% identity	92
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	125272
Contig ID	17227_1.R1010
5'-most EST	jC-alXLIB327435P4g02b1

Seq. No.	125273
Contig ID	17227_2.R1010
5'-most EST	jC-atXP52C183J17T7d2

Seq. No.	125274
Contig ID	17227_3.R1010
5'-most EST	LIB24-130-Q1-E1-F5

Seq. No. 125275

Contig ID	17233_1.R1010
5'-most EST	ARABLI-024-Q1-B1-G7
Method	BLASTN
NCBI GI	g4775269
BLAST score	133
E value	1.0e-68
Match length	338
% identity	98
NCBI Description	Arabidopsis thaliana srp30 gene, exons 1-12

Seq. No.	125276
Contig ID	17238_1.R1010
5'-most EST	jC-atXLIB327413P3e12b1
Method	BLASTX
NCBI GI	g4587549
BLAST score	526
E value	1.0e-53
Match length	111
% identity	35
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	125277
Contig ID	17240_1.R1010
5'-most EST	LIB3175-030-P1-K1-H9
Method	BLASTX
NCBI GI	g3080442
BLAST score	923
E value	1.0e-100
Match length	181
% identity	96
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	125278
Contig ID	17241_1.R1010
5'-most EST	LIB24-005-Q1-E1-C10
Method	BLASTN
NCBI GI	g4587641
BLAST score	249
E value	1.0e-137
Match length	465
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	125279
Contig ID	17242_1.R1010
5'-most EST	jC-atX24006Q1E1C11b1
Method	BLASTN
NCBI GI	g4406790
BLAST score	467
E value	0.0e+00
Match length	479
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1O16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125280
Contig ID	17246_1.R1010
5'-most EST	jC-atXLIB327415P1d10b1
Method	BLASTX
NCBI GI	g4335750
BLAST score	255
E value	9.0e-22
Match length	130
% identity	39
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	125281
Contig ID	17248_1.R1010
5'-most EST	LIB24-005-Q1-E1-C6
Method	BLASTN
NCBI GI	g4468976
BLAST score	298
E value	1.0e-167
Match length	359
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	125282
Contig ID	17249_1.R1010
5'-most EST	LIB24-005-Q1-E1-C7
Method	BLASTX
NCBI GI	g4584342
BLAST score	89
E value	7.0e-36
Match length	103
% identity	84
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	125283
Contig ID	17250_1.R1010
5'-most EST	jC-atXLIB327413P1f09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125284
Contig ID	17251_1.R1010
5'-most EST	LIB24-005-Q1-E1-D1
Method	BLASTX
NCBI GI	g399299
BLAST score	331
E value	9.0e-31

Match length	157
% identity	41
NCBI Description	CHROMOSOME REGION MAINTENANCE PROTEIN 1 >gi_4584830_emb_CAB40824.1_ (X15482) crm1 product [Schizosaccharomyces pombe]

Seq. No.	125285
Contig ID	17255_1.R1010
5'-most EST	LIB24-005-Q1-E1-D2
Method	BLASTX
NCBI GI	g122085
BLAST score	502
E value	8.0e-51
Match length	131
% identity	78
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	125286
Contig ID	17257_1.R1010
5'-most EST	LIB24-005-Q1-E1-D4
Method	BLASTN
NCBI GI	g4159708
BLAST score	256
E value	1.0e-142
Match length	412
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	125287
Contig ID	17259_1.R1010
5'-most EST	LIB24-005-Q1-E1-D8
Method	BLASTX
NCBI GI	g4587589

BLAST score	345
E value	2.0e-32
Match length	114
% identity	55
NCBI Description	(AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125288
Contig ID	17260_1.R1010
5'-most EST	LIB24-005-Q1-E1-D9
Method	BLASTN
NCBI GI	g4587641
BLAST score	389
E value	0.0e+00
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	125289
Contig ID	17261_1.R1010
5'-most EST	jC-atXLIB327413P1g05b1
Method	BLASTX
NCBI GI	g2618689
BLAST score	166
E value	2.0e-20
Match length	99
% identity	59
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	125290
Contig ID	17263_1.R1010
5'-most EST	jC-atXLIB327413P2g08b1
Method	BLASTN
NCBI GI	g540252
BLAST score	59
E value	5.0e-24
Match length	59
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	125291
Contig ID	17264_1.R1010
5'-most EST	jC-atXLIB327409P3b03b1
Method	BLASTX
NCBI GI	g2191128
BLAST score	1260
E value	1.0e-139
Match length	249
% identity	100
NCBI Description	(AF007269) belongs to the L5P family of ribosomal proteins [Arabidopsis thaliana]

Seq. No.	125292
Contig ID	17264_2.R1010
5'-most EST	g2413852
Method	BLASTX
NCBI GI	g3777600

BLAST score	64
E value	5.0e-13
Match length	109
% identity	45
NCBI Description	(AF095708) 50S ribosomal protein L5 [Oryza sativa]

Seq. No.	125293
Contig ID	17273_1.R1010
5'-most EST	LIB3175-079-P1-K1-C9
Method	BLASTN
NCBI GI	g4467131
BLAST score	192
E value	1.0e-104
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	125294
Contig ID	17277_1.R1010
5'-most EST	jC-atXP92CH4A7T7016d1

Seq. No.	125295
Contig ID	17282_1.R1010
5'-most EST	jC-atXLIB327413P1h08b1
Method	BLASTN
NCBI GI	g4415905
BLAST score	95
E value	8.0e-46
Match length	462
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125296
Contig ID	17283_1.R1010
5'-most EST	jC-atXLIB327428P4c08a2
Method	BLASTX
NCBI GI	g3334756
BLAST score	508
E value	4.0e-51
Match length	107
% identity	88
NCBI Description	(Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]

Seq. No.	125297
Contig ID	17283_2.R1010
5'-most EST	jC-atXLIB327433P2b10a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	88
E value	1.0e-41
Match length	145
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	125298
Contig ID	17288_1.R1010
5'-most EST	LIB3175-004-P1-K1-B10
Method	BLASTX
NCBI GI	g2146728
BLAST score	150
E value	1.0e-09
Match length	99
% identity	47
NCBI Description	cyclin cyc1b - Arabidopsis thaliana >gi_1360646 (L27223) cyclin [Arabidopsis thaliana]

Seq. No.	125299
Contig ID	17289_1.R1010
5'-most EST	LIB24-005-Q1-E1-G6
Method	BLASTX
NCBI GI	g1175386
BLAST score	145
E value	5.0e-09
Match length	99
% identity	38
NCBI Description	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi_2130289_pir__S58305 hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe) >gi_929892_emb_CAA90591_ (Z50728) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	125300
Contig ID	17293_2.R1010
5'-most EST	LIB24-005-Q1-E1-H1
Method	BLASTN
NCBI GI	g2618605
BLAST score	269
E value	1.0e-149
Match length	593
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	125301
Contig ID	17295_2.R1010
5'-most EST	LIB24-005-Q1-E1-H11
Method	BLASTN
NCBI GI	g2098816
BLAST score	40
E value	7.0e-13
Match length	84
% identity	87
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	125302
Contig ID	17298_1.R1010
5'-most EST	jC-atXLIB327413P4h10b1
Method	BLASTX
NCBI GI	g1168733
BLAST score	374

E value	1.0e-35
Match length	138
% identity	49
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_1076238_pir__S49443 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) A - loblolly pine >gi_558385_emb_CAA86072_ (Z37991) cinnamyl alcohol dehydrogenase [Pinus taeda]

Seq. No.	125303
Contig ID	17299_1.R1010
5'-most EST	LIB24-005-Q1-E1-H5
Method	BLASTX
NCBI GI	g3426039
BLAST score	281
E value	5.0e-25
Match length	120
% identity	53
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	125304
Contig ID	17302_1.R1010
5'-most EST	jC-atXP115C249M9T7022d1
Method	BLASTN
NCBI GI	g4469002
BLAST score	267
E value	1.0e-148
Match length	882
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	125305
Contig ID	17307_1.R1010
5'-most EST	g586995
Method	BLASTX
NCBI GI	g3249086
BLAST score	247
E value	5.0e-21
Match length	153
% identity	67
NCBI Description	(AC004473) Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) gb_AF006086 from Homo sapiens. EST gb_Z37222 comes [Arabidopsis thaliana]

Seq. No.	125306
Contig ID	17308_1.R1010
5'-most EST	jC-atXLIB327418P4d05b1
Method	BLASTX
NCBI GI	g3461843
BLAST score	69
E value	4.0e-18
Match length	49
% identity	100
NCBI Description	(AC005315) unknown protein [Arabidopsis thaliana]

Seq. No.	125307
Contig ID	17311_1.R1010

5'-most EST	LIB24-006-Q1-E1-A7
Method	BLASTN
NCBI GI	g1931636
BLAST score	623
E value	0.0e+00
Match length	709
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	125308
Contig ID	17316_1.R1010
5'-most EST	jC-atXLIB327413P2f02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	68
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125309
Contig ID	17318_1.R1010
5'-most EST	LIB24-006-Q1-E1-B4

Seq. No.	125310
Contig ID	17320_1.R1010
5'-most EST	jC-atXP85CG7G10T7b1
Method	BLASTX
NCBI GI	g1086833
BLAST score	394
E value	5.0e-38
Match length	166
% identity	42
NCBI Description	(U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No.	125311
Contig ID	17325_1.R1010
5'-most EST	g2733593

Seq. No.	125312
Contig ID	17328_1.R1010
5'-most EST	jC-alXLIB327434P1g06b1
Method	BLASTX
NCBI GI	g3377800
BLAST score	712
E value	2.0e-75
Match length	148
% identity	91
NCBI Description	(AF075597) similar to glycosyl hydrolases family 9 (PFam:glycosyl_hydro5.hmm, score: 100.70) [Arabidopsis thaliana]

Seq. No.	125313
Contig ID	17331_1.R1010

5'-most EST	jC-atXLIB327413P1f07b1
Method	BLASTN
NCBI GI	g2264367
BLAST score	441
E value	0.0e+00
Match length	441
% identity	73
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	125314
Contig ID	17333_1.R1010
5'-most EST	LIB3168-045-P1-K1-E12

Seq. No.	125315
Contig ID	17339_1.R1010
5'-most EST	jC-atXLIB327409P4e04b1
Method	BLASTX
NCBI GI	g4325338
BLAST score	560
E value	2.0e-72
Match length	173
% identity	83
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	125316
Contig ID	17340_1.R1010
5'-most EST	LIB24-006-Q1-E1-D3
Method	BLASTX
NCBI GI	g3925277
BLAST score	418
E value	1.0e-40
Match length	184
% identity	48
NCBI Description	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	125317
Contig ID	17340_2.R1010
5'-most EST	LIB24-133-Q1-E1-G3
Method	BLASTX
NCBI GI	g3925277
BLAST score	307
E value	1.0e-27
Match length	192
% identity	39
NCBI Description	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	125318
Contig ID	17343_1.R1010
5'-most EST	LIB3234-050-P1-K1-C6
Method	BLASTX

NCBI GI	g2651316
BLAST score	722
E value	2.0e-76
Match length	156
% identity	94
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	125319
Contig ID	17345_1.R1010
5'-most EST	jC-atX24005Q1E1E01b1
Method	BLASTN
NCBI GI	g4680765
BLAST score	281
E value	1.0e-157
Match length	567
% identity	98
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	125320
Contig ID	17346_1.R1010
5'-most EST	jC-atXLIB327417P3a06a1
Method	BLASTN
NCBI GI	g4757392
BLAST score	182
E value	5.0e-98
Match length	214
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	125321
Contig ID	17351_1.R1010
5'-most EST	jC-atXLIB327413P1g10b1
Method	BLASTX
NCBI GI	g4455313
BLAST score	561
E value	1.0e-57
Match length	143
% identity	72
NCBI Description	(AL035528) fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]

Seq. No.	125322
Contig ID	17357_1.R1010
5'-most EST	g2723059
Method	BLASTX
NCBI GI	g2275216
BLAST score	250
E value	3.0e-21
Match length	64
% identity	75
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]

Seq. No.	125323
Contig ID	17361_1.R1010

5'-most EST	jC-alXLIB327434P4f07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	80
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125324
Contig ID	17361_2.R1010
5'-most EST	LIB24-006-Q1-E1-F2

Seq. No.	125325
Contig ID	17362_1.R1010
5'-most EST	g2749391
Method	BLASTX
NCBI GI	g2738998
BLAST score	342
E value	5.0e-32
Match length	127
% identity	52
NCBI Description	(AF022458) CYP98A2p [Glycine max]

Seq. No.	125326
Contig ID	17369_1.R1010
5'-most EST	LIB24-006-Q1-E1-G10
Method	BLASTN
NCBI GI	g2760164
BLAST score	374
E value	0.0e+00
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	125327
Contig ID	17371_1.R1010
5'-most EST	jC-atXLIB327423P1h01b1
Method	BLASTX
NCBI GI	g115484
BLAST score	762
E value	5.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN 1 >gi_71684_pir__MCPZDC calmodulin - carrot >gi_478632_pir__S22971 calmodulin - trumpet lily >gi_541839_pir__S40301 calmodulin - Red bryony >gi_2129970_pir__S70768 calmodulin CAM81 - garden petunia >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota] >gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium longiflorum] >gi_169207 (M80836) calmodulin [Petunia hybrida] >gi_308900 (L18912) calmodulin [Lilium longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin [Malus domestica] >gi_535444 (U13882) calmodulin [Pisum sativum] >gi_445602_prf__1909349A calmodulin [Daucus

carota]

Seq. No.	125328
Contig ID	17371_2.R1010
5'-most EST	jC-atXP80C240D7T7s1
Method	BLASTX
NCBI GI	g3378652
BLAST score	287
E value	1.0e-25
Match length	59
% identity	57
NCBI Description	(AJ005039) CaM-1 [Nicotiana plumbaginifolia] >gi_3378654_emb_CAA06307_ (AJ005040) CaM-2 [Nicotiana plumbaginifolia]

Seq. No.	125329
Contig ID	17376_1.R1010
5'-most EST	jC-atXLIB327413P1h06b1
Method	BLASTX
NCBI GI	g3873913
BLAST score	169
E value	1.0e-11
Match length	144
% identity	33
NCBI Description	(Z71258) similar to Flavin-binding monooxygenase-like [Caenorhabditis elegans]

Seq. No.	125330
Contig ID	17379_1.R1010
5'-most EST	LIB24-006-Q1-E1-G9
Method	BLASTX
NCBI GI	g2341025
BLAST score	646
E value	8.0e-68
Match length	139
% identity	99
NCBI Description	(AC000104) F19P19.2 [Arabidopsis thaliana]

Seq. No.	125331
Contig ID	17383_1.R1010
5'-most EST	jC-atXLIB327413P4h09b1
Method	BLASTX
NCBI GI	g4539379
BLAST score	69
E value	5.2e+00
Match length	142
% identity	18
NCBI Description	(AL035526) gene 11-1 protein-like (fragment) [Arabidopsis thaliana]

Seq. No.	125332
Contig ID	17385_1.R1010
5'-most EST	jC-atXLIB327409P1d04b1
Method	BLASTX
NCBI GI	g3540190
BLAST score	630
E value	1.0e-65

Match length	130
% identity	94
NCBI Description	(AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	125333
Contig ID	17385_2.R1010
5'-most EST	LIB25-052-Q1-E1-E12
Method	BLASTN
NCBI GI	g3176693
BLAST score	277
E value	1.0e-154
Match length	522
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125334
Contig ID	17388_1.R1010
5'-most EST	LIB24-006-Q1-E1-H6
Method	BLASTN
NCBI GI	g3335331
BLAST score	290
E value	1.0e-162
Match length	485
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125335
Contig ID	17396_1.R1010
5'-most EST	jC-atXLIB327415P2b12b2
Method	BLASTX
NCBI GI	g416664
BLAST score	596
E value	8.0e-62
Match length	151
% identity	79
NCBI Description	PLASMA MEMBRANE ATPASE 4 (PROTON PUMP) >gi_485504_pir__S33548 H+-transporting ATPase (EC 3.6.1.35) type 4, plasma membrane - curled-leaved tobacco >gi_19704_emb_CAA47275_ (X66737) plasma membrane H+-ATPase [Nicotiana plumbaginifolia]

Seq. No.	125336
Contig ID	17403_1.R1010
5'-most EST	jC-atXLIB327415P3b03b1
Method	BLASTN
NCBI GI	g4220633
BLAST score	131
E value	3.0e-67
Match length	421
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	125337
Contig ID	17406_1.R1010

5'-most EST	jC-atXLIB327415P4b06b1
Method	BLASTN
NCBI GI	g3702729
BLAST score	276
E value	1.0e-154
Match length	371
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A11, complete sequence [Arabidopsis thaliana]

Seq. No.	125338
Contig ID	17409_1.R1010
5'-most EST	jC-atXLIB327426P1b01b1
Method	BLASTN
NCBI GI	g1946354
BLAST score	383
E value	0.0e+00
Match length	512
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	125339
Contig ID	17413_1.R1010
5'-most EST	jC-alXLIB327435P4g05b1
Method	BLASTX
NCBI GI	g4539454
BLAST score	542
E value	3.0e-55
Match length	163
% identity	74
NCBI Description	(AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]

Seq. No.	125340
Contig ID	17413_2.R1010
5'-most EST	jC-alX25048Q1E1C12b1
Method	BLASTX
NCBI GI	g2829876
BLAST score	450
E value	9.0e-57
Match length	126
% identity	96
NCBI Description	(AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No.	125341
Contig ID	17414_1.R1010
5'-most EST	jC-atXLIB327415P3b04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 125342

Contig ID	17416_1.R1010
5'-most EST	jC-alXLIB327434P4c05b1
Method	BLASTX
NCBI GI	g2911797
BLAST score	227
E value	2.0e-18
Match length	140
% identity	36
NCBI Description	(AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	125343
Contig ID	17419_1.R1010
5'-most EST	LIB24-007-Q1-E1-C2
Method	BLASTN
NCBI GI	g4512646
BLAST score	260
E value	1.0e-144
Match length	585
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No.	125344
Contig ID	17421_1.R1010
5'-most EST	LIB24-113-Q1-E1-B5
Method	BLASTX
NCBI GI	g4218120
BLAST score	464
E value	3.0e-46
Match length	137
% identity	66
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	125345
Contig ID	17422_1.R1010
5'-most EST	jC-atXLIB327406P4g09b2
Method	BLASTX
NCBI GI	g2760332
BLAST score	234
E value	3.0e-19
Match length	121
% identity	20
NCBI Description	(AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No.	125346
Contig ID	17428_1.R1010
5'-most EST	jC-atXLIB327415P2c07b2
Method	BLASTN
NCBI GI	g484109
BLAST score	246
E value	1.0e-135
Match length	682
% identity	99
NCBI Description	Arabidopsis thaliana chloroplast glyceraldehyde-3-phosphate dehydrogenase B subunit gene, 5'end

Seq. No.	125347
Contig ID	17428_2.R1010
5'-most EST	g2749604
Method	BLASTN
NCBI GI	g484109
BLAST score	245
E value	1.0e-135
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana chloroplast glyceraldehyde-3-phosphate dehydrogenase B subunit gene, 5'end

Seq. No.	125348
Contig ID	17429_1.R1010
5'-most EST	jC-atXLIB327415P1c08b1
Method	BLASTN
NCBI GI	g3702722
BLAST score	230
E value	1.0e-126
Match length	335
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No.	125349
Contig ID	17430_1.R1010
5'-most EST	LIB24-007-Q1-E1-D12
Method	BLASTX
NCBI GI	g1922242
BLAST score	339
E value	2.0e-31
Match length	104
% identity	100
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125350
Contig ID	17433_1.R1010
5'-most EST	jC-atXLIB327415P2c10b2
Method	BLASTX
NCBI GI	g2507617
BLAST score	480
E value	3.0e-48
Match length	145
% identity	63
NCBI Description	(U90341) chalcone synthase homolog PrChS1 [Pinus radiata]

Seq. No.	125351
Contig ID	17434_1.R1010
5'-most EST	g937289
Method	BLASTX
NCBI GI	g3721926
BLAST score	205
E value	6.0e-16
Match length	99
% identity	42
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	125352
Contig ID	17438_1.R1010
5'-most EST	jC-atXLIB327415P3c03b1
Method	BLASTX
NCBI GI	g3152605
BLAST score	313
E value	1.0e-28
Match length	61
% identity	100
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125353
Contig ID	17442_1.R1010
5'-most EST	LIB25-014-Q1-E1-H1
Method	BLASTX
NCBI GI	g3183219
BLAST score	210
E value	9.0e-17
Match length	127
% identity	38
NCBI Description	HYPOTHETICAL PROTEIN KIAA0112 (HA0609) >gi_434779_dbj_BAA04948_ (D25218) KIAA0112 [Homo sapiens]

Seq. No.	125354
Contig ID	17448_1.R1010
5'-most EST	jC-atXLIB327415P3c11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125355
Contig ID	17456_1.R1010
5'-most EST	jC-atXLIB327415P4c11b1

Seq. No.	125356
Contig ID	17457_1.R1010
5'-most EST	jC-atXLIB327407P1g06b2
Method	BLASTX
NCBI GI	g4371280
BLAST score	262
E value	1.0e-22
Match length	70
% identity	70
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125357
Contig ID	17462_1.R1010
5'-most EST	jC-atXLIB327415P1d07b1
Method	BLASTN
NCBI GI	g4757411
BLAST score	258

E value	1.0e-143
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	125358
Contig ID	17465_1.R1010
5'-most EST	g2393707
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	5.0e-17
Match length	47
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	125359
Contig ID	17465_2.R1010
5'-most EST	jC-atXLIB327415P2d04b2
Method	BLASTN
NCBI GI	g2564047
BLAST score	34
E value	2.0e-09
Match length	178
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	125360
Contig ID	17466_1.R1010
5'-most EST	g2581669
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	3.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125361
Contig ID	17466_2.R1010
5'-most EST	g2047877
Method	BLASTX
NCBI GI	g1673344
BLAST score	153
E value	8.0e-10
Match length	49
% identity	57
NCBI Description	(D64002) hypothetical protein [Synechocystis sp.]

Seq. No.	125362
Contig ID	17467_1.R1010
5'-most EST	jC-atX24061Q1E1F01b1

Seq. No.	125363
Contig ID	17470_1.R1010

5'-most EST	jC-atXLIB327415P1d11b1
Method	BLASTX
NCBI GI	g4193320
BLAST score	804
E value	6.0e-86
Match length	206
% identity	75
NCBI Description	(AF045473) histone deacetylase [Zea mays]

Seq. No.	125364
Contig ID	17476_1.R1010
5'-most EST	jC-atXLIB327415P4d02b1
Method	BLASTN
NCBI GI	g4678340
BLAST score	211
E value	1.0e-115
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)

Seq. No.	125365
Contig ID	17482_1.R1010
5'-most EST	jC-atXLIB327415P1b12b1
Method	BLASTX
NCBI GI	g4249382
BLAST score	348
E value	7.0e-33
Match length	121
% identity	53
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	125366
Contig ID	17485_1.R1010
5'-most EST	jC-atXLIB327420P1e01b1
Method	BLASTX
NCBI GI	g2833223
BLAST score	93
E value	5.0e-37
Match length	179
% identity	48
NCBI Description	SIK1 PROTEIN >gi_626457_pir__S48550 hypothetical protein YLR197w - yeast (Saccharomyces cerevisiae) >gi_544506 (U14913) Sik1p [Saccharomyces cerevisiae] >gi_984964 (U20237) Sik1p [Saccharomyces cerevisiae]

Seq. No.	125367
Contig ID	17485_2.R1010
5'-most EST	jC-atXLIB327415P4b01b1
Method	BLASTX
NCBI GI	g4160346
BLAST score	383
E value	9.0e-37
Match length	156
% identity	50

NCBI Description	(AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]

Seq. No.	125368
Contig ID	17488_1.R1010
5'-most EST	jC-atXLIB327415P1b11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125369
Contig ID	17490_1.R1010
5'-most EST	LIB25-041-Q1-E1-H7
Method	BLASTN
NCBI GI	g4580386
BLAST score	311
E value	1.0e-175
Match length	330
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	125370
Contig ID	17492_1.R1010
5'-most EST	jC-atXLIB327406P3f09b2
Method	BLASTX
NCBI GI	g3859568
BLAST score	207
E value	5.0e-16
Match length	46
% identity	78
NCBI Description	(AF098752) unknown [Oryza sativa]

Seq. No.	125371
Contig ID	17494_1.R1010
5'-most EST	jC-atXLIB327408P1b09b1
Method	BLASTX
NCBI GI	g3885343
BLAST score	243
E value	4.0e-20
Match length	93
% identity	45
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125372
Contig ID	17495_1.R1010
5'-most EST	jC-atXLIB327427P3e11b2
Method	BLASTX
NCBI GI	g3548801
BLAST score	440
E value	2.0e-43
Match length	149

% identity	54
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	125373
Contig ID	17495_2.R1010
5'-most EST	jC-atXLIB327421P4e11b1
Method	BLASTX
NCBI GI	g4056454
BLAST score	141
E value	2.0e-08
Match length	113
% identity	2
NCBI Description	(AC005990) Contains repeated region with similarity to gb_U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb_Z34165 and gb_Z18788 come from this gene. [Arabidopsis thaliana]

Seq. No.	125374
Contig ID	17496_1.R1010
5'-most EST	g2763711
Method	BLASTX
NCBI GI	g1561774
BLAST score	891
E value	3.0e-96
Match length	222
% identity	78
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	125375
Contig ID	17499_1.R1010
5'-most EST	jC-atXLIB327406P3f03b2
Method	BLASTX
NCBI GI	g99725
BLAST score	457
E value	1.0e-45
Match length	107
% identity	96
NCBI Description	glycine-rich protein PUTG1 - Arabidopsis thaliana >gi_16310_emb_CAA77884_ (Z11858) unknown [Arabidopsis thaliana]

Seq. No.	125376
Contig ID	17500_1.R1010
5'-most EST	LIB24-008-Q1-E1-B9
Method	BLASTN
NCBI GI	g3080352
BLAST score	236
E value	1.0e-130
Match length	490
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	125377
Contig ID	17503_1.R1010

5'-most EST	jC-atXLIB327415P4b12b1
Method	BLASTX
NCBI GI	g1730764
BLAST score	244
E value	3.0e-20
Match length	82
% identity	51
NCBI Description	HYPOTHETICAL 25.4 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION >gi_2131890_pir__S63051 hypothetical protein YNL110c - yeast (Saccharomyces cerevisiae) >gi_1183963_emb_CAA93397_ (Z69382) N1954 [Saccharomyces cerevisiae] >gi_1302030_emb_CAA95989_ (Z71386) ORF YNL110c [Saccharomyces cerevisiae]

Seq. No.	125378
Contig ID	17503_2.R1010
5'-most EST	g2042751

Seq. No.	125379
Contig ID	17504_1.R1010
5'-most EST	jC-atXP27C135B9T7d2
Method	BLASTX
NCBI GI	g4432832
BLAST score	989
E value	1.0e-107
Match length	197
% identity	96
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	125380
Contig ID	17504_2.R1010
5'-most EST	LIB24-008-Q1-E1-C12
Method	BLASTX
NCBI GI	g4432832
BLAST score	807
E value	2.0e-86
Match length	170
% identity	97
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	125381
Contig ID	17507_1.R1010
5'-most EST	g1217056
Method	BLASTX
NCBI GI	g3522938
BLAST score	60
E value	1.0e-25
Match length	209
% identity	35
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	125382
Contig ID	17508_1.R1010
5'-most EST	jC-atXLIB327415P3b10b1
Method	BLASTX
NCBI GI	g1480347
BLAST score	231

E value	6.0e-35
Match length	140
% identity	58
NCBI Description	(X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]

Seq. No.	125383
Contig ID	17508_2.R1010
5'-most EST	LIB3175-042-P1-K1-A11

Seq. No.	125384
Contig ID	17510_1.R1010
5'-most EST	g1217494
Method	BLASTN
NCBI GI	g3335331
BLAST score	769
E value	0.0e+00
Match length	781
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125385
Contig ID	17510_2.R1010
5'-most EST	jC-atXP114C240G13T7s1
Method	BLASTN
NCBI GI	g3335331
BLAST score	473
E value	0.0e+00
Match length	493
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125386
Contig ID	17516_1.R1010
5'-most EST	jC-atXLIB327415P1c09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	1.0e-25
Match length	77
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125387
Contig ID	17519_1.R1010
5'-most EST	jC-atXLIB327415P1c10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	63
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125388
Contig ID	17520_1.R1010
5'-most EST	jC-atXLIB327415P2c05b2
Method	BLASTX
NCBI GI	g2388578
BLAST score	1113
E value	1.0e-122
Match length	220
% identity	100
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	125389
Contig ID	17520_2.R1010
5'-most EST	jC-atXLIB327422P2h09b2
Method	BLASTX
NCBI GI	g2388578
BLAST score	453
E value	5.0e-45
Match length	87
% identity	100
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	125390
Contig ID	17521_1.R1010
5'-most EST	jC-atX24008Q1E1D06b1
Method	BLASTX
NCBI GI	g4056433
BLAST score	278
E value	2.0e-24
Match length	124
% identity	48
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	125391
Contig ID	17523_1.R1010
5'-most EST	jC-atXLIB327415P1c07b1
Method	BLASTX
NCBI GI	g107350
BLAST score	177
E value	1.0e-12
Match length	122
% identity	33
NCBI Description	Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5 protein [Homo sapiens]

Seq. No.	125392
Contig ID	17524_1.R1010
5'-most EST	LIB24-008-Q1-E1-E1

Seq. No.	125393
Contig ID	17525_1.R1010
5'-most EST	jC-atXLIB327415P4c05b1

Method	BLASTX
NCBI GI	g3860020
BLAST score	230
E value	1.0e-18
Match length	150
% identity	35
NCBI Description	(AF091091) unknown [Homo sapiens]

Seq. No.	125394
Contig ID	17526_1.R1010
5'-most EST	LIB24-008-Q1-E1-E12

Seq. No.	125395
Contig ID	17527_1.R1010
5'-most EST	jC-atX24008Q1E1E02b1

Seq. No.	125396
Contig ID	17533_1.R1010
5'-most EST	jC-atXLIB327415P4c03b1

Seq. No.	125397
Contig ID	17535_1.R1010
5'-most EST	LIB24-008-Q1-E1-F11
Method	BLASTX
NCBI GI	g4218120
BLAST score	1221
E value	1.0e-134
Match length	347
% identity	68
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	125398
Contig ID	17535_2.R1010
5'-most EST	LIB3176-116-P2-K1-G3
Method	BLASTN
NCBI GI	g2262155
BLAST score	49
E value	3.0e-18
Match length	68
% identity	93
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	125399
Contig ID	17536_1.R1010
5'-most EST	jC-alXLIB327435P3e10b1
Method	BLASTX
NCBI GI	g4406759
BLAST score	299
E value	6.0e-27
Match length	223
% identity	37
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125400
Contig ID	17537_1.R1010

5'-most EST	jC-atXLIB327415P3c12b1
Method	BLASTX
NCBI GI	g3212871
BLAST score	355
E value	2.0e-33
Match length	65
% identity	100
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	125401
Contig ID	17543_1.R1010
5'-most EST	jC-atXLIB327408P4c11b1
Method	BLASTX
NCBI GI	g4218120
BLAST score	587
E value	2.0e-60
Match length	162
% identity	66
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	125402
Contig ID	17551_1.R1010
5'-most EST	jC-atXLIB327417P3g04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	9.0e-22
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125403
Contig ID	17555_1.R1010
5'-most EST	LIB24-008-Q1-E1-G8
Method	BLASTX
NCBI GI	g2505878
BLAST score	197
E value	3.0e-15
Match length	135
% identity	79
NCBI Description	(Y12776) gene5; most likely [Arabidopsis thaliana]

Seq. No.	125404
Contig ID	17556_1.R1010
5'-most EST	jC-atX35024Q1E1H10b1
Method	BLASTN
NCBI GI	g4699904
BLAST score	739
E value	0.0e+00
Match length	766
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	125405
Contig ID	17556_2.R1010
5'-most EST	jC-atXLIB327427P4e04b2
Method	BLASTN
NCBI GI	g4699904
BLAST score	327
E value	0.0e+00
Match length	592
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	125406
Contig ID	17558_1.R1010
5'-most EST	g3450457
Method	BLASTN
NCBI GI	g2760164
BLAST score	324
E value	0.0e+00
Match length	344
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	125407
Contig ID	17569_1.R1010
5'-most EST	jC-atXP11C99C22T7096d1
Method	BLASTX
NCBI GI	g2262098
BLAST score	760
E value	9.0e-81
Match length	175
% identity	87
NCBI Description	(AC002343) HSP90 isolog [Arabidopsis thaliana]

Seq. No.	125408
Contig ID	17569_2.R1010
5'-most EST	LIB24-104-Q1-E2-E5
Method	BLASTX
NCBI GI	g462013
BLAST score	1964
E value	0.0e+00
Match length	492
% identity	78
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	125409
Contig ID	17569_5.R1010
5'-most EST	LIB24-095-Q1-E1-C2
Method	BLASTN
NCBI GI	g2262097
BLAST score	252
E value	1.0e-139
Match length	288

% identity	97
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	125410
Contig ID	17570_1.R1010
5'-most EST	jC-atXLIB327415P2b08b2
Method	BLASTN
NCBI GI	g3763944
BLAST score	368
E value	0.0e+00
Match length	388
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	125411
Contig ID	17575_1.R1010
5'-most EST	jC-atXLIB327415P1b07b1

Seq. No.	125412
Contig ID	17579_1.R1010
5'-most EST	LIB24-009-Q1-E1-A9
Method	BLASTN
NCBI GI	g3264774
BLAST score	333
E value	0.0e+00
Match length	624
% identity	97
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	125413
Contig ID	17590_1.R1010
5'-most EST	LIB24-009-Q1-E1-C1
Method	BLASTX
NCBI GI	g2804436
BLAST score	89
E value	5.0e-18
Match length	227
% identity	18
NCBI Description	(AF043695) Similar to mitochondrial carrier protein [Caenorhabditis elegans]

Seq. No.	125414
Contig ID	17593_1.R1010
5'-most EST	jC-atXLIB327415P1e07b1
Method	BLASTX
NCBI GI	g3912926
BLAST score	654
E value	1.0e-68
Match length	124
% identity	96
NCBI Description	(AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]

Seq. No.	125415
Contig ID	17595_1.R1010

5'-most EST	jC-atXP29C135J15T7057d1
Seq. No.	125416
Contig ID	17595_2.R1010
5'-most EST	g2047772
Seq. No.	125417
Contig ID	17598_1.R1010
5'-most EST	jC-atXLIB327415P3b08b1
Method	BLASTX
NCBI GI	g3687243
BLAST score	261
E value	2.0e-22
Match length	64
% identity	80
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]
Seq. No.	125418
Contig ID	17603_1.R1010
5'-most EST	jC-alXLIB327434P1a07b1
Method	BLASTX
NCBI GI	g3183570
BLAST score	254
E value	1.0e-21
Match length	116
% identity	43
NCBI Description	HYPOTHETICAL 36.8 KD PROTEIN IN DINF-QOR INTERGENIC REGION
Seq. No.	125419
Contig ID	17604_1.R1010
5'-most EST	jC-atXLIB327408P3f06a1
Method	BLASTN
NCBI GI	g2264317
BLAST score	211
E value	1.0e-115
Match length	479
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.	125420
Contig ID	17604_2.R1010
5'-most EST	jC-atXLIB327408P3f06b1
Method	BLASTN
NCBI GI	g2264317
BLAST score	184
E value	7.0e-99
Match length	491
% identity	48
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.	125421
Contig ID	17606_1.R1010
5'-most EST	jC-atXLIB327424P4a11b1
Method	BLASTN

NCBI GI g3426033
BLAST score 348
E value 0.0e+00
Match length 502
% identity 95
NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 125422
Contig ID 17609_1.R1010
5'-most EST LIB24-036-Q1-E1-G7

Seq. No. 125423
Contig ID 17617_1.R1010
5'-most EST jC-atXLIB327415P4c02b1
Method BLASTX
NCBI GI g3096935
BLAST score 302
E value 3.0e-27
Match length 128
% identity 52
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 125424
Contig ID 17619_1.R1010
5'-most EST g1054461
Method BLASTX
NCBI GI g4406775
BLAST score 241
E value 3.0e-20
Match length 129
% identity 39
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 125425
Contig ID 17623_1.R1010
5'-most EST g2597775

Seq. No. 125426
Contig ID 17623_2.R1010
5'-most EST jC-atXLIB327405P3c04b1

Seq. No. 125427
Contig ID 17626_1.R1010
5'-most EST LIB35-056-Q1-E2-F12
Method BLASTN
NCBI GI g2244991
BLAST score 343
E value 0.0e+00
Match length 545
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 125428
Contig ID 17630_1.R1010
5'-most EST jC-atXLIB327415P4c09b1

Method	BLASTX
NCBI GI	g3420052
BLAST score	697
E value	1.0e-73
Match length	137
% identity	99
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	125429
Contig ID	17631_1.R1010
5'-most EST	jC-atXLIB327426P2b03b1
Method	BLASTX
NCBI GI	g3758859
BLAST score	196
E value	7.0e-15
Match length	104
% identity	36
NCBI Description	(Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w), Hypothetical protein, len: 222 aa [Plasmodium falciparum]

Seq. No.	125430
Contig ID	17635_1.R1010
5'-most EST	jC-atX24059Q1E1E07b1

Seq. No.	125431
Contig ID	17636_1.R1010
5'-most EST	g1033278

Seq. No.	125432
Contig ID	17638_1.R1010
5'-most EST	jC-atXLIB327404P4b12b1
Method	BLASTN
NCBI GI	g2760165
BLAST score	355
E value	0.0e+00
Match length	450
% identity	70
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	125433
Contig ID	17640_1.R1010
5'-most EST	jC-alXLIB327435P4c12b1
Method	BLASTX
NCBI GI	g1814407
BLAST score	745
E value	3.0e-79
Match length	189
% identity	76
NCBI Description	(U84891) H+-transporting ATPase [Mesembryanthemum crystallinum]

Seq. No.	125434
Contig ID	17655_1.R1010
5'-most EST	jC-atXLIB327415P2b06b2
Method	BLASTX

NCBI GI	g3915032
BLAST score	487
E value	6.0e-49
Match length	128
% identity	73
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_508603 (L34346) stearoyl-acyl carrier protein desaturase [Glycine max]

Seq. No.	125435
Contig ID	17656_1.R1010
5'-most EST	jC-atXLIB327415P1b08b1
Method	BLASTN
NCBI GI	g1297184
BLAST score	432
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, co

Seq. No.	125436
Contig ID	17660_1.R1010
5'-most EST	jC-atX24059Q1E1C07b1
Method	BLASTX
NCBI GI	g2245068
BLAST score	73
E value	1.0e-78
Match length	154
% identity	97
NCBI Description	(Z97342) serine protease homolog [Arabidopsis thaliana]

Seq. No.	125437
Contig ID	17666_1.R1010
5'-most EST	jC-atXLIB327422P1b05b1
Method	BLASTN
NCBI GI	g4691223
BLAST score	250
E value	1.0e-138
Match length	477
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	125438
Contig ID	17666_2.R1010
5'-most EST	LIB3176-033-P1-K1-A10
Method	BLASTN
NCBI GI	g4691223
BLAST score	262
E value	1.0e-145
Match length	563
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	125439
Contig ID	17666_3.R1010
5'-most EST	jC-atXP63C205A3T7d2
Method	BLASTN
NCBI GI	g4691223
BLAST score	209
E value	1.0e-114
Match length	484
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	125440
Contig ID	17668_1.R1010
5'-most EST	jC-atXP40C164D8T7044a1
Method	BLASTX
NCBI GI	g2213600
BLAST score	477
E value	1.0e-47
Match length	91
% identity	99
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	125441
Contig ID	17669_1.R1010
5'-most EST	jC-atXLIB327415P4b03b1
Method	BLASTX
NCBI GI	g1352316
BLAST score	445
E value	4.0e-44
Match length	90
% identity	96
NCBI Description	DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1 [Arabidopsis thaliana]

Seq. No.	125442
Contig ID	17676_1.R1010
5'-most EST	g2749626

Seq. No.	125443
Contig ID	17676_2.R1010
5'-most EST	jC-atXLIB327415P4b10b1

Seq. No.	125444
Contig ID	17686_1.R1010
5'-most EST	jC-atXLIB327415P2c04b2
Method	BLASTN
NCBI GI	g2244747
BLAST score	63
E value	2.0e-26
Match length	195
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	125445

Contig ID	17687_1.R1010
5'-most EST	jC-atXLIB327415P2c03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125446
Contig ID	17688_1.R1010
5'-most EST	LIB24-049-Q1-E1-G2
Method	BLASTX
NCBI GI	g2809242
BLAST score	714
E value	1.0e-75
Match length	144
% identity	100
NCBI Description	(AC002560) F21B7.11 [Arabidopsis thaliana]

Seq. No.	125447
Contig ID	17690_1.R1010
5'-most EST	LIB24-010-Q1-E1-E10
Method	BLASTN
NCBI GI	g2264306
BLAST score	183
E value	2.0e-98
Match length	372
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	125448
Contig ID	17692_1.R1010
5'-most EST	jC-atXLIB327415P3c01b1
Method	BLASTN
NCBI GI	g2264317
BLAST score	39
E value	2.0e-12
Match length	119
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	125449
Contig ID	17693_1.R1010
5'-most EST	jC-atXLIB327409P3e05b1
Method	BLASTX
NCBI GI	g4467125
BLAST score	596
E value	9.0e-62
Match length	157
% identity	67
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	125450
Contig ID	17695_1.R1010
5'-most EST	LIB3234-097-P1-K1-C12
Method	BLASTX
NCBI GI	g1518540
BLAST score	552
E value	1.0e-56
Match length	116
% identity	92
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	125451
Contig ID	17702_1.R1010
5'-most EST	LIB24-010-Q1-E1-F12
Method	BLASTX
NCBI GI	g4204271
BLAST score	733
E value	7.0e-78
Match length	159
% identity	93
NCBI Description	(AC005223) Unknown protein [Arabidopsis thaliana]

Seq. No.	125452
Contig ID	17704_1.R1010
5'-most EST	jC-atXLIB327415P3c08b1
Method	BLASTX
NCBI GI	g2317909
BLAST score	628
E value	1.0e-65
Match length	121
% identity	99
NCBI Description	(U89959) CER1-like protein [Arabidopsis thaliana]

Seq. No.	125453
Contig ID	17708_1.R1010
5'-most EST	jC-atXLIB327415P2d02b2

Seq. No.	125454
Contig ID	17709_1.R1010
5'-most EST	jC-atXLIB327415P1d03b1
Method	BLASTN
NCBI GI	g2924651
BLAST score	357
E value	0.0e+00
Match length	361
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	125455
Contig ID	17709_2.R1010
5'-most EST	g1565688
Method	BLASTN
NCBI GI	g2924651
BLAST score	172
E value	8.0e-92
Match length	452

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	125456
Contig ID	17712_1.R1010
5'-most EST	jC-atXLIB327419P2h01b2
Method	BLASTX
NCBI GI	g2924512
BLAST score	437
E value	4.0e-43
Match length	117
% identity	77
NCBI Description	(AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No.	125457
Contig ID	17716_1.R1010
5'-most EST	jC-atXLIB327408P2h07b1
Method	BLASTX
NCBI GI	g2213629
BLAST score	733
E value	6.0e-78
Match length	146
% identity	97
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	125458
Contig ID	17716_2.R1010
5'-most EST	jC-atXLIB327415P2d08b2
Method	BLASTX
NCBI GI	g2213629
BLAST score	1110
E value	1.0e-122
Match length	210
% identity	100
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	125459
Contig ID	17727_1.R1010
5'-most EST	jC-atXLIB327427P2e05b1
Method	BLASTN
NCBI GI	g4757397
BLAST score	281
E value	1.0e-156
Match length	614
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBG14, complete sequence

Seq. No.	125460
Contig ID	17727_2.R1010
5'-most EST	jC-atXLIB327408P2c02b1
Method	BLASTN
NCBI GI	g4757397
BLAST score	619
E value	0.0e+00

Match length	808
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBG14, complete sequence

Seq. No.	125461
Contig ID	17727_3.R1010
5'-most EST	g936080
Method	BLASTX
NCBI GI	g555655
BLAST score	180
E value	4.0e-13
Match length	57
% identity	61
NCBI Description	(U06712) DNA-binding protein [Nicotiana tabacum]

Seq. No.	125462
Contig ID	17731_1.R1010
5'-most EST	jC-atXLIB327415P4d06b1
Method	BLASTX
NCBI GI	g4588003
BLAST score	764
E value	1.0e-98
Match length	347
% identity	57
NCBI Description	(AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No.	125463
Contig ID	17733_1.R1010
5'-most EST	jC-atXLIB327415P4d07b1
Method	BLASTX
NCBI GI	g2104536
BLAST score	816
E value	1.0e-87
Match length	152
% identity	99
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	125464
Contig ID	17734_1.R1010
5'-most EST	jC-atXLIB327415P3d11b1
Method	BLASTN
NCBI GI	g4432811
BLAST score	252
E value	1.0e-139
Match length	385
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125465
Contig ID	17735_1.R1010
5'-most EST	jC-atXLIB327415P2e03b2
Method	BLASTX
NCBI GI	g3413704
BLAST score	292

E value	4.0e-26
Match length	158
% identity	45
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125466
Contig ID	17739_1.R1010
5'-most EST	LIB24-081-Q1-E1-E2
Method	BLASTX
NCBI GI	g2062155
BLAST score	488
E value	3.0e-49
Match length	129
% identity	75
NCBI Description	(AC001645) mitochondrial processing peptidase alpha subunit precusor isolog [Arabidopsis thaliana]

Seq. No.	125467
Contig ID	17741_1.R1010
5'-most EST	jC-atXLIB327415P1e06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	9.0e-30
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125468
Contig ID	17742_1.R1010
5'-most EST	jC-atXLIB327415P3d12b1
Method	BLASTX
NCBI GI	g4006827
BLAST score	646
E value	2.0e-67
Match length	126
% identity	99
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	125469
Contig ID	17743_1.R1010
5'-most EST	jC-atXLIB327415P2e01b2
Method	BLASTN
NCBI GI	g3600045
BLAST score	184
E value	6.0e-99
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	125470
Contig ID	17744_1.R1010
5'-most EST	jC-atXLIB327415P2e02b2
Method	BLASTN
NCBI GI	g2656026
BLAST score	85

E value	8.0e-40
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	125471
Contig ID	17751_1.R1010
5'-most EST	jC-atXLIB327415P2e11b2
Method	BLASTN
NCBI GI	g2262155
BLAST score	165
E value	1.0e-87
Match length	448
% identity	98
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	125472
Contig ID	17756_1.R1010
5'-most EST	jC-atXLIB327415P2e08b2
Method	BLASTX
NCBI GI	g4580990
BLAST score	262
E value	1.0e-22
Match length	152
% identity	36
NCBI Description	(AF120335) putative transposase [Arabidopsis thaliana]

Seq. No.	125473
Contig ID	17770_1.R1010
5'-most EST	LIB35-051-Q1-E1-E10
Method	BLASTN
NCBI GI	g3236479
BLAST score	379
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	125474
Contig ID	17771_1.R1010
5'-most EST	g906969
Method	BLASTN
NCBI GI	g3650026
BLAST score	749
E value	0.0e+00
Match length	773
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125475
Contig ID	17784_1.R1010
5'-most EST	jC-atXLIB327415P1f09b1
Method	BLASTN

NCBI GI g4678315
BLAST score 373
E value 0.0e+00
Match length 401
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No. 125476
Contig ID 17789_1.R1010
5'-most EST jC-atXLIB327415P4f01b1

Seq. No. 125477
Contig ID 17791_1.R1010
5'-most EST jC-atXLIB327415P3f04b1
Method BLASTX
NCBI GI g4585977
BLAST score 579
E value 8.0e-60
Match length 118
% identity 90
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No. 125478
Contig ID 17792_1.R1010
5'-most EST g2748978
Method BLASTX
NCBI GI g4585991
BLAST score 349
E value 7.0e-64
Match length 212
% identity 58
NCBI Description (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]

Seq. No. 125479
Contig ID 17793_1.R1010
5'-most EST jC-atXLIB327421P4c06b1
Method BLASTX
NCBI GI g1806140
BLAST score 496
E value 4.0e-50
Match length 118
% identity 84
NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 125480
Contig ID 17800_1.R1010
5'-most EST jC-atXP115C124C13T7032d1
Method BLASTX
NCBI GI g4455248
BLAST score 641
E value 7.0e-67
Match length 137
% identity 100
NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No.	125481
Contig ID	17808_1.R1010
5'-most EST	LIB24-011-Q1-E1-H7
Method	BLASTX
NCBI GI	g4006884
BLAST score	449
E value	1.0e-44
Match length	98
% identity	90
NCBI Description	(Z99707) BEL1-like homeodomain protein [Arabidopsis thaliana]

Seq. No.	125482
Contig ID	17811_1.R1010
5'-most EST	jC-atXLIB327415P4d08b1
Method	BLASTN
NCBI GI	g4490734
BLAST score	299
E value	1.0e-167
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	125483
Contig ID	17813_1.R1010
5'-most EST	jC-atXmonuni26Aa09b1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	1.0e-22
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	125484
Contig ID	17823_1.R1010
5'-most EST	jC-atXP70C220O22T7038a1
Method	BLASTN
NCBI GI	g3687221
BLAST score	211
E value	1.0e-115
Match length	406
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125485
Contig ID	17827_1.R1010
5'-most EST	LIB35-022-Q1-E1-F10
Method	BLASTN
NCBI GI	g4757395
BLAST score	332
E value	0.0e+00
Match length	456
% identity	72
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No.	125486
Contig ID	17829_1.R1010
5'-most EST	LIB3176-113-P2-K1-B12
Method	BLASTN
NCBI GI	g2459406
BLAST score	392
E value	0.0e+00
Match length	1008
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125487
Contig ID	17830_1.R1010
5'-most EST	jC-atXLIB327415P4d12b1
Method	BLASTX
NCBI GI	g3328450
BLAST score	362
E value	5.0e-34
Match length	137
% identity	47
NCBI Description	(AE001280) hypothetical protein [Chlamydia trachomatis]

Seq. No.	125488
Contig ID	17831_1.R1010
5'-most EST	LIB3175-022-P1-K1-E11
Method	BLASTX
NCBI GI	g2462754
BLAST score	187
E value	9.0e-14
Match length	54
% identity	67
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	125489
Contig ID	17835_1.R1010
5'-most EST	jC-atXP98CH2H6T7053d1
Method	BLASTX
NCBI GI	g1931637
BLAST score	630
E value	1.0e-65
Match length	138
% identity	89
NCBI Description	(U95973) receptor-associated kinase isolog [Arabidopsis thaliana]

Seq. No.	125490
Contig ID	17843_1.R1010
5'-most EST	LIB24-019-Q1-E1-E1
Method	BLASTX
NCBI GI	g3935141
BLAST score	542
E value	1.0e-55
Match length	99
% identity	99

NCBI Description	(AC005106) T25N20.5 [Arabidopsis thaliana]
Seq. No.	125491
Contig ID	17845_1.R1010
5'-most EST	g957553
Method	BLASTX
NCBI GI	g2642448
BLAST score	218
E value	2.0e-17
Match length	149
% identity	26
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.	125492
Contig ID	17848_1.R1010
5'-most EST	jC-atXLIB327415P4e07b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	125493
Contig ID	17849_1.R1010
5'-most EST	g502190
Method	BLASTX
NCBI GI	g1172873
BLAST score	340
E value	1.0e-91
Match length	265
% identity	61
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.	125494
Contig ID	17850_1.R1010
5'-most EST	jC-atXLIB327417P3d03b1
Method	BLASTX
NCBI GI	g2529680
BLAST score	1733
E value	0.0e+00
Match length	358
% identity	94
NCBI Description	(AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]
Seq. No.	125495
Contig ID	17850_2.R1010
5'-most EST	jC-atXLIB327417P4d03a1
Method	BLASTX
NCBI GI	g2529680

BLAST score	357
E value	9.0e-34
Match length	80
% identity	94
NCBI Description	(AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]

Seq. No.	125496
Contig ID	17852_1.R1010
5'-most EST	LIB35-036-Q1-E1-F4
Method	BLASTN
NCBI GI	g4589409
BLAST score	198
E value	1.0e-107
Match length	419
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	125497
Contig ID	17852_2.R1010
5'-most EST	jC-atXmonuni26Ae06b1
Method	BLASTN
NCBI GI	g4589409
BLAST score	159
E value	4.0e-84
Match length	446
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	125498
Contig ID	17853_1.R1010
5'-most EST	jC-atXLIB327415P3e08b1
Method	BLASTX
NCBI GI	g4580476
BLAST score	297
E value	9.0e-27
Match length	98
% identity	59
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	125499
Contig ID	17854_1.R1010
5'-most EST	LIB24-012-Q1-E1-D5
Method	BLASTX
NCBI GI	g4678263
BLAST score	741
E value	6.0e-79
Match length	145
% identity	100
NCBI Description	(AL049657) brefeldin A-sensitive Golgi protein-like [Arabidopsis thaliana]

Seq. No.	125500
Contig ID	17857_1.R1010
5'-most EST	g2762358

Method	BLASTX
NCBI GI	g3776571
BLAST score	615
E value	3.0e-66
Match length	184
% identity	77
NCBI Description	(AC005388) T22H22.18 [Arabidopsis thaliana]

Seq. No.	125501
Contig ID	17858_1.R1010
5'-most EST	jC-atXLIB327415P4e06b1
Method	BLASTN
NCBI GI	g4415928
BLAST score	413
E value	0.0e+00
Match length	434
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125502
Contig ID	17862_1.R1010
5'-most EST	jC-atXLIB327415P2f02b2
Method	BLASTX
NCBI GI	g4490332
BLAST score	383
E value	3.0e-38
Match length	143
% identity	54
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	125503
Contig ID	17863_1.R1010
5'-most EST	jC-atXLIB327415P2f03b2
Method	BLASTX
NCBI GI	g4314376
BLAST score	54
E value	2.0e-22
Match length	94
% identity	63
NCBI Description	(AC006232) similar to PIG-L [Arabidopsis thaliana]

Seq. No.	125504
Contig ID	17865_1.R1010
5'-most EST	jC-atXLIB327415P4e12b1

Seq. No.	125505
Contig ID	17866_1.R1010
5'-most EST	jC-atXLIB327415P2g12b2
Method	BLASTX
NCBI GI	g3880026
BLAST score	409
E value	7.0e-40
Match length	132
% identity	52
NCBI Description	(Z75550) Similarity with Schizosaccharomyces hypothetical gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from

this gene [Caenorhabditis elegans]

Seq. No.	125506
Contig ID	17868_1.R1010
5'-most EST	LIB24-012-Q1-E1-E9
Method	BLASTX
NCBI GI	g3335366
BLAST score	271
E value	1.0e-23
Match length	105
% identity	47
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	125507
Contig ID	17869_1.R1010
5'-most EST	jC-atXLIB327423P1e01b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	125508
Contig ID	17869_2.R1010
5'-most EST	g937891
Method	BLASTN
NCBI GI	g540252
BLAST score	45
E value	9.0e-16
Match length	45
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	125509
Contig ID	17880_1.R1010
5'-most EST	jC-atXLIB327415P4f04b1
Method	BLASTX
NCBI GI	g3695061
BLAST score	286
E value	2.0e-25
Match length	91
% identity	60
NCBI Description	(AF064788) rac GTPase activating protein 2 [Lotus japonicus]

Seq. No.	125510
Contig ID	17881_1.R1010
5'-most EST	jC-atXLIB327407P1d12b2
Method	BLASTN
NCBI GI	g2191126
BLAST score	557
E value	0.0e+00
Match length	639
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	125511
Contig ID	17883_1.R1010
5'-most EST	jC-atXLIB327415P4f06b1
Method	BLASTX
NCBI GI	g4099831
BLAST score	674
E value	7.0e-71
Match length	125
% identity	98
NCBI Description	(U90264) bifunctional nuclease bfn1 [Arabidopsis thaliana]

Seq. No.	125512
Contig ID	17887_1.R1010
5'-most EST	jC-atXLIB327415P3f01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125513
Contig ID	17887_2.R1010
5'-most EST	LIB24-012-Q1-E1-G5

Seq. No.	125514
Contig ID	17888_1.R1010
5'-most EST	jC-atXLIB327415P4f02b1

Seq. No.	125515
Contig ID	17889_1.R1010
5'-most EST	jC-atXLIB327415P3f02b1
Method	BLASTN
NCBI GI	g4589440
BLAST score	220
E value	1.0e-120
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	125516
Contig ID	17890_1.R1010
5'-most EST	jC-atXLIB327415P3f03b1
Method	BLASTN
NCBI GI	g2853071
BLAST score	181
E value	4.0e-97
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No. 125517

Contig ID 17891_1.R1010
5'-most EST LIB24-102-Q1-E1-B4

Seq. No. 125518
Contig ID 17897_1.R1010
5'-most EST jC-atXLIB327415P4f11b1

Seq. No. 125519
Contig ID 17898_1.R1010
5'-most EST jC-atXLIB327416P3g06b1
Method BLASTX
NCBI GI g1351135
BLAST score 526
E value 1.0e-53
Match length 105
% identity 99
NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_436792_emb_CAA50317_ (X70990) sucrose synthase [Arabidopsis thaliana]

Seq. No. 125520
Contig ID 17901_1.R1010
5'-most EST jC-alX24005Q1E1E12a1

Seq. No. 125521
Contig ID 17903_1.R1010
5'-most EST jC-atXLIB327415P4d04b1
Method BLASTN
NCBI GI g3241923
BLAST score 262
E value 1.0e-145
Match length 416
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No. 125522
Contig ID 17915_1.R1010
5'-most EST g1053339

Seq. No. 125523
Contig ID 17917_1.R1010
5'-most EST jC-atXLIB327415P4d11b1
Method BLASTX
NCBI GI g1592545
BLAST score 197
E value 5.0e-15
Match length 125
% identity 37
NCBI Description (U37486) peroxisomal multifunctional enzyme type II [Rattus norvegicus]

Seq. No. 125524
Contig ID 17920_1.R1010
5'-most EST jC-atXLIB327414P4d02a2
Method BLASTX
NCBI GI g2464914

BLAST score	272
E value	1.0e-23
Match length	106
% identity	55
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125525
Contig ID	17920_3.R1010
5'-most EST	LIB24-013-Q1-E1-B4

Seq. No.	125526
Contig ID	17923_1.R1010
5'-most EST	jC-atXLIB327415P3d10b1
Method	BLASTX
NCBI GI	g4741186
BLAST score	316
E value	5.0e-29
Match length	85
% identity	78
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	125527
Contig ID	17932_1.R1010
5'-most EST	jC-atXLIB327415P4e02b1
Method	BLASTX
NCBI GI	g3776578
BLAST score	262
E value	2.0e-22
Match length	128
% identity	42
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	125528
Contig ID	17932_2.R1010
5'-most EST	g2757796
Method	BLASTN
NCBI GI	g4586349
BLAST score	86
E value	1.0e-40
Match length	90
% identity	99
NCBI Description	Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

Seq. No.	125529
Contig ID	17934_1.R1010
5'-most EST	jC-atXLIB327415P4e03b1
Method	BLASTX
NCBI GI	g3894393
BLAST score	209
E value	2.0e-17
Match length	294
% identity	6
NCBI Description	(AF053998) Hcr2-5D [Lycopersicon esculentum]

Seq. No.	125530

Contig ID	17935_1.R1010
5'-most EST	LIB24-041-Q1-E1-H6
Method	BLASTX
NCBI GI	g4679028
BLAST score	548
E value	6.0e-56
Match length	243
% identity	47
NCBI Description	(AF077207) HSPC021 [Homo sapiens]

Seq. No.	125531
Contig ID	17936_1.R1010
5'-most EST	jC-atXLIB327415P2e12b2
Method	BLASTN
NCBI GI	g4589444
BLAST score	446
E value	0.0e+00
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence

Seq. No.	125532
Contig ID	17937_1.R1010
5'-most EST	jC-atXLIB327415P4e01b1

Seq. No.	125533
Contig ID	17938_1.R1010
5'-most EST	jC-atXP73C223E15T7b1
Method	BLASTX
NCBI GI	g3249098
BLAST score	253
E value	2.0e-21
Match length	148
% identity	39
NCBI Description	(AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481 and gb_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No.	125534
Contig ID	17938_2.R1010
5'-most EST	g1054215

Seq. No.	125535
Contig ID	17941_1.R1010
5'-most EST	jC-atXLIB327415P4e10b1
Method	BLASTN
NCBI GI	g4097546
BLAST score	200
E value	1.0e-108
Match length	200
% identity	88
NCBI Description	Arabidopsis thaliana farnesylated protein ATFP3 mRNA, partial cds

Seq. No.	125536
Contig ID	17942_1.R1010
5'-most EST	jC-atXLIB327405P1f09b2

Seq. No.	125537
Contig ID	17949_1.R1010
5'-most EST	LIB3234-058-P1-K1-G7
Method	BLASTX
NCBI GI	g3426039
BLAST score	323
E value	9.0e-30
Match length	84
% identity	71
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	125538
Contig ID	17951_1.R1010
5'-most EST	LIB24-056-Q1-E2-B3
Method	BLASTX
NCBI GI	g4468813
BLAST score	333
E value	6.0e-31
Match length	136
% identity	46
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	125539
Contig ID	17953_2.R1010
5'-most EST	LIB3175-024-P1-K1-H5
Method	BLASTN
NCBI GI	g3985957
BLAST score	228
E value	1.0e-125
Match length	666
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	125540
Contig ID	17954_1.R1010
5'-most EST	g2413507
Method	BLASTN
NCBI GI	g3859658
BLAST score	440
E value	0.0e+00
Match length	504
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	125541
Contig ID	17954_2.R1010
5'-most EST	jC-atXLIB327415P1f05a1
Method	BLASTN
NCBI GI	g3859658
BLAST score	50
E value	5.0e-19
Match length	158
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No.	125542
Contig ID	17958_1.R1010
5'-most EST	jC-atXLIB327415P1f04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	5.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125543
Contig ID	17966_1.R1010
5'-most EST	jC-atXLIB327415P2f12b2
Method	BLASTX
NCBI GI	g1654140
BLAST score	406
E value	2.0e-39
Match length	105
% identity	75
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	125544
Contig ID	17968_1.R1010
5'-most EST	jC-atXLIB327415P2f10b2

Seq. No.	125545
Contig ID	17971_1.R1010
5'-most EST	jC-atXLIB327415P2f11b2
Method	BLASTN
NCBI GI	g2244829
BLAST score	339
E value	0.0e+00
Match length	570
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	125546
Contig ID	17973_1.R1010
5'-most EST	jC-atXLIB327415P4f08b1
Method	BLASTX
NCBI GI	g4262162
BLAST score	166
E value	3.0e-11
Match length	64
% identity	55
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	125547
Contig ID	17973_2.R1010
5'-most EST	g935576
Method	BLASTX

NCBI GI g2809251
BLAST score 180
E value 1.0e-23
Match length 122
% identity 46
NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No. 125548
Contig ID 17974_1.R1010
5'-most EST LIB25-001-Q1-E2-B1
Method BLASTX
NCBI GI g1174780
BLAST score 268
E value 2.0e-23
Match length 85
% identity 65
NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP 2) >gi_320135_pir__PQ0450 tryptophan synthase (EC 4.2.1.20) beta-2 chain precursor - maize (fragment) >gi_168574 (M76685) tryptophan synthase beta-subunit [Zea mays]

Seq. No. 125549
Contig ID 17975_1.R1010
5'-most EST jC-alX24049Q1E2D02b1
Method BLASTX
NCBI GI g3618320
BLAST score 247
E value 5.0e-21
Match length 56
% identity 79
NCBI Description (AB001888) zinc finger protein [Oryza sativa]

Seq. No. 125550
Contig ID 17976_1.R1010
5'-most EST LIB24-013-Q1-E1-H4
Method BLASTN
NCBI GI g3449325
BLAST score 225
E value 1.0e-123
Match length 407
% identity 63
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No. 125551
Contig ID 17977_1.R1010
5'-most EST LIB24-013-Q1-E1-H5

Seq. No. 125552
Contig ID 17982_1.R1010
5'-most EST jC-atXLIB327416P2c09b1
Method BLASTX
NCBI GI g4206197
BLAST score 408
E value 2.0e-68
Match length 138
% identity 67

NCBI Description	(AF071527) putative pre-mRNA splicing factor [Arabidopsis thaliana]

Seq. No.	125553
Contig ID	17983_1.R1010
5'-most EST	LIB35-047-Q1-E1-B8
Method	BLASTX
NCBI GI	g4586674
BLAST score	426
E value	1.0e-42
Match length	142
% identity	66
NCBI Description	(AB022714) signal peptidase 21kDa subunit [Rattus norvegicus]

Seq. No.	125554
Contig ID	17983_2.R1010
5'-most EST	jC-atXLIB327416P1c11b1
Method	BLASTX
NCBI GI	g4586674
BLAST score	440
E value	3.0e-43
Match length	170
% identity	52
NCBI Description	(AB022714) signal peptidase 21kDa subunit [Rattus norvegicus]

Seq. No.	125555
Contig ID	17983_3.R1010
5'-most EST	jC-atXLIB327416P1c11a1
Method	BLASTX
NCBI GI	g4586674
BLAST score	261
E value	1.0e-22
Match length	89
% identity	56
NCBI Description	(AB022714) signal peptidase 21kDa subunit [Rattus norvegicus]

Seq. No.	125556
Contig ID	17984_1.R1010
5'-most EST	jC-atX25073Q1E1F04b1
Method	BLASTX
NCBI GI	g3212866
BLAST score	265
E value	6.0e-23
Match length	82
% identity	67
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	125557
Contig ID	17985_1.R1010
5'-most EST	LIB25-062-Q1-E1-F2

Seq. No.	125558
Contig ID	17987_1.R1010
5'-most EST	jC-alXLIB327434P4d03b1

Method	BLASTN
NCBI GI	g3869074
BLAST score	291
E value	1.0e-162
Match length	587
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	125559
Contig ID	17987_2.R1010
5'-most EST	jC-alXLIB327434P4c07b1
Method	BLASTN
NCBI GI	g3869074
BLAST score	534
E value	0.0e+00
Match length	577
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	125560
Contig ID	17990_1.R1010
5'-most EST	g2762556
Method	BLASTX
NCBI GI	g1703227
BLAST score	161
E value	2.0e-83
Match length	226
% identity	67
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine aminotransferase [Hordeum vulgare]

Seq. No.	125561
Contig ID	17991_1.R1010
5'-most EST	jC-atXLIB327416P4c07b1

Seq. No.	125562
Contig ID	17995_1.R1010
5'-most EST	jC-alX24071Q1E1H03b1
Method	BLASTX
NCBI GI	g3128173
BLAST score	737
E value	2.0e-78
Match length	142
% identity	100
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125563
Contig ID	17996_1.R1010
5'-most EST	g398624

Seq. No.	125564
Contig ID	18002_1.R1010

5'-most EST	jC-atXLIB327427P2e03b1
Method	BLASTX
NCBI GI	g3980405
BLAST score	556
E value	8.0e-57
Match length	167
% identity	63
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	125565
Contig ID	18003_4.R1010
5'-most EST	LIB24-094-Q1-E1-H8

Seq. No.	125566
Contig ID	18007_1.R1010
5'-most EST	LIB3175-007-P1-K1-H6
Method	BLASTX
NCBI GI	g3128175
BLAST score	326
E value	5.0e-30
Match length	156
% identity	39
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	125567
Contig ID	18007_2.R1010
5'-most EST	jC-alXLIB327436P1b12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	5.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125568
Contig ID	18009_1.R1010
5'-most EST	LIB24-014-Q1-E1-C8
Method	BLASTN
NCBI GI	g3757512
BLAST score	332
E value	0.0e+00
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125569
Contig ID	18010_1.R1010
5'-most EST	jC-atXLIB327416P2d01b1
Method	BLASTN
NCBI GI	g3510339
BLAST score	283
E value	1.0e-158
Match length	422

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	125570
Contig ID	18011_1.R1010
5'-most EST	jC-atXLIB327416P1d05b1
Method	BLASTX
NCBI GI	g2244784
BLAST score	355
E value	5.0e-34
Match length	155
% identity	54
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125571
Contig ID	18016_1.R1010
5'-most EST	g2393656
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	8.0e-16
Match length	57
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125572
Contig ID	18016_2.R1010
5'-most EST	jC-atXLIB327416P1d07b1
Method	BLASTX
NCBI GI	g3763916
BLAST score	444
E value	5.0e-44
Match length	145
% identity	61
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	125573
Contig ID	18017_1.R1010
5'-most EST	jC-atXLIB327416P2d07b1
Method	BLASTX
NCBI GI	g4455222
BLAST score	315
E value	7.0e-29
Match length	88
% identity	70
NCBI Description	(AL035440) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125574
Contig ID	18025_1.R1010
5'-most EST	LIB24-014-Q1-E1-E2

Seq. No.	125575
Contig ID	18030_1.R1010
5'-most EST	jC-alXLIB327435P3f12b1

Method	BLASTN
NCBI GI	g1707006
BLAST score	317
E value	1.0e-178
Match length	396
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125576
Contig ID	18033_1.R1010
5'-most EST	LIB24-074-Q1-E1-G12
Method	BLASTX
NCBI GI	g4539452
BLAST score	486
E value	6.0e-49
Match length	163
% identity	56
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	125577
Contig ID	18035_1.R1010
5'-most EST	jC-atXLIB327416P3d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125578
Contig ID	18039_1.R1010
5'-most EST	LIB3177-018-P1-K2-A3
Method	BLASTX
NCBI GI	g4406759
BLAST score	315
E value	6.0e-29
Match length	160
% identity	45
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125579
Contig ID	18045_1.R1010
5'-most EST	jC-atXLIB327421P3c08b1

Seq. No.	125580
Contig ID	18046_1.R1010
5'-most EST	jC-atX24067Q1E1H05b1
Method	BLASTX
NCBI GI	g4507075
BLAST score	680
E value	1.0e-71
Match length	183
% identity	72

NCBI Description	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 >gi_2967452_dbj_BAA25173_ (AB010882) hSNF2H [Homo sapiens]

Seq. No.	125581
Contig ID	18049_1.R1010
5'-most EST	LIB24-014-Q1-E1-G6

Seq. No.	125582
Contig ID	18050_1.R1010
5'-most EST	jC-atXLIB327416P4d11b1
Method	BLASTN
NCBI GI	g4159706
BLAST score	563
E value	0.0e+00
Match length	666
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	125583
Contig ID	18055_1.R1010
5'-most EST	jC-atXLIB327416P2e10b1
Method	BLASTX
NCBI GI	g2191135
BLAST score	321
E value	1.0e-29
Match length	110
% identity	51
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	125584
Contig ID	18064_1.R1010
5'-most EST	jC-atXLIB327416P1c10b1
Method	BLASTX
NCBI GI	g4337207
BLAST score	650
E value	6.0e-98
Match length	228
% identity	82
NCBI Description	(AC006403) putative zinc-finger protein [Arabidopsis thaliana] >gi_4585205_gb_AAD25324.1_AF095588_1 (AF095588) C2H2 zinc finger protein FZF [Arabidopsis thaliana]

Seq. No.	125585
Contig ID	18065_1.R1010
5'-most EST	jC-atXLIB327416P2c10b1
Method	BLASTX
NCBI GI	g2459417
BLAST score	595
E value	2.0e-61
Match length	138
% identity	45
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	125586
Contig ID	18071_1.R1010
5'-most EST	LIB24-015-Q1-E1-A5
Method	BLASTN
NCBI GI	g4589435
BLAST score	400
E value	0.0e+00
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	125587
Contig ID	18076_1.R1010
5'-most EST	jC-atXLIB327416P4c09b1
Method	BLASTX
NCBI GI	g4115925
BLAST score	314
E value	2.0e-28
Match length	156
% identity	47
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	125588
Contig ID	18079_1.R1010
5'-most EST	jC-atXLIB327416P3c10b1
Method	BLASTX
NCBI GI	g1871195
BLAST score	666
E value	5.0e-70
Match length	128
% identity	98
NCBI Description	(U90439) Ca++ dependent protein kinase isolog [Arabidopsis thaliana] >gi_2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	125589
Contig ID	18082_1.R1010
5'-most EST	LIB24-015-Q1-E1-B5
Method	BLASTN
NCBI GI	g3738313
BLAST score	279
E value	1.0e-155
Match length	387
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125590
Contig ID	18093_1.R1010
5'-most EST	jC-atXP85C241I8T7b1
Method	BLASTX
NCBI GI	g2995953
BLAST score	301

E value	5.0e-27
Match length	118
% identity	53
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	125591
Contig ID	18094_1.R1010
5'-most EST	jC-atXLIB327404P2h11b1
Method	BLASTX
NCBI GI	g2213615
BLAST score	512
E value	9.0e-52
Match length	150
% identity	61
NCBI Description	(AC000103) F21J9.9 [Arabidopsis thaliana]

Seq. No.	125592
Contig ID	18098_1.R1010
5'-most EST	jC-atXLIB327416P2d06b1
Method	BLASTN
NCBI GI	g3449330
BLAST score	576
E value	0.0e+00
Match length	580
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	125593
Contig ID	18103_1.R1010
5'-most EST	jC-alXLIB327436P3e02b1
Method	BLASTX
NCBI GI	g3878134
BLAST score	213
E value	1.0e-16
Match length	60
% identity	62
NCBI Description	(Z68218) K01H12.1 [Caenorhabditis elegans]

Seq. No.	125594
Contig ID	18105_1.R1010
5'-most EST	LIB25-009-Q1-E1-E7
Method	BLASTX
NCBI GI	g4262226
BLAST score	291
E value	4.0e-26
Match length	87
% identity	63
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	125595
Contig ID	18107_1.R1010
5'-most EST	jC-atXLIB327408P3c06b1
Method	BLASTN
NCBI GI	g2252823
BLAST score	154
E value	7.0e-81

Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	125596
Contig ID	18110_1.R1010
5'-most EST	g2759645
Method	BLASTX
NCBI GI	g462195
BLAST score	440
E value	2.0e-43
Match length	112
% identity	75
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	125597
Contig ID	18112_1.R1010
5'-most EST	jC-atXLIB327423P1g02b1
Method	BLASTX
NCBI GI	g4680192
BLAST score	179
E value	1.0e-12
Match length	108
% identity	39
NCBI Description	(AF111710) hypothetical protein [Oryza sativa subsp. indica]

Seq. No.	125598
Contig ID	18115_1.R1010
5'-most EST	jC-atXLIB327416P2d11b1
Method	BLASTX
NCBI GI	g3540209
BLAST score	496
E value	4.0e-50
Match length	140
% identity	72
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	125599
Contig ID	18117_1.R1010
5'-most EST	jC-atXLIB327416P1d11b1

Seq. No.	125600
Contig ID	18124_1.R1010
5'-most EST	jC-atXmonuni26Cc01b1
Method	BLASTN
NCBI GI	g4512656
BLAST score	195
E value	1.0e-105
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	125601
Contig ID	18125_1.R1010
5'-most EST	jC-atXmonuni27Ba08b1
Method	BLASTX
NCBI GI	g4335737
BLAST score	263
E value	1.0e-22
Match length	112
% identity	29
NCBI Description	(AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	125602
Contig ID	18127_1.R1010
5'-most EST	jC-atXLIB327416P4d04b1
Method	BLASTX
NCBI GI	g133448
BLAST score	574
E value	3.0e-59
Match length	138
% identity	81
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN >gi_81503_pir__A29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta'' chain - spinach chloroplast >gi_295122 (M55297) RNA polymerase [Spinacia oleracea]

Seq. No.	125603
Contig ID	18132_1.R1010
5'-most EST	LIB24-015-Q1-E1-F9
Method	BLASTX
NCBI GI	g520515
BLAST score	173
E value	1.0e-12
Match length	99
% identity	41
NCBI Description	(U10337) RNA polymerase II, second largest subunit [Helobdella stagnalis]

Seq. No.	125604
Contig ID	18134_1.R1010
5'-most EST	jC-atXLIB327416P1e02b1
Method	BLASTN
NCBI GI	g4544405
BLAST score	252
E value	1.0e-139
Match length	772
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	125605
Contig ID	18136_1.R1010
5'-most EST	jC-atXLIB327416P2e03b1
Method	BLASTX
NCBI GI	g2208903
BLAST score	373

E value 1.0e-35
Match length 83
% identity 76
NCBI Description (AB004798) ascorbate oxidase [Arabidopsis thaliana]

Seq. No. 125606
Contig ID 18137_1.R1010
5'-most EST LIB25-001-Q1-E1-G10
Method BLASTX
NCBI GI g4680651
BLAST score 155
E value 3.0e-10
Match length 85
% identity 40
NCBI Description (AF132940) CGI-06 protein [Homo sapiens]

Seq. No. 125607
Contig ID 18138_1.R1010
5'-most EST jC-atXLIB327438P3g10a2
Method BLASTX
NCBI GI g2244885
BLAST score 397
E value 2.0e-38
Match length 161
% identity 54
NCBI Description (Z97338) strong similarity to UTP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 125608
Contig ID 18141_1.R1010
5'-most EST jC-atXLIB327416P3d10b1

Seq. No. 125609
Contig ID 18144_1.R1010
5'-most EST g1053695
Method BLASTX
NCBI GI g4503527
BLAST score 293
E value 3.0e-26
Match length 152
% identity 39
NCBI Description UNKNOWN >gi_1778051 (U62583) Prt1 homolog [Homo sapiens]

Seq. No. 125610
Contig ID 18148_1.R1010
5'-most EST jC-atXLIB327419P4d09b1
Method BLASTX
NCBI GI g2827536
BLAST score 637
E value 1.0e-66
Match length 136
% identity 88
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 125611
Contig ID 18150_1.R1010
5'-most EST jC-atXLIB327416P1e12b1

Method	BLASTN
NCBI GI	g2244788
BLAST score	479
E value	0.0e+00
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	125612
Contig ID	18154_1.R1010
5'-most EST	LIB24-015-Q1-E1-H7
Method	BLASTX
NCBI GI	g4689436
BLAST score	232
E value	7.0e-19
Match length	99
% identity	52
NCBI Description	(AF143096) peptidyl-prolyl cis-trans isomerase EPVH [Homo sapiens]

Seq. No.	125613
Contig ID	18155_1.R1010
5'-most EST	jC-atXLIB327416P1e05b1
Method	BLASTX
NCBI GI	g557472
BLAST score	255
E value	8.0e-22
Match length	126
% identity	45
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	125614
Contig ID	18155_2.R1010
5'-most EST	g2722905
Method	BLASTX
NCBI GI	g557472
BLAST score	263
E value	6.0e-23
Match length	124
% identity	48
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	125615
Contig ID	18158_1.R1010
5'-most EST	jC-atXLIB327416P2c04b1
Method	BLASTX
NCBI GI	g2131492
BLAST score	171
E value	5.0e-12
Match length	97
% identity	37
NCBI Description	hypothetical protein YDR438w - yeast (Saccharomyces cerevisiae) >gi_927694 (U33007) Ydr438wp; CAI: 0.11 [Saccharomyces cerevisiae]

Seq. No. 125616

Contig ID	18164_1.R1010
5'-most EST	jC-atXLIB327416P1c03b1
Method	BLASTX
NCBI GI	g3193320
BLAST score	647
E value	8.0e-68
Match length	137
% identity	98
NCBI Description	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No.	125617
Contig ID	18168_1.R1010
5'-most EST	LIB24-016-Q1-E1-B1

Seq. No.	125618
Contig ID	18170_1.R1010
5'-most EST	jC-atXLIB327416P3c03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	64
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125619
Contig ID	18173_1.R1010
5'-most EST	jC-atXLIB327416P4c06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125620
Contig ID	18174_1.R1010
5'-most EST	jC-atXLIB327416P4c05b1
Method	BLASTN
NCBI GI	g1871173
BLAST score	425
E value	0.0e+00
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	125621
Contig ID	18175_1.R1010
5'-most EST	jC-atXLIB327416P2c12b1
Method	BLASTN

NCBI GI	g4678196
BLAST score	403
E value	0.0e+00
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence, complete sequence

Seq. No.	125622
Contig ID	18182_1.R1010
5'-most EST	ARABLI-15-Q1-B1-A6
Method	BLASTX
NCBI GI	g1353163
BLAST score	352
E value	6.0e-33
Match length	113
% identity	58
NCBI Description	HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHROMOSOME III PRECURSOR >gi_1055071 (U39851) C23G10.2 gene product [Caenorhabditis elegans]

Seq. No.	125623
Contig ID	18182_2.R1010
5'-most EST	LIB3234-001-P1-K1-B9
Method	BLASTN
NCBI GI	g4519195
BLAST score	422
E value	0.0e+00
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	125624
Contig ID	18185_1.R1010
5'-most EST	jC-atXLIB327416P3c12b1
Method	BLASTX
NCBI GI	g4220477
BLAST score	271
E value	1.0e-23
Match length	130
% identity	48
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	125625
Contig ID	18186_1.R1010
5'-most EST	jC-atXLIB327406P4c05b2
Method	BLASTN
NCBI GI	g2252848
BLAST score	264
E value	1.0e-146
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	125626
Contig ID	18192_1.R1010

5'-most EST	LIB24-016-Q1-E1-D1
Method	BLASTX
NCBI GI	g3859594
BLAST score	56
E value	6.0e-43
Match length	165
% identity	66
NCBI Description	(AF104919) contains similarity to ribosomal protein L7Ae (Pfam: PF01248, E=0.0017, N=1) [Arabidopsis thaliana]

Seq. No.	125627
Contig ID	18193_1.R1010
5'-most EST	jC-atX24106Q1E1E12b1
Method	BLASTX
NCBI GI	g4567232
BLAST score	342
E value	6.0e-32
Match length	72
% identity	96
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	125628
Contig ID	18193_2.R1010
5'-most EST	g2597151
Method	BLASTX
NCBI GI	g4567232
BLAST score	150
E value	1.0e-09
Match length	31
% identity	97
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	125629
Contig ID	18195_1.R1010
5'-most EST	jC-atXLIB327409P1a02b1
Method	BLASTX
NCBI GI	g4263720
BLAST score	654
E value	2.0e-68
Match length	146
% identity	90
NCBI Description	(AC006223) putative cysteine proteinase inhibitor [Arabidopsis thaliana]

Seq. No.	125630
Contig ID	18196_1.R1010
5'-most EST	jC-atXLIB327423P1g11b1
Method	BLASTX
NCBI GI	g2435511
BLAST score	392
E value	4.0e-40
Match length	186
% identity	53
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	125631
Contig ID	18199_1.R1010
5'-most EST	LIB24-085-Q1-E1-D4

Seq. No.	125632
Contig ID	18201_1.R1010
5'-most EST	LIB25-067-Q1-E1-F7
Method	BLASTN
NCBI GI	g3510343
BLAST score	439
E value	0.0e+00
Match length	476
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	125633
Contig ID	18204_1.R1010
5'-most EST	jC-atXLIB327416P1d09b1
Method	BLASTN
NCBI GI	g4589429
BLAST score	556
E value	0.0e+00
Match length	556
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJM18, complete sequence

Seq. No.	125634
Contig ID	18208_1.R1010
5'-most EST	jC-atXLIB327416P1d10b1
Method	BLASTX
NCBI GI	g3643598
BLAST score	713
E value	1.0e-75
Match length	137
% identity	93
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	125635
Contig ID	18209_1.R1010
5'-most EST	jC-atXLIB327416P2d09b1
Method	BLASTN
NCBI GI	g2924653
BLAST score	173
E value	2.0e-92
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	125636
Contig ID	18212_1.R1010
5'-most EST	LIB25-052-Q1-E1-G9
Method	BLASTN

NCBI GI g4678315
BLAST score 178
E value 2.0e-95
Match length 316
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No. 125637
Contig ID 18213_1.R1010
5'-most EST LIB35-007-Q1-E1-D7
Method BLASTN
NCBI GI g3152602
BLAST score 472
E value 0.0e+00
Match length 484
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 125638
Contig ID 18227_1.R1010
5'-most EST jC-atXP98CH8B11T7063d1
Method BLASTN
NCBI GI g1946354
BLAST score 572
E value 0.0e+00
Match length 624
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No. 125639
Contig ID 18227_2.R1010
5'-most EST LIB3176-004-P1-K1-D12
Method BLASTN
NCBI GI g1946354
BLAST score 438
E value 0.0e+00
Match length 598
% identity 95
NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No. 125640
Contig ID 18227_3.R1010
5'-most EST jC-atXLIB327416P3d07b1
Method BLASTN
NCBI GI g1946354
BLAST score 310
E value 1.0e-174
Match length 413
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No. 125641

Contig ID	18231_1.R1010
5'-most EST	jC-atXLIB327425P1c03b1
Method	BLASTN
NCBI GI	g3763944
BLAST score	220
E value	1.0e-120
Match length	489
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	125642
Contig ID	18241_1.R1010
5'-most EST	g932878
Method	BLASTX
NCBI GI	g3094014
BLAST score	295
E value	3.0e-26
Match length	90
% identity	56
NCBI Description	(AF060862) unknown [Homo sapiens]

Seq. No.	125643
Contig ID	18244_1.R1010
5'-most EST	jC-atXLIB327408P3a01b1
Method	BLASTX
NCBI GI	g4559384
BLAST score	215
E value	7.0e-17
Match length	61
% identity	67
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	125644
Contig ID	18245_1.R1010
5'-most EST	LIB24-016-Q1-E1-H6

Seq. No.	125645
Contig ID	18246_1.R1010
5'-most EST	jC-atXLIB327408P3e09b1
Method	BLASTN
NCBI GI	g4314374
BLAST score	561
E value	0.0e+00
Match length	695
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125646
Contig ID	18251_1.R1010
5'-most EST	jC-atXLIB327416P4d07b1
Method	BLASTN
NCBI GI	g2618677
BLAST score	279
E value	1.0e-155
Match length	576

% identity	100
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	125647
Contig ID	18253_1.R1010
5'-most EST	jC-atXLIB327416P2c06b1
Method	BLASTX
NCBI GI	g3184285
BLAST score	214
E value	4.0e-17
Match length	73
% identity	58
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125648
Contig ID	18258_1.R1010
5'-most EST	LIB24-017-Q1-E1-B1
Method	BLASTX
NCBI GI	g3548808
BLAST score	756
E value	2.0e-80
Match length	149
% identity	93
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	125649
Contig ID	18258_2.R1010
5'-most EST	g2446011
Method	BLASTX
NCBI GI	g3548808
BLAST score	530
E value	5.0e-54
Match length	103
% identity	94
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	125650
Contig ID	18260_1.R1010
5'-most EST	jC-atXLIB327416P4c03b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	281
E value	1.0e-24
Match length	115
% identity	49
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	125651
Contig ID	18268_1.R1010
5'-most EST	jC-atXLIB327421P2f10b1
Method	BLASTX
NCBI GI	g3426051
BLAST score	729
E value	4.0e-77
Match length	162

% identity	92
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125652
Contig ID	18269_1.R1010
5'-most EST	jC-alXLIB327435P4d09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	5.0e-23
Match length	68
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125653
Contig ID	18271_1.R1010
5'-most EST	LIB24-017-Q1-E1-C11
Method	BLASTX
NCBI GI	g3445209
BLAST score	465
E value	9.0e-87
Match length	191
% identity	79
NCBI Description	(AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	125654
Contig ID	18274_1.R1010
5'-most EST	jC-alXLIB327434P1h10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125655
Contig ID	18282_1.R1010
5'-most EST	LIB24-017-Q1-E1-D12
Method	BLASTX
NCBI GI	g2505877
BLAST score	924
E value	1.0e-100
Match length	202
% identity	90
NCBI Description	(Y12776) dehydrogenase [Arabidopsis thaliana]

Seq. No.	125656
Contig ID	18290_1.R1010
5'-most EST	LIB25-032-Q1-E1-G2
Method	BLASTN
NCBI GI	g4220631
BLAST score	344
E value	0.0e+00

Match length	408
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	125657
Contig ID	18292_1.R1010
5'-most EST	LIB35-024-Q1-E1-D10
Method	BLASTX
NCBI GI	g4325282
BLAST score	580
E value	8.0e-60
Match length	159
% identity	66
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	125658
Contig ID	18294_2.R1010
5'-most EST	LIB3175-064-P1-K1-C10
Method	BLASTX
NCBI GI	g2924773
BLAST score	759
E value	5.0e-81
Match length	152
% identity	99
NCBI Description	(AC002334) putative mitochondrial chaperonin HSP60 precursor [Arabidopsis thaliana]

Seq. No.	125659
Contig ID	18298_1.R1010
5'-most EST	LIB24-119-Q1-E1-G9
Method	BLASTX
NCBI GI	g4115364
BLAST score	600
E value	2.0e-62
Match length	125
% identity	93
NCBI Description	(AC005957) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	125660
Contig ID	18302_1.R1010
5'-most EST	LIB24-017-Q1-E1-F10

Seq. No.	125661
Contig ID	18302_2.R1010
5'-most EST	jC-atXLIB327419P3h05b2

Seq. No.	125662
Contig ID	18308_1.R1010
5'-most EST	LIB24-093-Q1-E1-B3
Method	BLASTN
NCBI GI	g22598
BLAST score	387
E value	0.0e+00

Match length	412
% identity	92
NCBI Description	A.thaliana APG gene encoding a novel proline-rich protein

Seq. No.	125663
Contig ID	18311_1.R1010
5'-most EST	jC-atXLIB327417P1d11b1
Method	BLASTX
NCBI GI	g2191187
BLAST score	339
E value	2.0e-31
Match length	125
% identity	55
NCBI Description	(AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No.	125664
Contig ID	18322_1.R1010
5'-most EST	jC-atXLIB327416P3d06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	3.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125665
Contig ID	18323_1.R1010
5'-most EST	jC-atX25097Q1E1A09b1
Method	BLASTX
NCBI GI	g1067224
BLAST score	321
E value	2.0e-29
Match length	157
% identity	42
NCBI Description	(Z67999) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]

Seq. No.	125666
Contig ID	18323_2.R1010
5'-most EST	jC-atXP92CH2A2T7030d1
Method	BLASTX
NCBI GI	g1352075
BLAST score	1066
E value	1.0e-116
Match length	230
% identity	83
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi_669059_emb_CAA59162_ (X84684) beta-galactosidase [Brassica oleracea]

Seq. No.	125667
Contig ID	18323_4.R1010
5'-most EST	jC-atX24017Q1E1G09b1

Method	BLASTX
NCBI GI	g1352075
BLAST score	466
E value	1.0e-46
Match length	102
% identity	81
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi_669059_emb_CAA59162_ (X84684) beta-galactosidase [Brassica oleracea]

Seq. No.	125668
Contig ID	18326_1.R1010
5'-most EST	g957883
Method	BLASTX
NCBI GI	g3702339
BLAST score	937
E value	1.0e-101
Match length	213
% identity	87
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	125669
Contig ID	18327_1.R1010
5'-most EST	LIB35-056-Q1-E2-G3

Seq. No.	125670
Contig ID	18330_1.R1010
5'-most EST	jC-atXLIB327416P2e05b1
Method	BLASTX
NCBI GI	g728749
BLAST score	289
E value	7.0e-26
Match length	90
% identity	62
NCBI Description	TAPETUM-SPECIFIC PROTEIN A9 PRECURSOR >gi_81684_pir__S22467 gene A9 protein - rape >gi_17742_emb_CAA43890_ (X61751) A9 [Brassica napus]

Seq. No.	125671
Contig ID	18332_1.R1010
5'-most EST	jC-atXLIB327419P2a02b2
Method	BLASTN
NCBI GI	g3228389
BLAST score	162
E value	8.0e-86
Match length	446
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	125672
Contig ID	18333_1.R1010
5'-most EST	LIB24-018-Q1-E1-A12

Seq. No.	125673
Contig ID	18335_1.R1010

5'-most EST	LIB3168-035-P1-K1-H5
Seq. No.	125674
Contig ID	18335_2.R1010
5'-most EST	jC-atXLIB327419P2a03b2
Seq. No.	125675
Contig ID	18336_1.R1010
5'-most EST	jC-atXLIB327419P3a04b2
Seq. No.	125676
Contig ID	18339_1.R1010
5'-most EST	LIB3234-050-P1-K1-B12
Method	BLASTN
NCBI GI	g4262221
BLAST score	338
E value	0.0e+00
Match length	617
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	125677
Contig ID	18340_1.R1010
5'-most EST	g2048070
Method	BLASTX
NCBI GI	g4204265
BLAST score	377
E value	4.0e-36
Match length	148
% identity	52
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]
Seq. No.	125678
Contig ID	18340_2.R1010
5'-most EST	LIB3176-109-P1-K1-F7
Method	BLASTN
NCBI GI	g2351061
BLAST score	287
E value	1.0e-160
Match length	678
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.	125679
Contig ID	18342_1.R1010
5'-most EST	g2445976
Method	BLASTN
NCBI GI	g3128143
BLAST score	346
E value	0.0e+00
Match length	548
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	125680
Contig ID	18342_2.R1010
5'-most EST	jC-atXLIB327419P3e01b2
Method	BLASTN
NCBI GI	g3128143
BLAST score	239
E value	1.0e-131
Match length	532
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	125681
Contig ID	18343_1.R1010
5'-most EST	LIB3176-119-P2-K1-H6
Method	BLASTN
NCBI GI	g4583545
BLAST score	315
E value	1.0e-177
Match length	315
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for chloroplast GrpE protein

Seq. No.	125682
Contig ID	18359_1.R1010
5'-most EST	LIB3177-099-P1-K1-A11
Method	BLASTX
NCBI GI	g2983203
BLAST score	145
E value	5.0e-09
Match length	57
% identity	42
NCBI Description	(AE000696) polypeptide deformylase [Aquifex aeolicus]

Seq. No.	125683
Contig ID	18362_1.R1010
5'-most EST	LIB24-106-Q1-E1-B4
Method	BLASTN
NCBI GI	g3451055
BLAST score	236
E value	1.0e-130
Match length	447
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	125684
Contig ID	18363_1.R1010
5'-most EST	jC-atXLIB327419P3d02b2
Method	BLASTX
NCBI GI	g2262113
BLAST score	352
E value	4.0e-45
Match length	128
% identity	66
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	125685
Contig ID	18366_1.R1010
5'-most EST	LIB3234-057-P1-K1-E5
Method	BLASTX
NCBI GI	g4519671
BLAST score	330
E value	4.0e-30
Match length	193
% identity	45
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	125686
Contig ID	18371_1.R1010
5'-most EST	jC-atXLIB327430P2b05b1
Method	BLASTX
NCBI GI	g1706103
BLAST score	622
E value	1.0e-64
Match length	234
% identity	50
NCBI Description	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT) >gi_1363022_pir__A56351 cleavage and polyadenylation specificity factor 100K chain - bovine >gi_599683_emb_CAA53535_ (X75931) Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit [Bos taurus]

Seq. No.	125687
Contig ID	18373_1.R1010
5'-most EST	jC-atXLIB327419P2c05b2
Method	BLASTX
NCBI GI	g1174846
BLAST score	808
E value	2.0e-86
Match length	150
% identity	99
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3) >gi_1076425_pir__S43782 ubiquitin-conjugating enzyme UBC3 - Arabidopsis thaliana >gi_431262 (L19352) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	125688
Contig ID	18373_2.R1010
5'-most EST	LIB3168-073-P1-K1-B6
Method	BLASTX
NCBI GI	g1174846
BLAST score	225
E value	1.0e-33
Match length	72
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3) >gi_1076425_pir__S43782 ubiquitin-conjugating enzyme UBC3 - Arabidopsis thaliana >gi_431262 (L19352) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	125689
Contig ID	18378_1.R1010
5'-most EST	LIB24-019-Q1-E1-A10
Method	BLASTX
NCBI GI	g4006921
BLAST score	1057
E value	1.0e-116
Match length	205
% identity	98
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	125690
Contig ID	18382_1.R1010
5'-most EST	g634196
Method	BLASTX
NCBI GI	g2244924
BLAST score	301
E value	3.0e-27
Match length	76
% identity	72
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	125691
Contig ID	18382_2.R1010
5'-most EST	LIB24-019-Q1-E1-A3
Method	BLASTX
NCBI GI	g2244924
BLAST score	415
E value	2.0e-40
Match length	102
% identity	75
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	125692
Contig ID	18389_1.R1010
5'-most EST	jC-atXLIB327421P2e04b1
Method	BLASTX
NCBI GI	g3123100
BLAST score	216
E value	8.0e-26
Match length	138
% identity	51
NCBI Description	HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I >gi_4490640_emb_CAB11472.1_ (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ _ECOLI, P32698, hypothetical 15.7 kd protein, (138aa), fast a scores, opt:403, E(): 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe]

Seq. No.	125693
Contig ID	18389_2.R1010
5'-most EST	jC-atXLIB327422P1a08b1
Method	BLASTX
NCBI GI	g4586231
BLAST score	86
E value	6.0e-16
Match length	136

% identity 43
NCBI Description (AJ237788) hypothetical protein yjbQ [Salmonella enterica]

Seq. No. 125694
Contig ID 18389_3.R1010
5'-most EST g2048382

Seq. No. 125695
Contig ID 18391_1.R1010
5'-most EST jC-atXLIB327419P2a12b2
Method BLASTX
NCBI GI g4759224
BLAST score 184
E value 2.0e-13
Match length 105
% identity 40
NCBI Description TFAR19 novel apoptosis-related gene >gi_2407068 (AF014955) TFAR19 [Homo sapiens]

Seq. No. 125696
Contig ID 18391_3.R1010
5'-most EST jC-atX24019Q1E1B11a1

Seq. No. 125697
Contig ID 18392_1.R1010
5'-most EST jC-atXLIB327416P3g01b1
Method BLASTX
NCBI GI g2642443
BLAST score 374
E value 8.0e-36
Match length 119
% identity 64
NCBI Description (AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 125698
Contig ID 18396_1.R1010
5'-most EST LIB25-001-Q1-E2-C5
Method BLASTX
NCBI GI g2500376
BLAST score 488
E value 4.0e-49
Match length 95
% identity 100
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]

Seq. No. 125699
Contig ID 18398_1.R1010
5'-most EST g2722430
Method BLASTX
NCBI GI g3080435
BLAST score 604
E value 6.0e-67
Match length 129
% identity 100
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	125700
Contig ID	18402_1.R1010
5'-most EST	LIB3234-049-P1-K1-E1

Seq. No.	125701
Contig ID	18406_1.R1010
5'-most EST	jC-atXLIB327427P4b07b2
Method	BLASTX
NCBI GI	g4056456
BLAST score	305
E value	1.0e-27
Match length	61
% identity	98
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	125702
Contig ID	18410_1.R1010
5'-most EST	jC-atXLIB327408P3a10b1
Method	BLASTN
NCBI GI	g3985931
BLAST score	305
E value	1.0e-171
Match length	1119
% identity	39
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	125703
Contig ID	18414_1.R1010
5'-most EST	jC-atXLIB327419P4c01b1
Method	BLASTX
NCBI GI	g3135611
BLAST score	550
E value	2.0e-61
Match length	155
% identity	77
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	125704
Contig ID	18418_1.R1010
5'-most EST	jC-atXmonuni26Ce12b1
Method	BLASTX
NCBI GI	g3618214
BLAST score	206
E value	9.0e-16
Match length	186
% identity	32
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	125705
Contig ID	18420_1.R1010
5'-most EST	jC-atXLIB327419P2b09b2
Method	BLASTN

NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125706
Contig ID	18423_1.R1010
5'-most EST	LIB24-019-Q1-E1-E5
Method	BLASTX
NCBI GI	g2880051
BLAST score	492
E value	2.0e-49
Match length	100
% identity	94
NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No.	125707
Contig ID	18425_1.R1010
5'-most EST	jC-atXLIB327419P4b04b1
Method	BLASTN
NCBI GI	g2351071
BLAST score	179
E value	7.0e-96
Match length	499
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	125708
Contig ID	18426_1.R1010
5'-most EST	jC-atX24049Q1E1A01b1
Method	BLASTX
NCBI GI	g1170606
BLAST score	202
E value	9.0e-16
Match length	55
% identity	71
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	125709
Contig ID	18430_1.R1010
5'-most EST	LIB24-019-Q1-E1-F3

Seq. No.	125710
Contig ID	18433_1.R1010
5'-most EST	LIB24-019-Q1-E1-F6
Method	BLASTN

NCBI GI	g2673901
BLAST score	235
E value	1.0e-129
Match length	359
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125711
Contig ID	18435_1.R1010
5'-most EST	jC-atXLIB327419P3f07b2
Method	BLASTX
NCBI GI	g4587680
BLAST score	425
E value	9.0e-42
Match length	121
% identity	68
NCBI Description	(AC007197) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	125712
Contig ID	18441_1.R1010
5'-most EST	jC-atXLIB327419P4b10b1
Method	BLASTN
NCBI GI	g4757401
BLAST score	288
E value	1.0e-161
Match length	332
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	125713
Contig ID	18454_1.R1010
5'-most EST	jC-atXLIB327418P4h11b1

Seq. No.	125714
Contig ID	18459_1.R1010
5'-most EST	g935433

Seq. No.	125715
Contig ID	18459_2.R1010
5'-most EST	LIB25-037-Q1-E1-F10
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	4.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	125716
Contig ID	18459_4.R1010
5'-most EST	jC-atXP102CE5D12T7031d1

Seq. No.	125717
Contig ID	18460_1.R1010
5'-most EST	jC-atXLIB327418P4h09b1

Seq. No.	125718
Contig ID	18461_1.R1010
5'-most EST	LIB3175-060-P1-K1-H12

Seq. No.	125719
Contig ID	18463_1.R1010
5'-most EST	jC-atXLIB327419P2a07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	5.0e-22
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125720
Contig ID	18464_1.R1010
5'-most EST	jC-atXP98CH2H10T7b1
Method	BLASTN
NCBI GI	g3264774
BLAST score	323
E value	0.0e+00
Match length	583
% identity	100
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	125721
Contig ID	18466_1.R1010
5'-most EST	LIB3175-075-P1-K1-A11
Method	BLASTX
NCBI GI	g1586940
BLAST score	269
E value	1.0e-23
Match length	92
% identity	54
NCBI Description	Ser/Thr kinase [Lycopersicon esculentum]

Seq. No.	125722
Contig ID	18473_1.R1010
5'-most EST	LIB24-020-Q1-E1-C11
Method	BLASTX
NCBI GI	g3319343
BLAST score	302
E value	1.0e-27
Match length	77
% identity	71
NCBI Description	(AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.91) [Arabidopsis thaliana]

Seq. No.	125723
Contig ID	18474_1.R1010
5'-most EST	g1053440
Method	BLASTX
NCBI GI	g3892054

BLAST score 618
E value 2.0e-64
Match length 152
% identity 80
NCBI Description (AC002330) putative glycosyltransferase [Arabidopsis thaliana]

Seq. No. 125724
Contig ID 18475_1.R1010
5'-most EST jC-atXLIB327419P3a06b2
Method BLASTX
NCBI GI g731284
BLAST score 153
E value 7.0e-10
Match length 148
% identity 31
NCBI Description HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION >gi_1077482_pir__S51971 probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae) >gi_595536 (U12980) Yal048cp [Saccharomyces cerevisiae]

Seq. No. 125725
Contig ID 18479_1.R1010
5'-most EST LIB25-039-Q1-E1-A9
Method BLASTX
NCBI GI g2829881
BLAST score 120
E value 2.0e-32
Match length 102
% identity 77
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 125726
Contig ID 18481_1.R1010
5'-most EST jC-atXLIB327405P3c10b1
Method BLASTN
NCBI GI g3510347
BLAST score 654
E value 0.0e+00
Match length 745
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 125727
Contig ID 18483_1.R1010
5'-most EST jC-atXLIB327419P4a11b1
Method BLASTN
NCBI GI g2582640
BLAST score 68
E value 2.0e-29
Match length 75
% identity 99
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 125728

Contig ID	18485_1.R1010
5'-most EST	jC-atXLIB327419P4a12b1
Method	BLASTN
NCBI GI	g4388714
BLAST score	411
E value	0.0e+00
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125729
Contig ID	18488_1.R1010
5'-most EST	LIB24-060-Q1-E1-H8
Method	BLASTX
NCBI GI	g3023848
BLAST score	639
E value	6.0e-67
Match length	136
% identity	32
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	125730
Contig ID	18494_1.R1010
5'-most EST	LIB25-110-Q1-E1-E6
Method	BLASTN
NCBI GI	g4063737
BLAST score	430
E value	0.0e+00
Match length	454
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125731
Contig ID	18509_1.R1010
5'-most EST	jC-atX24113Q1E1D09b1

Seq. No.	125732
Contig ID	18511_1.R1010
5'-most EST	jC-atXLIB327419P2b11b2
Method	BLASTX
NCBI GI	g2245009
BLAST score	324
E value	1.0e-45
Match length	119
% identity	83
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125733
Contig ID	18513_1.R1010
5'-most EST	jC-atX24032Q1E1A04b1

Seq. No.	125734

Contig ID	18523_1.R1010
5'-most EST	jC-atX24116Q1E1E06b1
Method	BLASTN
NCBI GI	g3402671
BLAST score	46
E value	1.0e-16
Match length	179
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125735
Contig ID	18529_1.R1010
5'-most EST	jC-atXLIB327418P3d07b1
Method	BLASTN
NCBI GI	g3738313
BLAST score	131
E value	2.0e-67
Match length	359
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125736
Contig ID	18529_2.R1010
5'-most EST	LIB24-020-Q1-E1-H7
Method	BLASTN
NCBI GI	g3738313
BLAST score	358
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125737
Contig ID	18532_1.R1010
5'-most EST	jC-atXLIB327404P2d02b1
Method	BLASTX
NCBI GI	g3776561
BLAST score	597
E value	1.0e-61
Match length	125
% identity	99
NCBI Description	(AC005388) Identical to DNA for acyl carrier protein (ACP) gene A2 gb_X57699 from A. thaliana. ESTs gb_W43252, gb_T42821, gb_N65229, gb_N97267, gb_F15491 and gb_AA040955 come from this gene. [Arabidopsis thaliana]

Seq. No.	125738
Contig ID	18532_2.R1010
5'-most EST	g2413948
Method	BLASTN
NCBI GI	g3659491
BLAST score	206
E value	1.0e-112
Match length	505

% identity	54
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	125739
Contig ID	18532_3.R1010
5'-most EST	g2412774
Method	BLASTX
NCBI GI	g3776558
BLAST score	527
E value	2.0e-53
Match length	136
% identity	82
NCBI Description	(AC005388) Identical to gb_L14814 DNA for tissue-specific acyl carrier protein isoform 2 from A. thaliana. ESTs gb_AA597351, gb_T41805, gb_H36871, gb_R30210, gb_AA042549, gb_Z47650, gb_H76304 and gb_AA597348 come from this gene. [Arabidopsi

Seq. No.	125740
Contig ID	18535_1.R1010
5'-most EST	jC-atXLIB327418P4h12b1
Method	BLASTX
NCBI GI	g3257978
BLAST score	345
E value	3.0e-32
Match length	170
% identity	46
NCBI Description	(AP000006) 249aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No.	125741
Contig ID	18535_2.R1010
5'-most EST	LIB3168-040-P1-K1-H12
Method	BLASTX
NCBI GI	g3257978
BLAST score	396
E value	3.0e-38
Match length	159
% identity	50
NCBI Description	(AP000006) 249aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No.	125742
Contig ID	18536_1.R1010
5'-most EST	LIB24-021-Q1-E1-A3
Method	BLASTX
NCBI GI	g4406814
BLAST score	597
E value	1.0e-61
Match length	119
% identity	100
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	125743
Contig ID	18540_1.R1010

5'-most EST	LIB24-021-Q1-E1-A7
Method	BLASTN
NCBI GI	g2980757
BLAST score	331
E value	0.0e+00
Match length	353
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	125744
Contig ID	18541_1.R1010
5'-most EST	LIB24-021-Q1-E1-A8
Method	BLASTX
NCBI GI	g2583123
BLAST score	166
E value	3.0e-11
Match length	38
% identity	74
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	125745
Contig ID	18544_1.R1010
5'-most EST	LIB24-021-Q1-E1-B12
Method	BLASTN
NCBI GI	g2264304
BLAST score	317
E value	1.0e-178
Match length	389
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	125746
Contig ID	18548_1.R1010
5'-most EST	jC-atX35010Q1E1F08b1

Seq. No.	125747
Contig ID	18551_1.R1010
5'-most EST	jC-atXLIB327419P2a06b2
Method	BLASTX
NCBI GI	g4325375
BLAST score	775
E value	8.0e-83
Match length	153
% identity	100
NCBI Description	(AF128396) similar to arginases (Pfam: PF00491, Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]

Seq. No.	125748
Contig ID	18555_1.R1010
5'-most EST	jC-atXLIB327419P4a05b1
Method	BLASTN
NCBI GI	g4220633
BLAST score	72
E value	7.0e-32

Match length	470
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	125749
Contig ID	18562_1.R1010
5'-most EST	g2763417
Method	BLASTX
NCBI GI	g4262182
BLAST score	152
E value	2.0e-09
Match length	136
% identity	37
NCBI Description	(AC005508) 44123 [Arabidopsis thaliana]

Seq. No.	125750
Contig ID	18565_1.R1010
5'-most EST	jC-atXLIB327419P3a11b2

Seq. No.	125751
Contig ID	18567_1.R1010
5'-most EST	jC-atXLIB327419P3a12b2
Method	BLASTX
NCBI GI	g486784
BLAST score	240
E value	4.0e-20
Match length	97
% identity	51
NCBI Description	Golgi-associated particle 102K chain - human

Seq. No.	125752
Contig ID	18568_1.R1010
5'-most EST	jC-atXLIB327419P2b01b2
Method	BLASTX
NCBI GI	g4725941
BLAST score	862
E value	1.0e-92
Match length	189
% identity	86
NCBI Description	(AL049730) putative pollen-specific protein [Arabidopsis thaliana]

Seq. No.	125753
Contig ID	18570_1.R1010
5'-most EST	jC-atXLIB327420P3a03b1
Method	BLASTX
NCBI GI	g3335353
BLAST score	710
E value	6.0e-75
Match length	226
% identity	60
NCBI Description	(AC004512) Similar to cytochrome P450 gb_X90458 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	125754
Contig ID	18576_1.R1010

5'-most EST	jC-atXLIB327419P2b06b2
Method	BLASTN
NCBI GI	g2656032
BLAST score	200
E value	1.0e-108
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	125755
Contig ID	18580_1.R1010
5'-most EST	jC-atXLIB327419P2b04b2
Method	BLASTX
NCBI GI	g4049353
BLAST score	486
E value	7.0e-49
Match length	157
% identity	60
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	125756
Contig ID	18581_1.R1010
5'-most EST	LIB25-101-Q1-E1-E9
Method	BLASTX
NCBI GI	g4581162
BLAST score	471
E value	5.0e-47
Match length	114
% identity	77
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	125757
Contig ID	18581_2.R1010
5'-most EST	g905654

Seq. No.	125758
Contig ID	18583_1.R1010
5'-most EST	jC-atXLIB327419P2b05b2
Method	BLASTX
NCBI GI	g4704662
BLAST score	636
E value	3.0e-66
Match length	139
% identity	91
NCBI Description	(AF116860) uracil phosphoribosyltransferase 1 [Arabidopsis thaliana]

Seq. No.	125759
Contig ID	18584_1.R1010
5'-most EST	g406620
Method	BLASTN
NCBI GI	g4580744
BLAST score	93
E value	2.0e-44
Match length	565

% identity	96
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	125760
Contig ID	18584_2.R1010
5'-most EST	LIB25-039-Q1-E1-B5
Method	BLASTN
NCBI GI	g4580744
BLAST score	259
E value	1.0e-144
Match length	385
% identity	100
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	125761
Contig ID	18585_1.R1010
5'-most EST	jC-atXLIB327419P3b01b2
Method	BLASTN
NCBI GI	g2244788
BLAST score	278
E value	1.0e-155
Match length	435
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	125762
Contig ID	18586_1.R1010
5'-most EST	jC-atXLIB327419P3b02b2
Method	BLASTN
NCBI GI	g4092472
BLAST score	506
E value	0.0e+00
Match length	803
% identity	100
NCBI Description	Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	125763
Contig ID	18589_1.R1010
5'-most EST	LIB24-127-Q1-E1-A11
Method	BLASTX
NCBI GI	g4559358
BLAST score	270
E value	3.0e-23
Match length	97
% identity	49
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	125764
Contig ID	18590_1.R1010
5'-most EST	LIB25-012-Q1-E1-C7
Method	BLASTN
NCBI GI	g2827538

BLAST score	219
E value	1.0e-120
Match length	307
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	125765
Contig ID	18597_1.R1010
5'-most EST	jC-atXLIB327425P3e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125766
Contig ID	18597_2.R1010
5'-most EST	LIB3175-076-P1-K1-D8
Method	BLASTX
NCBI GI	g3894197
BLAST score	53
E value	2.0e-37
Match length	191
% identity	46
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125767
Contig ID	18601_1.R1010
5'-most EST	jC-atXLIB327419P3b09b2

Seq. No.	125768
Contig ID	18601_2.R1010
5'-most EST	LIB3176-102-P1-K1-G2

Seq. No.	125769
Contig ID	18601_3.R1010
5'-most EST	g3450170

Seq. No.	125770
Contig ID	18601_5.R1010
5'-most EST	LIB24-053-Q1-E2-F8
Method	BLASTX
NCBI GI	g267547
BLAST score	152
E value	6.0e-10
Match length	129
% identity	14
NCBI Description	HYPOTHETICAL 52.8 KD PROTEIN R08D7.1 IN CHROMOSOME III >gi_102508_pir__S24457 hypothetical protein R08D7.1 - Caenorhabditis elegans >gi_3878934_emb_CAA78047_ (Z12017) predicted using Genefinder; basic-rich; cDNA EST yk328f6.3 comes from this gene; cDNA EST yk328f6.5 comes from this gene; cDNA EST yk393c3.5 comes from this gene

[Caenorhabditis elegans]

Seq. No.	125771
Contig ID	18605_1.R1010
5'-most EST	jC-atXLIB327419P4b08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	9.0e-25
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125772
Contig ID	18609_1.R1010
5'-most EST	LIB24-021-Q1-E1-H4
Method	BLASTX
NCBI GI	g2129640
BLAST score	753
E value	3.0e-80
Match length	146
% identity	98
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	125773
Contig ID	18612_1.R1010
5'-most EST	jC-atXLIB327419P2c01b2
Method	BLASTX
NCBI GI	g3834302
BLAST score	1009
E value	1.0e-110
Match length	226
% identity	88
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	125774
Contig ID	18613_1.R1010
5'-most EST	LIB24-022-Q1-E1-A7
Method	BLASTN
NCBI GI	g2656030
BLAST score	302
E value	1.0e-169
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	125775
Contig ID	18616_1.R1010
5'-most EST	jC-atXLIB327430P1b07b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	65
E value	6.0e-28
Match length	81
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125776
Contig ID	18619_1.R1010
5'-most EST	jC-atXLIB327419P2c10b2
Method	BLASTX
NCBI GI	g3334323
BLAST score	658
E value	4.0e-69
Match length	154
% identity	83
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_ (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No.	125777
Contig ID	18622_1.R1010
5'-most EST	jC-atXLIB327419P3c11b2
Method	BLASTX
NCBI GI	g4115363
BLAST score	121
E value	4.0e-06
Match length	170
% identity	8
NCBI Description	(AC005957) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	125778
Contig ID	18625_1.R1010
5'-most EST	jC-atXLIB327419P4c10b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	1.0e-09
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125779
Contig ID	18632_1.R1010
5'-most EST	jC-atXLIB327419P4c08b1

Seq. No.	125780
Contig ID	18637_1.R1010
5'-most EST	LIB35-008-Q1-E1-G10
Method	BLASTN
NCBI GI	g2252823
BLAST score	321
E value	0.0e+00
Match length	418

% identity 99
NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 125781
Contig ID 18639_1.R1010
5'-most EST jC-alXLIB327436P1b05b1
Method BLASTN
NCBI GI g2582640
BLAST score 61
E value 2.0e-25
Match length 76
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 125782
Contig ID 18640_1.R1010
5'-most EST jC-atXLIB327419P2d04b2
Method BLASTN
NCBI GI g2582640
BLAST score 58
E value 1.0e-23
Match length 74
% identity 95
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 125783
Contig ID 18641_1.R1010
5'-most EST jC-atX22053Q1E1B04b1
Method BLASTX
NCBI GI g4455368
BLAST score 961
E value 1.0e-104
Match length 181
% identity 99
NCBI Description (AL035524) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 125784
Contig ID 18649_1.R1010
5'-most EST jC-atXLIB327419P4d02b1

Seq. No. 125785
Contig ID 18650_1.R1010
5'-most EST LIB25-078-Q1-E1-D7

Seq. No. 125786
Contig ID 18650_2.R1010
5'-most EST jC-atXLIB327408P2g03b1

Seq. No. 125787
Contig ID 18654_1.R1010
5'-most EST g899214
Method BLASTX
NCBI GI g4567265
BLAST score 63

E value	6.0e-78
Match length	149
% identity	100
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	125788
Contig ID	18656_1.R1010
5'-most EST	jC-atXLIB327419P2d12b2
Method	BLASTX
NCBI GI	g4678275
BLAST score	437
E value	3.0e-43
Match length	89
% identity	96
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	125789
Contig ID	18662_1.R1010
5'-most EST	g2446056
Method	BLASTN
NCBI GI	g4567237
BLAST score	501
E value	0.0e+00
Match length	508
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	125790
Contig ID	18662_2.R1010
5'-most EST	g1054405
Method	BLASTN
NCBI GI	g4567237
BLAST score	337
E value	0.0e+00
Match length	353
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	125791
Contig ID	18662_3.R1010
5'-most EST	LIB3176-050-P1-K1-G11
Method	BLASTN
NCBI GI	g4567237
BLAST score	383
E value	0.0e+00
Match length	447
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	125792
Contig ID	18663_1.R1010
5'-most EST	jC-atXLIB327419P3d11b1
Method	BLASTN
NCBI GI	g4558521

BLAST score	109
E value	3.0e-54
Match length	325
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	125793
Contig ID	18664_1.R1010
5'-most EST	jC-alXLIB327436P2g12b1
Method	BLASTX
NCBI GI	g1778762
BLAST score	266
E value	4.0e-23
Match length	67
% identity	79
NCBI Description	(U77666) pollen coat protein homolog [Brassica rapa]

Seq. No.	125794
Contig ID	18668_1.R1010
5'-most EST	jC-atX22054Q1E2G09b1
Method	BLASTN
NCBI GI	g2351073
BLAST score	296
E value	1.0e-165
Match length	489
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	125795
Contig ID	18669_1.R1010
5'-most EST	LIB24-022-Q1-E1-F10
Method	BLASTX
NCBI GI	g2129455
BLAST score	275
E value	5.0e-24
Match length	154
% identity	41
NCBI Description	chlorophyll a/b-binding protein (clone GC7 and others) - Euglena gracilis (var. bacillaris) (fragment)

Seq. No.	125796
Contig ID	18676_1.R1010
5'-most EST	jC-atXLIB327419P2e04b2
Method	BLASTX
NCBI GI	g3386621
BLAST score	900
E value	5.0e-97
Match length	220
% identity	80
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	125797
Contig ID	18678_1.R1010
5'-most EST	jC-atX24025Q1E1E03b1
Method	BLASTX

NCBI GI	g4006816
BLAST score	217
E value	1.0e-17
Match length	54
% identity	81
NCBI Description	(AC005970) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	125798
Contig ID	18680_1.R1010
5'-most EST	jC-atXLIB327419P3e03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	6.0e-19
Match length	77
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125799
Contig ID	18681_1.R1010
5'-most EST	jC-atXLIB327419P4e04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125800
Contig ID	18682_1.R1010
5'-most EST	jC-atXLIB327419P3e04b2

Seq. No.	125801
Contig ID	18685_1.R1010
5'-most EST	jC-atXLIB327419P4e05b1
Method	BLASTN
NCBI GI	g2924729
BLAST score	160
E value	2.0e-84
Match length	339
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	125802
Contig ID	18685_2.R1010
5'-most EST	LIB3234-058-P1-K1-A11
Method	BLASTN
NCBI GI	g2924729
BLAST score	306
E value	1.0e-171
Match length	661
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	125803
Contig ID	18694_1.R1010
5'-most EST	jC-atXLIB327407P1a12b2
Method	BLASTX
NCBI GI	g2642446
BLAST score	880
E value	5.0e-95
Match length	174
% identity	100
NCBI Description	(AC002391) similar to auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	125804
Contig ID	18702_1.R1010
5'-most EST	jC-atXLIB327422P2g01b2
Method	BLASTN
NCBI GI	g4220627
BLAST score	363
E value	0.0e+00
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	125805
Contig ID	18704_1.R1010
5'-most EST	jC-alXLIB327434P1g04b1
Method	BLASTX
NCBI GI	g4432861
BLAST score	663
E value	3.0e-69
Match length	206
% identity	69
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125806
Contig ID	18707_1.R1010
5'-most EST	jC-atXLIB327408P1e07b1
Method	BLASTX
NCBI GI	g4585879
BLAST score	397
E value	3.0e-38
Match length	95
% identity	81
NCBI Description	(AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

Seq. No.	125807
Contig ID	18713_1.R1010
5'-most EST	jC-atXLIB327419P3c09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25

Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125808
Contig ID	18729_1.R1010
5'-most EST	LIB3177-069-P1-K1-A5
Method	BLASTN
NCBI GI	g3869062
BLAST score	203
E value	1.0e-110
Match length	603
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	125809
Contig ID	18732_1.R1010
5'-most EST	g453914
Method	BLASTX
NCBI GI	g1169585
BLAST score	566
E value	3.0e-58
Match length	112
% identity	96
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_885894 (U20179) fructose 1,6-bisphosphatase [Brassica napus]

Seq. No.	125810
Contig ID	18736_1.R1010
5'-most EST	g315886
Method	BLASTX
NCBI GI	g4503523
BLAST score	310
E value	2.0e-28
Match length	127
% identity	48
NCBI Description	UNKNOWN >gi_2351378 (U54558) translation initiation factor eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313) EIF3-P66 [Homo sapiens]

Seq. No.	125811
Contig ID	18737_1.R1010
5'-most EST	jC-atXLIB327419P4d03b1
Method	BLASTX
NCBI GI	g2947070
BLAST score	805
E value	1.0e-110
Match length	207
% identity	75
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	125812

Contig ID	18742_1.R1010
5'-most EST	jC-atXLIB327419P4d01b1
Method	BLASTX
NCBI GI	g2529662
BLAST score	484
E value	2.0e-48
Match length	107
% identity	89
NCBI Description	(AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana]

Seq. No.	125813
Contig ID	18742_2.R1010
5'-most EST	LIB35-053-Q1-E1-E8
Method	BLASTX
NCBI GI	g2529662
BLAST score	489
E value	3.0e-49
Match length	108
% identity	89
NCBI Description	(AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana]

Seq. No.	125814
Contig ID	18743_1.R1010
5'-most EST	jC-atXLIB327419P3d09b2
Method	BLASTN
NCBI GI	g4589427
BLAST score	370
E value	0.0e+00
Match length	426
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	125815
Contig ID	18745_1.R1010
5'-most EST	LIB24-023-Q1-E1-E11
Method	BLASTX
NCBI GI	g2317902
BLAST score	953
E value	1.0e-103
Match length	190
% identity	94
NCBI Description	(U89959) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125816
Contig ID	18752_1.R1010
5'-most EST	LIB3176-069-P1-K1-G8

Seq. No.	125817
Contig ID	18752_2.R1010
5'-most EST	jC-atXLIB327422P2h06b2

Seq. No.	125818
Contig ID	18757_1.R1010
5'-most EST	jC-atXLIB327419P2e07b2
Method	BLASTN
NCBI GI	g4314374
BLAST score	251
E value	1.0e-139
Match length	455
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125819
Contig ID	18760_1.R1010
5'-most EST	jC-alXLIB327434P1b05a1

Seq. No.	125820
Contig ID	18760_2.R1010
5'-most EST	LIB24-023-Q1-E1-F4
Method	BLASTX
NCBI GI	g1438881
BLAST score	529
E value	8.0e-54
Match length	147
% identity	64
NCBI Description	(U43839) GmCK2p [Glycine max]

Seq. No.	125821
Contig ID	18763_1.R1010
5'-most EST	LIB24-023-Q1-E1-F7
Method	BLASTX
NCBI GI	g2435519
BLAST score	649
E value	5.0e-68
Match length	152
% identity	84
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	125822
Contig ID	18764_1.R1010
5'-most EST	jC-atXLIB327419P2e05b2
Method	BLASTX
NCBI GI	g4506225
BLAST score	441
E value	1.0e-43
Match length	137
% identity	33
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 >gi_3914474_sp_Q99460_PSD1_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S1 (P112) >gi_1808578_dbj_BAA07918_ (D44466) proteasome subunit p112 [Homo sapiens]

Seq. No.	125823
Contig ID	18772_1.R1010

5'-most EST	jC-atXLIB327419P3e05b2
Seq. No.	125824
Contig ID	18775_1.R1010
5'-most EST	LIB24-023-Q1-E1-G7
Method	BLASTX
NCBI GI	g544075
BLAST score	523
E value	2.0e-53
Match length	124
% identity	28
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_486768_pir__S35312 coatomer complex chain beta' - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop [Bos taurus]
Seq. No.	125825
Contig ID	18778_1.R1010
5'-most EST	jC-atXLIB327419P4e11b1
Seq. No.	125826
Contig ID	18788_1.R1010
5'-most EST	LIB24-024-Q1-E1-A1
Method	BLASTN
NCBI GI	g4519193
BLAST score	494
E value	0.0e+00
Match length	609
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence
Seq. No.	125827
Contig ID	18795_1.R1010
5'-most EST	jC-atXLIB327419P2c07b2
Seq. No.	125828
Contig ID	18799_1.R1010
5'-most EST	jC-atXLIB327419P3c04b2
Method	BLASTN
NCBI GI	g3510336
BLAST score	362
E value	0.0e+00
Match length	362
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.	125829
Contig ID	18808_1.R1010
5'-most EST	jC-atXLIB327419P4c04b1
Seq. No.	125830
Contig ID	18809_1.R1010
5'-most EST	jC-atXLIB327419P2d02b2
Method	BLASTN
NCBI GI	g2673901

BLAST score 390
E value 0.0e+00
Match length 581
% identity 96
NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 125831
Contig ID 18814_1.R1010
5'-most EST jC-atXLIB327419P4c12b1
Method BLASTX
NCBI GI g4263695
BLAST score 841
E value 2.0e-90
Match length 193
% identity 16
NCBI Description (AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No. 125832
Contig ID 18815_1.R1010
5'-most EST jC-atX22051Q1E1A08b1

Seq. No. 125833
Contig ID 18816_1.R1010
5'-most EST jC-atXLIB327419P2d01b2
Method BLASTX
NCBI GI g2119927
BLAST score 812
E value 6.0e-87
Match length 172
% identity 92
NCBI Description translation elongation factor G, chloroplast - soybean

Seq. No. 125834
Contig ID 18817_1.R1010
5'-most EST jC-atXP85CG8A10T7b1
Method BLASTX
NCBI GI g1709786
BLAST score 1350
E value 1.0e-149
Match length 276
% identity 100
NCBI Description PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi_541894_pir__JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi_166815 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi_1632776_emb_CAA70148_ (Y08951) T5r protein [Arabidopsis thaliana]

Seq. No. 125835
Contig ID 18819_1.R1010
5'-most EST jC-atX22053Q1E1C03b1
Method BLASTX
NCBI GI g2262117
BLAST score 296
E value 1.0e-26

Match length	63
% identity	86
NCBI Description	(AC002343) auxin inducible protein isolog [Arabidopsis thaliana]

Seq. No.	125836
Contig ID	18821_1.R1010
5'-most EST	jC-atX22051Q1E1C06b1
Method	BLASTX
NCBI GI	g465820
BLAST score	597
E value	1.0e-61
Match length	161
% identity	65
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi_280536_pir__S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154) C40H1.6 [Caenorhabditis elegans]

Seq. No.	125837
Contig ID	18822_1.R1010
5'-most EST	g550259
Method	BLASTX
NCBI GI	g2760330
BLAST score	643
E value	4.0e-67
Match length	136
% identity	91
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No.	125838
Contig ID	18824_1.R1010
5'-most EST	LIB24-024-Q1-E1-D3

Seq. No.	125839
Contig ID	18829_1.R1010
5'-most EST	LIB24-024-Q1-E1-D8
Method	BLASTN
NCBI GI	g16567
BLAST score	46
E value	1.0e-16
Match length	46
% identity	100
NCBI Description	A.thaliana tRNA-Trp gene (clone 2)

Seq. No.	125840
Contig ID	18831_1.R1010
5'-most EST	jC-atXLIB327419P4d05b1

Seq. No.	125841
Contig ID	18832_1.R1010
5'-most EST	LIB24-081-Q1-E1-C10
Method	BLASTX
NCBI GI	g2558655
BLAST score	614
E value	4.0e-64
Match length	128

% identity	93
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	125842
Contig ID	18833_1.R1010
5'-most EST	jC-atXLIB327415P3c03a1
Method	BLASTX
NCBI GI	g3152605
BLAST score	462
E value	4.0e-46
Match length	87
% identity	99
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125843
Contig ID	18837_1.R1010
5'-most EST	LIB3168-032-P1-K1-E10
Method	BLASTX
NCBI GI	g4585872
BLAST score	373
E value	6.0e-37
Match length	160
% identity	55
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	125844
Contig ID	18847_1.R1010
5'-most EST	jC-atXLIB327419P3e07b2
Method	BLASTX
NCBI GI	g4115918
BLAST score	400
E value	7.0e-51
Match length	136
% identity	80
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	125845
Contig ID	18848_1.R1010
5'-most EST	jC-atXLIB327419P2e03b2
Method	BLASTN
NCBI GI	g4589435
BLAST score	84
E value	3.0e-39
Match length	372
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	125846
Contig ID	18850_1.R1010
5'-most EST	jC-atXLIB327418P2d04b2
Method	BLASTX
NCBI GI	g2760332
BLAST score	558
E value	3.0e-57
Match length	106

% identity	100
NCBI Description	(AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No.	125847
Contig ID	18855_1.R1010
5'-most EST	jC-atXP108C180H11T7022d1
Method	BLASTX
NCBI GI	g4585976
BLAST score	1094
E value	1.0e-120
Match length	205
% identity	100
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	125848
Contig ID	18855_2.R1010
5'-most EST	LIB3168-057-P1-K1-A12
Method	BLASTX
NCBI GI	g4585976
BLAST score	580
E value	1.0e-80
Match length	190
% identity	80
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	125849
Contig ID	18856_1.R1010
5'-most EST	jC-atX22052Q1E1H04b1
Method	BLASTN
NCBI GI	g4468103
BLAST score	386
E value	0.0e+00
Match length	386
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	125850
Contig ID	18858_1.R1010
5'-most EST	jC-atX24025Q1E1F09b1
Method	BLASTN
NCBI GI	g3894179
BLAST score	408
E value	0.0e+00
Match length	555
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125851
Contig ID	18859_1.R1010
5'-most EST	jC-atX22052Q1E1H10b1
Method	BLASTX
NCBI GI	g3377849
BLAST score	409
E value	2.0e-45
Match length	126

% identity	15
NCBI Description	(AF076274) similar to receptor protein kinases [Arabidopsis thaliana]

Seq. No.	125852
Contig ID	18866_1.R1010
5'-most EST	jC-atXLIB327406P2h08b1
Method	BLASTX
NCBI GI	g2497542
BLAST score	1045
E value	1.0e-114
Match length	242
% identity	85
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	125853
Contig ID	18873_1.R1010
5'-most EST	jC-atXP123C118K4T7077d1
Method	BLASTX
NCBI GI	g2088659
BLAST score	467
E value	2.0e-46
Match length	92
% identity	100
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	125854
Contig ID	18873_2.R1010
5'-most EST	jC-atXLIB327414P3b02a1
Method	BLASTX
NCBI GI	g2088659
BLAST score	458
E value	2.0e-45
Match length	92
% identity	99
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	125855
Contig ID	18874_1.R1010
5'-most EST	jC-alXLIB327434P1f11b1
Method	BLASTN
NCBI GI	g4235150
BLAST score	527
E value	0.0e+00
Match length	527
% identity	61
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	125856
Contig ID	18874_2.R1010
5'-most EST	jC-atXLIB327420P2e06a2
Method	BLASTN
NCBI GI	g4587582

BLAST score	391
E value	0.0e+00
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	125857
Contig ID	18878_1.R1010
5'-most EST	LIB3175-038-P1-K1-F9
Method	BLASTN
NCBI GI	g2749918
BLAST score	402
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125858
Contig ID	18881_1.R1010
5'-most EST	LIB3177-046-P1-K2-E9
Method	BLASTX
NCBI GI	g3128168
BLAST score	514
E value	5.0e-52
Match length	161
% identity	60
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	125859
Contig ID	18888_1.R1010
5'-most EST	jC-atXP29C135K12T7081d1
Method	BLASTX
NCBI GI	g1871195
BLAST score	715
E value	2.0e-75
Match length	187
% identity	74
NCBI Description	(U90439) Ca++ dependent protein kinase isolog [Arabidopsis thaliana] >gi_2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	125860
Contig ID	18894_1.R1010
5'-most EST	LIB3234-052-P1-K1-C9

Seq. No.	125861
Contig ID	18896_1.R1010
5'-most EST	LIB24-110-Q1-E1-C8
Method	BLASTX
NCBI GI	g2982266
BLAST score	1050
E value	1.0e-114
Match length	232
% identity	87

NCBI Description	(AF051216) probable fibrillarin [Picea mariana]

Seq. No.	125862
Contig ID	18897_1.R1010
5'-most EST	LIB35-026-Q1-E1-A8
Method	BLASTN
NCBI GI	g3241926
BLAST score	259
E value	1.0e-143
Match length	522
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	125863
Contig ID	18903_1.R1010
5'-most EST	LIB35-031-Q1-E1-F5

Seq. No.	125864
Contig ID	18907_1.R1010
5'-most EST	jC-atXLIB327419P2d08b2
Method	BLASTX
NCBI GI	g4689108
BLAST score	232
E value	4.0e-19
Match length	112
% identity	40
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens]

Seq. No.	125865
Contig ID	18908_1.R1010
5'-most EST	jC-atXLIB327419P2d09b2
Method	BLASTN
NCBI GI	g4376087
BLAST score	136
E value	3.0e-70
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	125866
Contig ID	18909_1.R1010
5'-most EST	LIB24-025-Q1-E1-D2
Method	BLASTN
NCBI GI	g4581103
BLAST score	327
E value	0.0e+00
Match length	455
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	125867
Contig ID	18911_1.R1010
5'-most EST	LIB24-025-Q1-E1-D4
Method	BLASTX

NCBI GI g3885329
BLAST score 648
E value 4.0e-68
Match length 124
% identity 100
NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 125868
Contig ID 18913_1.R1010
5'-most EST LIB3177-068-P1-K1-C1
Method BLASTX
NCBI GI g2829868
BLAST score 130
E value 1.0e-82
Match length 180
% identity 92
NCBI Description (AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No. 125869
Contig ID 18918_1.R1010
5'-most EST jC-atXLIB327419P3d05b2
Method BLASTX
NCBI GI g3184281
BLAST score 399
E value 2.0e-55
Match length 138
% identity 78
NCBI Description (AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 125870
Contig ID 18920_1.R1010
5'-most EST jC-atXLIB327424P4c11b1
Method BLASTX
NCBI GI g2924512
BLAST score 593
E value 4.0e-61
Match length 193
% identity 66
NCBI Description (AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No. 125871
Contig ID 18920_2.R1010
5'-most EST jC-atXLIB327419P3d03b2
Method BLASTX
NCBI GI g2924512
BLAST score 452
E value 1.0e-44
Match length 222
% identity 80
NCBI Description (AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No. 125872
Contig ID 18923_1.R1010
5'-most EST LIB24-025-Q1-E1-E7

Seq. No.	125873
Contig ID	18924_1.R1010
5'-most EST	jC-atXLIB327419P4d04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	9.0e-28
Match length	65
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125874
Contig ID	18928_1.R1010
5'-most EST	g1054321
Method	BLASTX
NCBI GI	g114122
BLAST score	250
E value	3.0e-23
Match length	87
% identity	63
NCBI Description	ADP-RIBOSYLATION FACTOR 2 >gi_423228_pir__A45422 ADP-ribosylation factor 2 - bovine >gi_2137127_pir__JC4946 ADP-ribosylation factor type 2 - mouse >gi_162682 (J03794) ADP-ribosylation factor protein [Bos taurus] >gi_163668 (M88292) ADP-ribosylation factor 2 [Bos taurus] >gi_304249 (M88287) ADP-ribosylation factor 2 [Bos taurus] >gi_438864 (L12381) ADP-ribosylation factor 2 [Rattus norvegicus] >gi_1565209_dbj_BAA13491_ (D87899) ARF2 [Mus musculus] >gi_740260_prf__2004472B phospholipase D-activating factor [Bos taurus]

Seq. No.	125875
Contig ID	18932_1.R1010
5'-most EST	LIB3234-047-P1-K1-F8
Method	BLASTX
NCBI GI	g4038039
BLAST score	311
E value	2.0e-28
Match length	73
% identity	81
NCBI Description	(AC005936) putative proteinase inhibitor II [Arabidopsis thaliana]

Seq. No.	125876
Contig ID	18932_2.R1010
5'-most EST	g2413411
Method	BLASTX
NCBI GI	g4038039
BLAST score	311
E value	2.0e-28
Match length	73
% identity	81
NCBI Description	(AC005936) putative proteinase inhibitor II [Arabidopsis thaliana]

Seq. No. 125877

Contig ID	18934_1.R1010
5'-most EST	jC-atXP29C139G17T7014d1
Method	BLASTX
NCBI GI	g2829893
BLAST score	777
E value	6.0e-98
Match length	200
% identity	92
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	125878
Contig ID	18934_2.R1010
5'-most EST	jC-atXLIB327419P4d12b1
Method	BLASTX
NCBI GI	g4234941
BLAST score	621
E value	1.0e-64
Match length	183
% identity	70
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	125879
Contig ID	18935_1.R1010
5'-most EST	jC-atXLIB327419P2e12b2
Method	BLASTX
NCBI GI	g3132476
BLAST score	1036
E value	1.0e-113
Match length	206
% identity	100
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	125880
Contig ID	18937_1.R1010
5'-most EST	LIB25-100-Q1-E1-B12
Method	BLASTN
NCBI GI	g4538990
BLAST score	267
E value	1.0e-148
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	125881
Contig ID	18946_1.R1010
5'-most EST	LIB24-025-Q1-E1-G9
Method	BLASTN
NCBI GI	g4581138
BLAST score	826
E value	0.0e+00
Match length	850
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	125882
Contig ID	18949_1.R1010
5'-most EST	jC-atXLIB327419P4e08b1
Method	BLASTX
NCBI GI	g4544449
BLAST score	310
E value	4.0e-49
Match length	108
% identity	98
NCBI Description	(AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No.	125883
Contig ID	18955_1.R1010
5'-most EST	jC-atXLIB327419P2e06b2
Method	BLASTN
NCBI GI	g2337888
BLAST score	116
E value	4.0e-58
Match length	433
% identity	85
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	125884
Contig ID	18955_3.R1010
5'-most EST	jC-atXP78CF4E6T7b1
Method	BLASTN
NCBI GI	g2337888
BLAST score	45
E value	7.0e-16
Match length	153
% identity	83
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	125885
Contig ID	18957_1.R1010
5'-most EST	LIB24-025-Q1-E1-H8
Method	BLASTX
NCBI GI	g3128213
BLAST score	735
E value	3.0e-78
Match length	143
% identity	99
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125886
Contig ID	18961_1.R1010
5'-most EST	LIB24-116-Q1-E1-H2
Method	BLASTN
NCBI GI	g3413696
BLAST score	289
E value	1.0e-162
Match length	293
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125887
Contig ID	18962_1.R1010
5'-most EST	LIB25-039-Q1-E1-G6

Seq. No.	125888
Contig ID	18964_1.R1010
5'-most EST	jC-atXLIB327419P2f02b2
Method	BLASTN
NCBI GI	g2696018
BLAST score	306
E value	1.0e-172
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	125889
Contig ID	18973_1.R1010
5'-most EST	LIB3176-074-P1-K1-A7
Method	BLASTX
NCBI GI	g2511693
BLAST score	564
E value	8.0e-58
Match length	210
% identity	55
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	125890
Contig ID	18990_1.R1010
5'-most EST	jC-atXLIB327419P4f11b1
Method	BLASTX
NCBI GI	g2213547
BLAST score	265
E value	7.0e-23
Match length	161
% identity	47
NCBI Description	(Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe]

Seq. No.	125891
Contig ID	18991_1.R1010
5'-most EST	jC-alXLIB327434P3b08b1
Method	BLASTX
NCBI GI	g3122724
BLAST score	351
E value	6.0e-33
Match length	69
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	125892
Contig ID	18992_1.R1010
5'-most EST	jC-atXLIB327419P2g01b2
Method	BLASTX
NCBI GI	g2194132

BLAST score	716
E value	7.0e-76
Match length	146
% identity	95
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	125893
Contig ID	18993_1.R1010
5'-most EST	LIB24-026-Q1-E1-D2
Method	BLASTN
NCBI GI	g3449332
BLAST score	178
E value	3.0e-95
Match length	453
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSF19, complete sequence [Arabidopsis thaliana]

Seq. No.	125894
Contig ID	18997_1.R1010
5'-most EST	LIB25-007-Q1-E1-B5

Seq. No.	125895
Contig ID	18999_1.R1010
5'-most EST	jC-atXP100C251J21T7b1
Method	BLASTN
NCBI GI	g2352026
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cloning vector pRS421 with 2micron MET15 marker, complete sequence

Seq. No.	125896
Contig ID	18999_2.R1010
5'-most EST	g1053962

Seq. No.	125897
Contig ID	19002_1.R1010
5'-most EST	g933596

Seq. No.	125898
Contig ID	19013_1.R1010
5'-most EST	jC-atXLIB327419P4g02b1
Method	BLASTX
NCBI GI	g3121844
BLAST score	117
E value	3.0e-18
Match length	132
% identity	49
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_1652668_dbj_BAA17588_ (D90907) phosphatidate cytidylyltransferase [Synechocystis sp.]

Seq. No.	125899
Contig ID	19014_1.R1010
5'-most EST	jC-atXLIB327405P3c08b1
Method	BLASTN
NCBI GI	g3687221
BLAST score	163
E value	3.0e-86
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125900
Contig ID	19017_1.R1010
5'-most EST	LIB24-026-Q1-E1-F7
Method	BLASTN
NCBI GI	g4165340
BLAST score	47
E value	4.0e-17
Match length	103
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125901
Contig ID	19022_1.R1010
5'-most EST	jC-atXLIB327419P3g09b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	376
E value	0.0e+00
Match length	388
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	125902
Contig ID	19023_1.R1010
5'-most EST	jC-atXLIB327419P4g10b1
Method	BLASTX
NCBI GI	g4512651
BLAST score	285
E value	3.0e-25
Match length	123
% identity	44
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	125903
Contig ID	19027_1.R1010
5'-most EST	jC-atXP15C106E4T7d1
Method	BLASTN
NCBI GI	g3510345
BLAST score	317
E value	1.0e-178
Match length	413

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	125904
Contig ID	19031_1.R1010
5'-most EST	LIB24-026-Q1-E1-H2
Method	BLASTN
NCBI GI	g2494106
BLAST score	624
E value	0.0e+00
Match length	624
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125905
Contig ID	19034_1.R1010
5'-most EST	LIB25-058-P1-E1-C7
Method	BLASTX
NCBI GI	g3355468
BLAST score	429
E value	4.0e-42
Match length	123
% identity	76
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	125906
Contig ID	19042_1.R1010
5'-most EST	LIB25-021-Q1-E1-B11
Method	BLASTN
NCBI GI	g2252639
BLAST score	55
E value	5.0e-22
Match length	209
% identity	84
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	125907
Contig ID	19047_1.R1010
5'-most EST	LIB24-027-Q1-E1-A8
Method	BLASTN
NCBI GI	g4733953
BLAST score	21
E value	9.1e-02
Match length	418
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	125908
Contig ID	19048_1.R1010
5'-most EST	jC-atX22056Q1E1C09b1

Seq. No.	125909

Contig ID	19052_1.R1010
5'-most EST	g2733888
Method	BLASTX
NCBI GI	g2497980
BLAST score	80
E value	2.7e-01
Match length	176
% identity	56
NCBI Description	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_1419252_emb_CAA90275_ (Z49974) adenine nucleotide carrier [Schizosaccharomyces pombe] >gi_3150257_emb_CAA19176_ (AL023634) adp/atp translocase [Schizosaccharomyces pombe]

Seq. No.	125910
Contig ID	19056_1.R1010
5'-most EST	g899166
Method	BLASTN
NCBI GI	g4589433
BLAST score	401
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNI5, complete sequence

Seq. No.	125911
Contig ID	19057_1.R1010
5'-most EST	jC-atXLIB327419P2f08b2
Method	BLASTN
NCBI GI	g3608126
BLAST score	222
E value	1.0e-121
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125912
Contig ID	19061_1.R1010
5'-most EST	jC-atXLIB327419P3f06b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	252
E value	3.0e-21
Match length	165
% identity	18
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	125913
Contig ID	19071_2.R1010
5'-most EST	LIB24-027-Q1-E1-D11
Method	BLASTX
NCBI GI	g3128231
BLAST score	242
E value	2.0e-20

Match length	142
% identity	11
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337370 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125914
Contig ID	19076_1.R1010
5'-most EST	jC-atXLIB327419P3f11b1
Method	BLASTX
NCBI GI	g4335714
BLAST score	359
E value	4.0e-34
Match length	73
% identity	97
NCBI Description	(AC006248) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	125915
Contig ID	19088_1.R1010
5'-most EST	jC-atXLIB327419P2g08b2
Method	BLASTX
NCBI GI	g4262229
BLAST score	638
E value	9.0e-67
Match length	127
% identity	100
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	125916
Contig ID	19090_1.R1010
5'-most EST	jC-atXLIB327426P1d03b1
Method	BLASTX
NCBI GI	g2262163
BLAST score	442
E value	9.0e-44
Match length	94
% identity	90
NCBI Description	(AC002329) hypothetical protein similar to F5J6.10 [Arabidopsis thaliana]

Seq. No.	125917
Contig ID	19090_2.R1010
5'-most EST	jC-atXP29C139I6T7046d1
Method	BLASTX
NCBI GI	g2262165
BLAST score	618
E value	2.0e-85
Match length	167
% identity	97
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	125918
Contig ID	19092_1.R1010
5'-most EST	jC-atXLIB327419P3g01b2
Method	BLASTN

NCBI GI g3341671
BLAST score 218
E value 1.0e-119
Match length 411
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 125919
Contig ID 19100_1.R1010
5'-most EST g2748076
Method BLASTX
NCBI GI g3757519
BLAST score 477
E value 9.0e-48
Match length 122
% identity 80
NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No. 125920
Contig ID 19102_1.R1010
5'-most EST jC-atXLIB327419P4g09b1
Method BLASTN
NCBI GI g2264321
BLAST score 194
E value 1.0e-104
Match length 564
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 125921
Contig ID 19108_1.R1010
5'-most EST jC-atXLIB327419P4g07b1
Method BLASTN
NCBI GI g2582640
BLAST score 59
E value 3.0e-24
Match length 75
% identity 95
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 125922
Contig ID 19116_1.R1010
5'-most EST g2749510
Method BLASTX
NCBI GI g4689108
BLAST score 190
E value 4.0e-14
Match length 56
% identity 62
NCBI Description (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]

Seq. No. 125923
Contig ID 19118_1.R1010
5'-most EST ARABLI-18-Q1-B1-D1

Method	BLASTN
NCBI GI	g2979540
BLAST score	443
E value	0.0e+00
Match length	482
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125924
Contig ID	19122_1.R1010
5'-most EST	LIB24-027-Q1-E1-H8
Method	BLASTX
NCBI GI	g4007792
BLAST score	447
E value	4.0e-44
Match length	150
% identity	57
NCBI Description	(AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]

Seq. No.	125925
Contig ID	19123_1.R1010
5'-most EST	jC-atXLIB327419P2h05b2
Method	BLASTX
NCBI GI	g4586056
BLAST score	660
E value	3.0e-69
Match length	145
% identity	86
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	125926
Contig ID	19132_1.R1010
5'-most EST	LIB24-028-Q1-E1-A6
Method	BLASTX
NCBI GI	g4455210
BLAST score	76
E value	1.0e-69
Match length	151
% identity	95
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	125927
Contig ID	19136_1.R1010
5'-most EST	jC-alXLIB327436P2h09b1

Seq. No.	125928
Contig ID	19138_1.R1010
5'-most EST	LIB25-038-Q1-E1-A2

Seq. No.	125929
Contig ID	19139_1.R1010
5'-most EST	jC-atXLIB327419P2f06b2
Method	BLASTN
NCBI GI	g4415928

BLAST score	442
E value	0.0e+00
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125930
Contig ID	19145_1.R1010
5'-most EST	g2722291
Method	BLASTX
NCBI GI	g2864602
BLAST score	402
E value	6.0e-39
Match length	119
% identity	67
NCBI Description	(Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No.	125931
Contig ID	19147_1.R1010
5'-most EST	LIB3175-043-P1-K1-G5
Method	BLASTX
NCBI GI	g4128133
BLAST score	237
E value	8.0e-20
Match length	91
% identity	51
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	125932
Contig ID	19152_1.R1010
5'-most EST	jC-atXLIB327419P4f04b1
Method	BLASTN
NCBI GI	g2244788
BLAST score	353
E value	0.0e+00
Match length	614
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	125933
Contig ID	19154_1.R1010
5'-most EST	jC-atXLIB327419P3f05b2
Method	BLASTX
NCBI GI	g4741942
BLAST score	580
E value	8.0e-72
Match length	185
% identity	81
NCBI Description	(AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No.	125934
Contig ID	19156_1.R1010
5'-most EST	jC-atXLIB327408P2a09b1
Method	BLASTX
NCBI GI	g3021336

BLAST score 235
E value 2.0e-19
Match length 96
% identity 55
NCBI Description (AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No. 125935
Contig ID 19158_1.R1010
5'-most EST jC-atXP50C179J3T7037d1
Method BLASTN
NCBI GI g3941523
BLAST score 49
E value 5.0e-18
Match length 49
% identity 100
NCBI Description Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No. 125936
Contig ID 19158_2.R1010
5'-most EST g906803

Seq. No. 125937
Contig ID 19159_1.R1010
5'-most EST jC-atXP92CH3H9T7055d1
Method BLASTN
NCBI GI g4519188
BLAST score 152
E value 1.0e-79
Match length 567
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No. 125938
Contig ID 19163_1.R1010
5'-most EST jC-atXLIB327419P3f09b1
Method BLASTX
NCBI GI g1652297
BLAST score 210
E value 2.0e-16
Match length 131
% identity 37
NCBI Description (D90904) hypothetical protein [Synechocystis sp.]

Seq. No. 125939
Contig ID 19168_1.R1010
5'-most EST jC-atXP43C169E21T7039d1
Method BLASTX
NCBI GI g3510256
BLAST score 224
E value 6.0e-18
Match length 82
% identity 50
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 125940

Contig ID	19168_2.R1010
5'-most EST	jC-atXLIB327431P2d09a1
Method	BLASTX
NCBI GI	g3510256
BLAST score	198
E value	4.0e-15
Match length	71
% identity	49
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	125941
Contig ID	19180_1.R1010
5'-most EST	jC-atXLIB327419P2g04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	5.0e-26
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	125942
Contig ID	19187_1.R1010
5'-most EST	jC-atXLIB327408P3b02b1
Method	BLASTN
NCBI GI	g1865682
BLAST score	515
E value	0.0e+00
Match length	1047
% identity	95
NCBI Description	A.thaliana 16 kb chromosome 1 DNA fragment

Seq. No.	125943
Contig ID	19187_3.R1010
5'-most EST	jC-atXLIB327422P1a11b1
Method	BLASTN
NCBI GI	g1865682
BLAST score	106
E value	3.0e-52
Match length	366
% identity	94
NCBI Description	A.thaliana 16 kb chromosome 1 DNA fragment

Seq. No.	125944
Contig ID	19190_1.R1010
5'-most EST	LIB3168-051-P1-K1-D3
Method	BLASTX
NCBI GI	g16245
BLAST score	960
E value	1.0e-104
Match length	211
% identity	91
NCBI Description	(X51514) precursor acetolactate synthase (670 AA) [Arabidopsis thaliana]

Seq. No. 125945

Contig ID	19193_1.R1010
5'-most EST	LIB3168-093-P1-K1-A8
Method	BLASTX
NCBI GI	g4734009
BLAST score	318
E value	4.0e-29
Match length	140
% identity	46
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125946
Contig ID	19193_2.R1010
5'-most EST	LIB3175-062-P1-K1-C7
Method	BLASTX
NCBI GI	g4734009
BLAST score	107
E value	3.0e-11
Match length	85
% identity	49
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	125947
Contig ID	19195_1.R1010
5'-most EST	jC-atXP11C98J3T7061d1
Method	BLASTX
NCBI GI	g2924509
BLAST score	695
E value	3.0e-73
Match length	224
% identity	61
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	125948
Contig ID	19195_2.R1010
5'-most EST	LIB24-136-Q1-E1-E10
Method	BLASTX
NCBI GI	g2924509
BLAST score	586
E value	2.0e-60
Match length	235
% identity	52
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	125949
Contig ID	19198_1.R1010
5'-most EST	jC-atXP3C80D12T7007a1
Method	BLASTX
NCBI GI	g1351359
BLAST score	288
E value	1.0e-25
Match length	61
% identity	79
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein

- potato >gi_488712_emb_CAA55860_ (X79273)
ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	125950
Contig ID	19198_2.R1010
5'-most EST	LIB3176-069-P1-K1-E10
Method	BLASTX
NCBI GI	g1351359
BLAST score	62
E value	8.0e-21
Match length	65
% identity	75
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein - potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	125951
Contig ID	19199_1.R1010
5'-most EST	jC-atXLIB327419P4g04b1

Seq. No.	125952
Contig ID	19199_2.R1010
5'-most EST	g2412741
Method	BLASTN
NCBI GI	g4757409
BLAST score	33
E value	6.0e-09
Match length	96
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	125953
Contig ID	19202_1.R1010
5'-most EST	jC-alXLIB327434P1f01b1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	7.0e-23
Match length	125
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	125954
Contig ID	19204_1.R1010
5'-most EST	jC-atXP71CF1D2T7032d1

Seq. No.	125955
Contig ID	19204_2.R1010
5'-most EST	jC-atXLIB327431P1g06a1
Method	BLASTN
NCBI GI	g836895
BLAST score	37
E value	4.0e-11
Match length	51

% identity	96
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	125956
Contig ID	19205_1.R1010
5'-most EST	LIB3175-032-P1-K1-F12
Method	BLASTX
NCBI GI	g2462825
BLAST score	377
E value	5.0e-36
Match length	95
% identity	76
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	125957
Contig ID	19212_1.R1010
5'-most EST	jC-atXLIB327419P3g11b2
Method	BLASTN
NCBI GI	g3063438
BLAST score	465
E value	0.0e+00
Match length	469
% identity	100
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	125958
Contig ID	19215_1.R1010
5'-most EST	jC-atXLIB327403P3b03b2
Method	BLASTX
NCBI GI	g4056433
BLAST score	360
E value	4.0e-34
Match length	142
% identity	55
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	125959
Contig ID	19224_1.R1010
5'-most EST	jC-alXLIB327434P3b12a1
Method	BLASTX
NCBI GI	g3928090
BLAST score	183
E value	2.0e-13
Match length	99
% identity	40
NCBI Description	(AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No.	125960
Contig ID	19227_1.R1010
5'-most EST	LIB24-029-Q1-E1-B11
Method	BLASTX
NCBI GI	g3880625
BLAST score	349
E value	1.0e-32

Match length	154
% identity	47
NCBI Description	(Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge

Seq. No.	125961
Contig ID	19228_1.R1010
5'-most EST	ARABLI-16-Q1-B1-B11
Method	BLASTX
NCBI GI	g3450842
BLAST score	501
E value	1.0e-50
Match length	202
% identity	57
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	125962
Contig ID	19233_1.R1010
5'-most EST	jC-atXLIB327408P2c12b1
Method	BLASTX
NCBI GI	g4006899
BLAST score	376
E value	1.0e-35
Match length	121
% identity	56
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	125963
Contig ID	19235_1.R1010
5'-most EST	jC-atXP11C98E12T7050d1

Seq. No.	125964
Contig ID	19235_2.R1010
5'-most EST	g623694
Method	BLASTX
NCBI GI	g4633127
BLAST score	175
E value	2.0e-12
Match length	113
% identity	29
NCBI Description	(AF110134) GlsA [Volvox carteri f. nagariensis] >gi_4633129_gb_AAD26633.1_AF110135_1 (AF110135) GlsA [Volvox carteri f. nagariensis]

Seq. No.	125965
Contig ID	19235_3.R1010
5'-most EST	g2048898

Seq. No.	125966
Contig ID	19238_1.R1010
5'-most EST	jC-atXLIB327419P2f01b2

Seq. No. 125967

Contig ID	19242_1.R1010
5'-most EST	jC-atXP29C138J21T7039d1
Method	BLASTX
NCBI GI	g3264611
BLAST score	410
E value	1.0e-39
Match length	93
% identity	89
NCBI Description	(AF061511) seven in absentia homolog [Zea mays]

Seq. No.	125968
Contig ID	19242_2.R1010
5'-most EST	jC-atXLIB327419P3f04b2
Method	BLASTX
NCBI GI	g4584255
BLAST score	270
E value	4.0e-29
Match length	86
% identity	76
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	125969
Contig ID	19249_1.R1010
5'-most EST	LIB24-029-Q1-E1-E1

Seq. No.	125970
Contig ID	19250_1.R1010
5'-most EST	LIB3234-096-P1-K1-E4
Method	BLASTX
NCBI GI	g4115943
BLAST score	767
E value	8.0e-82
Match length	148
% identity	98
NCBI Description	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]

Seq. No.	125971
Contig ID	19251_1.R1010
5'-most EST	g2758989

Seq. No.	125972
Contig ID	19262_2.R1010
5'-most EST	jC-atXLIB327419P4g03b1

Seq. No.	125973
Contig ID	19269_1.R1010
5'-most EST	LIB25-009-Q1-E1-C4
Method	BLASTX
NCBI GI	g2245004
BLAST score	420
E value	2.0e-41
Match length	81
% identity	100
NCBI Description	(Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No.	125974
Contig ID	19270_1.R1010
5'-most EST	jC-atXLIB327419P4g12b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	61
E value	3.0e-25
Match length	240
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	125975
Contig ID	19270_2.R1010
5'-most EST	jC-atXLIB327420P1c04b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	39
E value	3.0e-12
Match length	225
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	125976
Contig ID	19275_1.R1010
5'-most EST	jC-atXLIB327419P2h02b2
Method	BLASTX
NCBI GI	g3785989
BLAST score	642
E value	3.0e-67
Match length	134
% identity	89
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	125977
Contig ID	19285_1.R1010
5'-most EST	jC-atXLIB327419P2h09b2

Seq. No.	125978
Contig ID	19286_1.R1010
5'-most EST	jC-atXP117C141O5T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	125979
Contig ID	19286_2.R1010
5'-most EST	LIB3177-097-P1-K1-E3
Method	BLASTX
NCBI GI	g4160280

BLAST score	1505
E value	1.0e-168
Match length	430
% identity	63
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	125980
Contig ID	19287_1.R1010
5'-most EST	g930698

Seq. No.	125981
Contig ID	19292_1.R1010
5'-most EST	jC-atXP119C209E19T7047a1
Method	BLASTX
NCBI GI	g3402716
BLAST score	424
E value	2.0e-41
Match length	164
% identity	59
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	125982
Contig ID	19292_2.R1010
5'-most EST	jC-atXLIB327431P2e01a1
Method	BLASTX
NCBI GI	g3402716
BLAST score	232
E value	5.0e-19
Match length	122
% identity	47
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	125983
Contig ID	19292_5.R1010
5'-most EST	jC-atXLIB327431P2e01b1
Method	BLASTX
NCBI GI	g3402716
BLAST score	179
E value	6.0e-13
Match length	74
% identity	51
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	125984
Contig ID	19293_1.R1010
5'-most EST	LIB24-030-Q1-E1-B7
Method	BLASTX
NCBI GI	g2462746
BLAST score	174
E value	6.0e-31
Match length	86
% identity	90
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	125985
Contig ID	19295_1.R1010

5'-most EST	LIB3175-032-P1-K1-C9
Method	BLASTX
NCBI GI	g112925
BLAST score	330
E value	3.0e-30
Match length	184
% identity	42
NCBI Description	41-2 PROTEIN ANTIGEN PRECURSOR >gi_320938_pir__A45503 41-2 protein antigen precursor - Plasmodium falciparum >gi_160039 (J04656) 41-2 protein antigen [Plasmodium falciparum]

Seq. No.	125986
Contig ID	19298_1.R1010
5'-most EST	jC-atXLIB327426P3b12b1
Method	BLASTX
NCBI GI	g2245082
BLAST score	653
E value	2.0e-68
Match length	147
% identity	88
NCBI Description	(Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No.	125987
Contig ID	19301_1.R1010
5'-most EST	LIB3176-091-P1-K1-A10
Method	BLASTN
NCBI GI	g4220637
BLAST score	394
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	125988
Contig ID	19304_1.R1010
5'-most EST	LIB24-030-Q1-E1-C9
Method	BLASTN
NCBI GI	g2191157
BLAST score	387
E value	0.0e+00
Match length	584
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	125989
Contig ID	19304_2.R1010
5'-most EST	jC-atX24070Q1E1D01b1
Method	BLASTN
NCBI GI	g2191157
BLAST score	390
E value	0.0e+00
Match length	491
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	125990
Contig ID	19305_1.R1010
5'-most EST	LIB24-030-Q1-E1-D1
Method	BLASTN
NCBI GI	g3399678
BLAST score	313
E value	1.0e-175
Match length	834
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125991
Contig ID	19309_1.R1010
5'-most EST	jC-atXLIB327419P3g02b2
Method	BLASTX
NCBI GI	g3738328
BLAST score	443
E value	8.0e-44
Match length	111
% identity	73
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	125992
Contig ID	19317_1.R1010
5'-most EST	LIB24-030-Q1-E1-E6
Method	BLASTX
NCBI GI	g2245128
BLAST score	207
E value	2.0e-16
Match length	63
% identity	67
NCBI Description	(Z97344) peroxidase [Arabidopsis thaliana]

Seq. No.	125993
Contig ID	19321_1.R1010
5'-most EST	LIB25-061-Q1-E1-H4

Seq. No.	125994
Contig ID	19321_2.R1010
5'-most EST	jC-atXP11C99A16T7088d1

Seq. No.	125995
Contig ID	19331_1.R1010
5'-most EST	jC-atXLIB327419P4h05b1
Method	BLASTN
NCBI GI	g531832
BLAST score	55
E value	7.0e-22
Match length	59
% identity	98
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	125996
Contig ID	19347_1.R1010
5'-most EST	jC-atXLIB327420P1c12b1

Method	BLASTX
NCBI GI	g4263712
BLAST score	574
E value	6.0e-59
Match length	143
% identity	78
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	125997
Contig ID	19348_1.R1010
5'-most EST	jC-alX24086Q1E1D04b1
Method	BLASTX
NCBI GI	g3894183
BLAST score	233
E value	2.0e-19
Match length	130
% identity	42
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	125998
Contig ID	19351_1.R1010
5'-most EST	LIB3177-090-P1-K1-E12
Method	BLASTN
NCBI GI	g2584827
BLAST score	248
E value	1.0e-137
Match length	551
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	125999
Contig ID	19351_2.R1010
5'-most EST	jC-atXP104CE10A8T7b1
Method	BLASTN
NCBI GI	g2584827
BLAST score	299
E value	1.0e-167
Match length	510
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126000
Contig ID	19352_1.R1010
5'-most EST	LIB24-031-Q1-E1-A3
Method	BLASTN
NCBI GI	g2623294
BLAST score	368
E value	0.0e+00
Match length	482
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126001

Contig ID	19353_1.R1010
5'-most EST	jC-atXLIB327437P2g09a2
Method	BLASTX
NCBI GI	g1841464
BLAST score	143
E value	9.0e-09
Match length	103
% identity	21
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	126002
Contig ID	19353_2.R1010
5'-most EST	jC-atXLIB327437P2g08a2
Method	BLASTX
NCBI GI	g3386614
BLAST score	551
E value	2.0e-56
Match length	122
% identity	50
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	126003
Contig ID	19361_1.R1010
5'-most EST	LIB25-056-Q1-E1-H2
Method	BLASTX
NCBI GI	g4006878
BLAST score	311
E value	3.0e-28
Match length	95
% identity	59
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	126004
Contig ID	19370_1.R1010
5'-most EST	LIB24-031-Q1-E1-C3
Method	BLASTN
NCBI GI	g3366536
BLAST score	268
E value	1.0e-149
Match length	448
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	126005
Contig ID	19372_1.R1010
5'-most EST	LIB24-031-Q1-E1-C6

Seq. No.	126006
Contig ID	19378_1.R1010
5'-most EST	jC-atXLIB327421P4g01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	4.0e-24
Match length	70

% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126007
Contig ID	19379_1.R1010
5'-most EST	LIB24-031-Q1-E1-D2
Method	BLASTX
NCBI GI	g2443890
BLAST score	583
E value	2.0e-60
Match length	104
% identity	100
NCBI Description	(AC002294) similar to NAM (gp_X92205_1321924) and CUC2 (gp_AB002560_1944132) proteins [Arabidopsis thaliana]

Seq. No.	126008
Contig ID	19384_1.R1010
5'-most EST	jC-atXP40C161L8T7d1
Method	BLASTX
NCBI GI	g3785983
BLAST score	281
E value	1.0e-31
Match length	112
% identity	67
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126009
Contig ID	19384_2.R1010
5'-most EST	LIB24-041-Q1-E1-C10
Method	BLASTX
NCBI GI	g3785983
BLAST score	353
E value	2.0e-33
Match length	90
% identity	70
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126010
Contig ID	19386_1.R1010
5'-most EST	jC-atXLIB327437P2h10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126011
Contig ID	19388_1.R1010
5'-most EST	LIB3177-077-P1-K1-A9
Method	BLASTX
NCBI GI	g3249072
BLAST score	216
E value	3.0e-17

Match length	81
% identity	52
NCBI Description	(AC004473) Contains similarity to hypothetical 43.1 KD protein in NDK-GCPE intergenic region gb_493519 from E. coli sequence gb_U02965. [Arabidopsis thaliana]

Seq. No.	126012
Contig ID	19389_1.R1010
5'-most EST	LIB24-031-Q1-E1-E12
Method	BLASTN
NCBI GI	g4467094
BLAST score	351
E value	0.0e+00
Match length	462
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	126013
Contig ID	19394_1.R1010
5'-most EST	LIB3177-076-P1-K1-E4

Seq. No.	126014
Contig ID	19396_1.R1010
5'-most EST	g2762787
Method	BLASTN
NCBI GI	g3386593
BLAST score	108
E value	1.0e-53
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126015
Contig ID	19398_1.R1010
5'-most EST	LIB24-031-Q1-E1-F10
Method	BLASTX
NCBI GI	g4585907
BLAST score	559
E value	5.0e-58
Match length	148
% identity	79
NCBI Description	(AC006298) unknown protein [Arabidopsis thaliana]

Seq. No.	126016
Contig ID	19400_1.R1010
5'-most EST	jC-alXLIB327435P3a02b1
Method	BLASTX
NCBI GI	g3063698
BLAST score	786
E value	6.0e-84
Match length	167
% identity	98
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 126017

Contig ID	19402_1.R1010
5'-most EST	jC-atXLIB327403P3f02b1
Method	BLASTX
NCBI GI	g4759160
BLAST score	169
E value	1.0e-11
Match length	64
% identity	50
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	126018
Contig ID	19402_2.R1010
5'-most EST	jC-atX24033Q1E1E06b1
Method	BLASTX
NCBI GI	g4759160
BLAST score	318
E value	6.0e-29
Match length	92
% identity	59
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	126019
Contig ID	19402_3.R1010
5'-most EST	jC-atXLIB327421P3f08b1
Method	BLASTX
NCBI GI	g4759160
BLAST score	315
E value	1.0e-28
Match length	97
% identity	56
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	126020
Contig ID	19402_4.R1010
5'-most EST	jC-atXLIB327437P4h05b2
Method	BLASTX
NCBI GI	g4759160
BLAST score	221
E value	3.0e-18
Match length	72
% identity	56
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	126021
Contig ID	19408_1.R1010

5'-most EST	LIB3177-038-P1-K2-H4
Method	BLASTX
NCBI GI	g1168530
BLAST score	591
E value	4.0e-61
Match length	118
% identity	95
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK2 >gi_99748_pir__S24586 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase [Arabidopsis thaliana]

Seq. No.	126022
Contig ID	19424_1.R1010
5'-most EST	LIB24-064-Q1-E1-A2
Method	BLASTX
NCBI GI	g4581162
BLAST score	421
E value	1.0e-41
Match length	85
% identity	99
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	126023
Contig ID	19426_1.R1010
5'-most EST	LIB24-032-Q1-E1-A3

Seq. No.	126024
Contig ID	19437_1.R1010
5'-most EST	jC-atXLIB327437P4g01b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	42
E value	5.0e-14
Match length	46
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	126025
Contig ID	19437_2.R1010
5'-most EST	g1158363
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126026
Contig ID	19437_3.R1010
5'-most EST	g1053998

Seq. No.	126027

Contig ID	19439_1.R1010
5'-most EST	g2393704
Method	BLASTN
NCBI GI	g3169169
BLAST score	501
E value	0.0e+00
Match length	532
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126028
Contig ID	19440_1.R1010
5'-most EST	LIB24-032-Q1-E1-C12
Method	BLASTN
NCBI GI	g4741184
BLAST score	438
E value	0.0e+00
Match length	501
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	126029
Contig ID	19441_1.R1010
5'-most EST	LIB24-032-Q1-E1-C6
Method	BLASTX
NCBI GI	g4506221
BLAST score	406
E value	3.0e-39
Match length	186
% identity	45
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No.	126030
Contig ID	19442_1.R1010
5'-most EST	LIB24-032-Q1-E1-C7

Seq. No.	126031
Contig ID	19462_1.R1010
5'-most EST	jC-atXLIB327404P1g09b1

Seq. No.	126032
Contig ID	19480_1.R1010
5'-most EST	LIB24-033-Q1-E1-A11
Method	BLASTN
NCBI GI	g3821780
BLAST score	25
E value	4.0e-04
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	126033
Contig ID	19483_1.R1010

5'-most EST	LIB24-033-Q1-E1-A3
Method	BLASTX
NCBI GI	g3935173
BLAST score	315
E value	8.0e-36
Match length	244
% identity	41
NCBI Description	(AC004557) F17L21.16 [Arabidopsis thaliana]

Seq. No.	126034
Contig ID	19485_1.R1010
5'-most EST	LIB24-033-Q1-E1-A6
Method	BLASTN
NCBI GI	g4589445
BLAST score	46
E value	9.0e-17
Match length	254
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	126035
Contig ID	19487_1.R1010
5'-most EST	jC-atXLIB327437P2g03b1
Method	BLASTN
NCBI GI	g3135250
BLAST score	357
E value	0.0e+00
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126036
Contig ID	19491_1.R1010
5'-most EST	LIB24-033-Q1-E1-B11
Method	BLASTX
NCBI GI	g4415925
BLAST score	636
E value	1.0e-66
Match length	125
% identity	100
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	126037
Contig ID	19495_1.R1010
5'-most EST	LIB25-076-Q1-E1-G4
Method	BLASTN
NCBI GI	g3176695
BLAST score	33
E value	7.0e-09
Match length	57
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	126038
Contig ID	19503_1.R1010
5'-most EST	jC-atXLIB327437P3g05b3
Method	BLASTN
NCBI GI	g2827698
BLAST score	206
E value	1.0e-112
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)

Seq. No.	126039
Contig ID	19505_1.R1010
5'-most EST	jC-atXLIB327407P2f04b1

Seq. No.	126040
Contig ID	19506_1.R1010
5'-most EST	LIB24-033-Q1-E1-C6
Method	BLASTN
NCBI GI	g4469002
BLAST score	206
E value	1.0e-112
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	126041
Contig ID	19508_2.R1010
5'-most EST	g899215
Method	BLASTX
NCBI GI	g4567265
BLAST score	317
E value	3.0e-29
Match length	63
% identity	100
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	126042
Contig ID	19514_1.R1010
5'-most EST	LIB25-002-Q1-E1-A4
Method	BLASTN
NCBI GI	g3659491
BLAST score	459
E value	0.0e+00
Match length	497
% identity	100
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	126043
Contig ID	19518_1.R1010
5'-most EST	LIB3168-022-P1-K1-D7
Method	BLASTX
NCBI GI	g4679028

BLAST score	331
E value	6.0e-31
Match length	134
% identity	49
NCBI Description	(AF077207) HSPC021 [Homo sapiens]

Seq. No.	126044
Contig ID	19522_1.R1010
5'-most EST	jC-atXLIB327418P1c07b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	308
E value	5.0e-28
Match length	117
% identity	57
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	126045
Contig ID	19524_1.R1010
5'-most EST	LIB3176-088-P1-K1-E7
Method	BLASTX
NCBI GI	g4544375
BLAST score	480
E value	6.0e-48
Match length	119
% identity	75
NCBI Description	(AC006920) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	126046
Contig ID	19525_1.R1010
5'-most EST	LIB3168-041-P1-K1-F2
Method	BLASTN
NCBI GI	g4220635
BLAST score	159
E value	4.0e-84
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	126047
Contig ID	19530_1.R1010
5'-most EST	LIB25-006-Q1-E1-B8
Method	BLASTN
NCBI GI	g1946354
BLAST score	71
E value	1.0e-31
Match length	252
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	126048
Contig ID	19532_1.R1010
5'-most EST	LIB3176-083-P1-K1-C2
Method	BLASTN

NCBI GI g2760829
BLAST score 402
E value 0.0e+00
Match length 651
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126049
Contig ID 19532_2.R1010
5'-most EST LIB35-052-Q1-E1-H7
Method BLASTN
NCBI GI g2760829
BLAST score 308
E value 1.0e-173
Match length 321
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126050
Contig ID 19550_1.R1010
5'-most EST LIB3176-070-P1-K1-H6
Method BLASTX
NCBI GI g4006902
BLAST score 198
E value 2.0e-15
Match length 89
% identity 47
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 126051
Contig ID 19559_1.R1010
5'-most EST jC-atXP20C114B3T7012a1
Method BLASTN
NCBI GI g2618605
BLAST score 267
E value 1.0e-148
Match length 563
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 126052
Contig ID 19559_2.R1010
5'-most EST jC-atXLIB327427P2d06b1
Method BLASTN
NCBI GI g2618605
BLAST score 214
E value 1.0e-117
Match length 434
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 126053
Contig ID 19563_1.R1010

5'-most EST	jC-atXP37C156G19T7d2
Method	BLASTX
NCBI GI	g400515
BLAST score	238
E value	1.0e-19
Match length	84
% identity	54
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8) (CI-B8) >gi_346540_pir__S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine >gi_246_emb_CAA44904_ (X63219) NADH dehydrogenase [Bos taurus]

Seq. No.	126054
Contig ID	19566_1.R1010
5'-most EST	LIB24-034-Q1-E1-B2
Method	BLASTX
NCBI GI	g3193298
BLAST score	255
E value	5.0e-22
Match length	86
% identity	57
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	126055
Contig ID	19570_1.R1010
5'-most EST	jC-atXLIB327402P4a02b1
Method	BLASTN
NCBI GI	g3798728
BLAST score	281
E value	1.0e-157
Match length	392
% identity	97
NCBI Description	Arabidopsis thaliana transgenic line A DNA, 3'-junction region

Seq. No.	126056
Contig ID	19572_1.R1010
5'-most EST	jC-atXP85C241B16T7b1
Method	BLASTX
NCBI GI	g2642429
BLAST score	657
E value	8.0e-69
Match length	132
% identity	99
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	126057
Contig ID	19576_1.R1010
5'-most EST	LIB24-034-Q1-E1-C4
Method	BLASTN
NCBI GI	g4490734
BLAST score	341
E value	0.0e+00
Match length	341
% identity	100

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	126058
Contig ID	19590_1.R1010
5'-most EST	LIB24-034-Q1-E1-E3
Method	BLASTX
NCBI GI	g1778374
BLAST score	229
E value	6.0e-19
Match length	117
% identity	46
NCBI Description	(U81287) glycine-rich RNA-binding protein PsGRBP [Pisum sativum]

Seq. No.	126059
Contig ID	19591_1.R1010
5'-most EST	LIB24-034-Q1-E1-E9
Method	BLASTX
NCBI GI	g4689376
BLAST score	668
E value	2.0e-70
Match length	139
% identity	38
NCBI Description	(AF138872) zinc finger protein 3 [Arabidopsis thaliana]

Seq. No.	126060
Contig ID	19603_1.R1010
5'-most EST	jC-atXLIB327409P3c09a1
Method	BLASTX
NCBI GI	g549732
BLAST score	224
E value	6.0e-18
Match length	82
% identity	51
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_ (Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF [Saccharomyces cerevisiae]

Seq. No.	126061
Contig ID	19607_1.R1010
5'-most EST	LIB24-035-Q1-E1-A5

Seq. No.	126062
Contig ID	19610_1.R1010
5'-most EST	LIB24-118-Q1-E1-A11
Method	BLASTX
NCBI GI	g114121
BLAST score	323
E value	6.0e-30
Match length	100
% identity	61
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_101185_pir__B36167

ADP-ribosylation factor 1 - yeast (Saccharomyces cerevisiae) >gi_171073 (J03276) ADP-ribosylation factor [Saccharomyces cerevisiae] >gi_1004303_emb_CAA58255_ (X83276) ADP-ribosylationfactor 2 [Saccharomyces cerevisiae] >gi_1431314_emb_CAA98769_ (Z74240) ORF YDL192w [Saccharomyces cerevisiae]

Seq. No.	126063
Contig ID	19612_1.R1010
5'-most EST	LIB24-035-Q1-E1-B10
Method	BLASTN
NCBI GI	g3399678
BLAST score	312
E value	1.0e-175
Match length	538
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126064
Contig ID	19613_1.R1010
5'-most EST	jC-atXP24035Q1E1B11b1

Seq. No.	126065
Contig ID	19613_2.R1010
5'-most EST	jC-atXP2C78G10T7d1

Seq. No.	126066
Contig ID	19614_1.R1010
5'-most EST	jC-atXLIB327402P4c05b1

Seq. No.	126067
Contig ID	19618_1.R1010
5'-most EST	jC-atXLIB327401P4a04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	66
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126068
Contig ID	19623_1.R1010
5'-most EST	LIB24-035-Q1-E1-C3
Method	BLASTX
NCBI GI	g4567246
BLAST score	829
E value	5.0e-89
Match length	195
% identity	86
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	126069
Contig ID	19624_1.R1010
5'-most EST	LIB24-110-Q1-E1-E1

Seq. No.	126070
Contig ID	19626_1.R1010
5'-most EST	LIB24-035-Q1-E1-C8
Method	BLASTX
NCBI GI	g2217970
BLAST score	169
E value	7.0e-12
Match length	105
% identity	11
NCBI Description	(Z97074) p40 [Homo sapiens]

Seq. No.	126071
Contig ID	19632_1.R1010
5'-most EST	jC-atXLIB327437P4d10a2
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	1.0e-17
Match length	48
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	126072
Contig ID	19633_1.R1010
5'-most EST	jC-atXLIB327406P3g01b2
Method	BLASTN
NCBI GI	g3522932
BLAST score	411
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126073
Contig ID	19634_1.R1010
5'-most EST	LIB24-035-Q1-E1-D6
Method	BLASTX
NCBI GI	g2547036
BLAST score	498
E value	5.0e-50
Match length	200
% identity	50
NCBI Description	(Y13920) ribosomal protein S2 [Triticum aestivum]

Seq. No.	126074
Contig ID	19634_2.R1010
5'-most EST	jC-atX24035Q1E1D06b1
Method	BLASTX
NCBI GI	g2547036
BLAST score	228
E value	7.0e-19
Match length	83
% identity	57
NCBI Description	(Y13920) ribosomal protein S2 [Triticum aestivum]

Seq. No.	126075
Contig ID	19635_1.R1010
5'-most EST	LIB24-035-Q1-E1-D7
Method	BLASTX
NCBI GI	g1169689
BLAST score	157
E value	3.0e-10
Match length	96
% identity	35
NCBI Description	FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKPA PRECURSOR (PPIASE) (ROTAMASE) >gi_2121124_pir__I65035 fkpA protein - Escherichia coli >gi_606281 (U18997) ORF_f270 [Escherichia coli] >gi_862300 (L28082) fkpA gene product [Escherichia coli] >gi_1789745 (AE000410) FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli]

Seq. No.	126076
Contig ID	19640_1.R1010
5'-most EST	jC-atXLIB327402P1d11b1
Method	BLASTN
NCBI GI	g2656026
BLAST score	322
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	126077
Contig ID	19641_1.R1010
5'-most EST	jC-atXLIB327401P3a11b2
Method	BLASTX
NCBI GI	g3414809
BLAST score	156
E value	3.0e-10
Match length	148
% identity	3
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	126078
Contig ID	19645_1.R1010
5'-most EST	LIB24-035-Q1-E1-F1
Method	BLASTN
NCBI GI	g3046855
BLAST score	468
E value	0.0e+00
Match length	578
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	126079
Contig ID	19652_1.R1010
5'-most EST	jC-atXLIB327402P4d09b1
Method	BLASTX
NCBI GI	g4210504

BLAST score 718
E value 4.0e-76
Match length 150
% identity 97
NCBI Description (AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No. 126080
Contig ID 19653_1.R1010
5'-most EST jC-atX24035Q1E1F06b1
Method BLASTN
NCBI GI g4455348
BLAST score 429
E value 0.0e+00
Match length 433
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No. 126081
Contig ID 19656_1.R1010
5'-most EST jC-atXLIB327402P4d06b1
Method BLASTX
NCBI GI g4468986
BLAST score 174
E value 7.0e-74
Match length 216
% identity 59
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 126082
Contig ID 19660_1.R1010
5'-most EST LIB24-035-Q1-E1-G2
Method BLASTN
NCBI GI g3702734
BLAST score 358
E value 0.0e+00
Match length 401
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No. 126083
Contig ID 19665_1.R1010
5'-most EST LIB24-035-Q1-E1-G8
Method BLASTX
NCBI GI g2739010
BLAST score 273
E value 5.0e-24
Match length 75
% identity 68
NCBI Description (AF022464) CYP77A3p [Glycine max]

Seq. No. 126084
Contig ID 19667_1.R1010
5'-most EST jC-atXLIB327402P1e11b1
Method BLASTX

NCBI GI	g3894158
BLAST score	612
E value	1.0e-63
Match length	149
% identity	81
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	126085
Contig ID	19668_1.R1010
5'-most EST	LIB3234-084-Q1-K1-H11
Method	BLASTX
NCBI GI	g3758833
BLAST score	391
E value	1.0e-37
Match length	172
% identity	47
NCBI Description	(Y18225) MtN6 [Medicago truncatula]

Seq. No.	126086
Contig ID	19672_1.R1010
5'-most EST	LIB35-034-Q1-E1-H3
Method	BLASTX
NCBI GI	g4115379
BLAST score	414
E value	2.0e-40
Match length	149
% identity	56
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	126087
Contig ID	19675_1.R1010
5'-most EST	LIB24-036-Q1-E1-A5
Method	BLASTN
NCBI GI	g3985958
BLAST score	61
E value	7.0e-26
Match length	85
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	126088
Contig ID	19679_1.R1010
5'-most EST	LIB3177-063-P1-K1-H12
Method	BLASTX
NCBI GI	g2245021
BLAST score	800
E value	9.0e-86
Match length	166
% identity	96
NCBI Description	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]

Seq. No.	126089
Contig ID	19681_1.R1010

5'-most EST	LIB24-036-Q1-E1-B11
Method	BLASTX
NCBI GI	g4469023
BLAST score	615
E value	5.0e-64
Match length	164
% identity	75
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	126090
Contig ID	19686_1.R1010
5'-most EST	jC-atXLIB327402P4c03b1
Method	BLASTN
NCBI GI	g3738313
BLAST score	383
E value	0.0e+00
Match length	435
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126091
Contig ID	19696_1.R1010
5'-most EST	jC-atXLIB327402P4c11b1
Method	BLASTX
NCBI GI	g4309734
BLAST score	161
E value	8.0e-11
Match length	65
% identity	49
NCBI Description	(AC006439) putative 26S proteosome regulatory subunit 8 [Arabidopsis thaliana]

Seq. No.	126092
Contig ID	19701_1.R1010
5'-most EST	jC-atXLIB327402P1c05b1
Method	BLASTN
NCBI GI	g3766106
BLAST score	248
E value	1.0e-137
Match length	657
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126093
Contig ID	19706_1.R1010
5'-most EST	jC-atXLIB327409P3c10b1
Method	BLASTX
NCBI GI	g4056433
BLAST score	353
E value	2.0e-33
Match length	119
% identity	60
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	126094
Contig ID	19706_3.R1010
5'-most EST	jC-atXLIB327406P4h06b2
Method	BLASTX
NCBI GI	g4056433
BLAST score	228
E value	1.0e-18
Match length	138
% identity	40
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	126095
Contig ID	19709_1.R1010
5'-most EST	g315369
Method	BLASTX
NCBI GI	g2245118
BLAST score	379
E value	2.0e-36
Match length	139
% identity	63
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126096
Contig ID	19710_1.R1010
5'-most EST	jC-atXLIB327401P4a12b2
Method	BLASTX
NCBI GI	g2190187
BLAST score	210
E value	2.0e-16
Match length	75
% identity	56
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	126097
Contig ID	19718_1.R1010
5'-most EST	LIB25-020-Q1-E1-H12
Method	BLASTX
NCBI GI	g4220464
BLAST score	606
E value	4.0e-63
Match length	118
% identity	99
NCBI Description	(AC006216) Similar to gb_Y09437 myrosinase binding protein from Brassica napus. [Arabidopsis thaliana]

Seq. No.	126098
Contig ID	19719_1.R1010
5'-most EST	jC-atXLIB327402P4d05b1
Method	BLASTX
NCBI GI	g4056434
BLAST score	269
E value	2.0e-23
Match length	74
% identity	78
NCBI Description	(AC005990) Similar to OBP32pep protein gb_U37698 from

Arabidopsis thaliana. [Arabidopsis thaliana]

Seq. No.	126099
Contig ID	19720_1.R1010
5'-most EST	jC-atXP121C95J21T7060d1
Method	BLASTX
NCBI GI	g2760839
BLAST score	546
E value	8.0e-56
Match length	187
% identity	58
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	126100
Contig ID	19723_1.R1010
5'-most EST	jC-atXLIB327402P1e05b1
Method	BLASTX
NCBI GI	g3927836
BLAST score	429
E value	7.0e-43
Match length	145
% identity	68
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	126101
Contig ID	19725_1.R1010
5'-most EST	g2048932
Method	BLASTN
NCBI GI	g3831448
BLAST score	142
E value	7.0e-74
Match length	324
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126102
Contig ID	19726_1.R1010
5'-most EST	jC-atXLIB327402P1e06b1
Method	BLASTX
NCBI GI	g1946331
BLAST score	667
E value	4.0e-70
Match length	146
% identity	90
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	126103
Contig ID	19728_1.R1010
5'-most EST	jC-atXLIB327406P2a05b1
Method	BLASTX
NCBI GI	g1171429
BLAST score	243
E value	7.0e-32
Match length	127
% identity	34

NCBI Description	(U44028) CKC [Arabidopsis thaliana]

Seq. No.	126104
Contig ID	19731_1.R1010
5'-most EST	LIB25-044-Q1-E1-A1
Method	BLASTX
NCBI GI	g125576
BLAST score	448
E value	3.0e-44
Match length	148
% identity	72
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	126105
Contig ID	19731_2.R1010
5'-most EST	g906967
Method	BLASTX
NCBI GI	g125576
BLAST score	352
E value	2.0e-44
Match length	123
% identity	76
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	126106
Contig ID	19731_3.R1010
5'-most EST	g2047391
Method	BLASTX
NCBI GI	g125576
BLAST score	389
E value	7.0e-48
Match length	135
% identity	79
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	126107
Contig ID	19731_4.R1010
5'-most EST	LIB3176-044-P1-K1-B1
Method	BLASTX
NCBI GI	g125576
BLAST score	96
E value	1.0e-140
Match length	267
% identity	92
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	126108
Contig ID	19732_1.R1010
5'-most EST	jC-atXLIB327402P1e10b1
Method	BLASTX
NCBI GI	g2370595
BLAST score	265
E value	5.0e-23
Match length	139
% identity	45
NCBI Description	(AJ001414) GTPase activating protein [Yarrowia lipolytica]

Seq. No.	126109
Contig ID	19733_1.R1010
5'-most EST	LIB24-036-Q1-E1-H10

Seq. No.	126110
Contig ID	19734_1.R1010
5'-most EST	LIB25-057-Q1-E1-H12
Method	BLASTX
NCBI GI	g2244945
BLAST score	272
E value	5.0e-24
Match length	52
% identity	100
NCBI Description	(Z97339) similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 6 (FRAGMENT) [Arabidopsis thaliana]

Seq. No.	126111
Contig ID	19738_1.R1010
5'-most EST	jC-atXLIB327405P4f04a1
Method	BLASTX
NCBI GI	g2245066
BLAST score	310
E value	3.0e-28
Match length	117
% identity	49
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	126112
Contig ID	19742_1.R1010
5'-most EST	LIB35-052-Q1-E1-F12
Method	BLASTX
NCBI GI	g4240207
BLAST score	206
E value	4.0e-16
Match length	119
% identity	38
NCBI Description	(AB020666) KIAA0859 protein [Homo sapiens]

Seq. No.	126113
Contig ID	19744_1.R1010
5'-most EST	LIB25-049-Q1-E1-D7

Method	BLASTN
NCBI GI	g2760173
BLAST score	40
E value	8.0e-13
Match length	60
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	126114
Contig ID	19745_1.R1010
5'-most EST	g3450569
Method	BLASTX
NCBI GI	g4586248
BLAST score	389
E value	3.0e-37
Match length	101
% identity	76
NCBI Description	(AL049640) growth factor like protein [Arabidopsis thaliana]

Seq. No.	126115
Contig ID	19749_1.R1010
5'-most EST	LIB24-037-Q1-E1-B12
Method	BLASTX
NCBI GI	g4734006
BLAST score	300
E value	2.0e-27
Match length	120
% identity	52
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126116
Contig ID	19750_1.R1010
5'-most EST	LIB24-037-Q1-E1-C10

Seq. No.	126117
Contig ID	19751_1.R1010
5'-most EST	LIB3168-031-P1-K1-G1
Method	BLASTN
NCBI GI	g2924655
BLAST score	149
E value	5.0e-78
Match length	543
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence [Arabidopsis thaliana]

Seq. No.	126118
Contig ID	19752_1.R1010
5'-most EST	jC-atXLIB327402P4c09b1
Method	BLASTX
NCBI GI	g3758859
BLAST score	193
E value	2.0e-14
Match length	100
% identity	32

NCBI Description	(Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w), Hypothetical protein, len: 222 aa [Plasmodium falciparum]

Seq. No.	126119
Contig ID	19753_1.R1010
5'-most EST	LIB24-037-Q1-E1-C9
Method	BLASTX
NCBI GI	g4028601
BLAST score	151
E value	8.0e-10
Match length	127
% identity	35
NCBI Description	(AF105229) beta-galactosidase [Cloning vector pHR'-CMVLacZ]

Seq. No.	126120
Contig ID	19754_1.R1010
5'-most EST	jC-atXLIB327402P4d02b1
Method	BLASTX
NCBI GI	g4512678
BLAST score	725
E value	6.0e-77
Match length	139
% identity	100
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	126121
Contig ID	19757_1.R1010
5'-most EST	jC-atXP73CF2F12T7b1
Method	BLASTN
NCBI GI	g3046848
BLAST score	264
E value	1.0e-146
Match length	1243
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	126122
Contig ID	19758_1.R1010
5'-most EST	LIB3176-112-P1-K1-G2
Method	BLASTX
NCBI GI	g4539307
BLAST score	341
E value	7.0e-32
Match length	69
% identity	100
NCBI Description	(AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	126123
Contig ID	19759_1.R1010
5'-most EST	jC-atXLIB327402P1d09b1
Method	BLASTX
NCBI GI	g2245141
BLAST score	577
E value	1.0e-59
Match length	112

% identity	100
NCBI Description	(Z97344) acetylornithine deacetylase [Arabidopsis thaliana]

Seq. No.	126124
Contig ID	19762_1.R1010
5'-most EST	jC-atX24037Q1E1F10b1
Method	BLASTX
NCBI GI	g4432832
BLAST score	585
E value	1.0e-60
Match length	148
% identity	81
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	126125
Contig ID	19778_1.R1010
5'-most EST	g872001

Seq. No.	126126
Contig ID	19781_1.R1010
5'-most EST	jC-atX24037Q1E2A08b1
Method	BLASTX
NCBI GI	g4467156
BLAST score	126
E value	4.0e-11
Match length	72
% identity	48
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	126127
Contig ID	19789_1.R1010
5'-most EST	jC-atXLIB327401P4a03b2
Method	BLASTX
NCBI GI	g4587526
BLAST score	429
E value	6.0e-42
Match length	198
% identity	45
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come from this gene

Seq. No.	126128
Contig ID	19797_1.R1010
5'-most EST	jC-atXLIB327401P3a05b2
Method	BLASTN
NCBI GI	g4589437
BLAST score	432
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	126129
Contig ID	19806_1.R1010

5'-most EST	jC-atXLIB327402P1d01b1
Method	BLASTX
NCBI GI	g4741201
BLAST score	629
E value	1.0e-65
Match length	144
% identity	22
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	126130
Contig ID	19808_1.R1010
5'-most EST	LIB24-037-Q1-E2-D8
Method	BLASTX
NCBI GI	g1723693
BLAST score	82
E value	3.0e-14
Match length	76
% identity	62
NCBI Description	HYPOTHETICAL 69.9 KD PROTEIN IN MIC1-SRB5 INTERGENIC REGION >gi_2132607_pir__S64410 probable membrane protein YGR103w - yeast (Saccharomyces cerevisiae) >gi_1323159_emb_CAA97106_ (Z72888) ORF YGR103w [Saccharomyces cerevisiae]

Seq. No.	126131
Contig ID	19815_1.R1010
5'-most EST	LIB3175-024-P1-K1-G3
Method	BLASTN
NCBI GI	g4757401
BLAST score	56
E value	1.0e-22
Match length	68
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	126132
Contig ID	19817_1.R1010
5'-most EST	LIB3176-053-P1-K1-A5

Seq. No.	126133
Contig ID	19832_2.R1010
5'-most EST	jC-alX25042Q1E1C04b1
Method	BLASTX
NCBI GI	g2213602
BLAST score	422
E value	2.0e-41
Match length	112
% identity	77
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	126134
Contig ID	19832_3.R1010
5'-most EST	jC-atXLIB327402P3d11b1
Method	BLASTX
NCBI GI	g2213602
BLAST score	529
E value	6.0e-54

Match length	148
% identity	77
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	126135
Contig ID	19850_1.R1010
5'-most EST	LIB24-038-Q1-E1-A2
Method	BLASTN
NCBI GI	g2337888
BLAST score	163
E value	2.0e-86
Match length	390
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	126136
Contig ID	19853_1.R1010
5'-most EST	LIB25-028-Q1-E1-C2
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	5.0e-11
Match length	60
% identity	55
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	126137
Contig ID	19854_1.R1010
5'-most EST	LIB25-049-Q1-E1-C4
Method	BLASTX
NCBI GI	g3355480
BLAST score	602
E value	1.0e-62
Match length	118
% identity	100
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	126138
Contig ID	19855_1.R1010
5'-most EST	LIB25-073-Q1-E1-F3
Method	BLASTN
NCBI GI	g2656029
BLAST score	209
E value	1.0e-114
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	126139
Contig ID	19860_1.R1010
5'-most EST	jC-alXLIB327435P2f07a1
Method	BLASTN
NCBI GI	g4757414
BLAST score	137

E value	7.0e-71
Match length	448
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	126140
Contig ID	19863_1.R1010
5'-most EST	LIB25-026-Q1-E1-G9
Method	BLASTN
NCBI GI	g2337888
BLAST score	225
E value	1.0e-123
Match length	587
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	126141
Contig ID	19864_1.R1010
5'-most EST	jC-atXP115C247K15T7073d1
Method	BLASTX
NCBI GI	g2160182
BLAST score	225
E value	4.0e-18
Match length	148
% identity	37
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	126142
Contig ID	19864_2.R1010
5'-most EST	jC-atXLIB327404P2h07b1
Method	BLASTX
NCBI GI	g2160182
BLAST score	240
E value	9.0e-20
Match length	148
% identity	39
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	126143
Contig ID	19866_1.R1010
5'-most EST	LIB3176-006-P1-K1-F7
Method	BLASTX
NCBI GI	g2464912
BLAST score	239
E value	1.0e-19
Match length	191
% identity	15
NCBI Description	(Z99708) salt-inducible like protein [Arabidopsis thaliana]

Seq. No.	126144
Contig ID	19868_1.R1010
5'-most EST	jC-atXLIB327401P3a06b2
Method	BLASTX

NCBI GI	g1931653
BLAST score	166
E value	2.0e-11
Match length	106
% identity	38
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	126145
Contig ID	19877_1.R1010
5'-most EST	g3228576

Seq. No.	126146
Contig ID	19877_2.R1010
5'-most EST	jC-atXLIB327424P1a10b2
Method	BLASTX
NCBI GI	g1076509
BLAST score	286
E value	3.0e-25
Match length	199
% identity	36
NCBI Description	chloroplast RNA binding protein - kidney bean >gi_558629_emb_CAA57551_ (X82030) chloroplast RNA binding protein [Phaseolus vulgaris]

Seq. No.	126147
Contig ID	19877_3.R1010
5'-most EST	g935784

Seq. No.	126148
Contig ID	19880_1.R1010
5'-most EST	LIB24-038-Q1-E1-D3
Method	BLASTN
NCBI GI	g2494106
BLAST score	331
E value	0.0e+00
Match length	343
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126149
Contig ID	19882_1.R1010
5'-most EST	jC-atXLIB327402P1d08b1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	3.0e-19
Match length	58
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	126150
Contig ID	19884_1.R1010
5'-most EST	jC-atXLIB327427P4a07b2
Method	BLASTN
NCBI GI	g2264307
BLAST score	330

E value	0.0e+00
Match length	603
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	126151
Contig ID	19885_1.R1010
5'-most EST	jC-atXLIB327431P4g03a1
Method	BLASTN
NCBI GI	g4519194
BLAST score	336
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	126152
Contig ID	19887_1.R1010
5'-most EST	jC-atXLIB327424P1c02b2
Method	BLASTX
NCBI GI	g3298538
BLAST score	744
E value	4.0e-79
Match length	141
% identity	100
NCBI Description	(AC004681) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126153
Contig ID	19890_1.R1010
5'-most EST	jC-atXLIB327402P1d12b1
Method	BLASTN
NCBI GI	g2924768
BLAST score	350
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126154
Contig ID	19892_1.R1010
5'-most EST	LIB3177-044-P1-K2-F3
Method	BLASTX
NCBI GI	g1172568
BLAST score	243
E value	2.0e-20
Match length	90
% identity	56
NCBI Description	LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (PTPASE) (SMALL TYROSINE PHOSPHATASE) >gi_1076916_pir__A55446 protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular weight - fission yeast (Schizosaccharomyces pombe) >gi_602992 (L33929) low Mr protein tyrosine phosphatase [Schizosaccharomyces pombe]

Seq. No.	126155
Contig ID	19897_1.R1010
5'-most EST	jC-atXLIB327402P1e01b1
Method	BLASTN
NCBI GI	g3449311
BLAST score	371
E value	0.0e+00
Match length	410
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15I22, complete sequence [Arabidopsis thaliana]

Seq. No.	126156
Contig ID	19901_1.R1010
5'-most EST	ARABLI-11-Q1-B1-F7
Method	BLASTX
NCBI GI	g2213629
BLAST score	215
E value	6.0e-17
Match length	202
% identity	27
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	126157
Contig ID	19905_1.R1010
5'-most EST	jC-atXLIB327413P1f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126158
Contig ID	19907_1.R1010
5'-most EST	LIB25-099-Q1-E1-F10
Method	BLASTX
NCBI GI	g3128175
BLAST score	165
E value	4.0e-11
Match length	172
% identity	27
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	126159
Contig ID	19911_1.R1010
5'-most EST	jC-atXLIB327402P3e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	69
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	126160
Contig ID	19917_1.R1010
5'-most EST	jC-atXLIB327402P4e05b1
Method	BLASTX
NCBI GI	g2335108
BLAST score	534
E value	1.0e-54
Match length	126
% identity	79
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	126161
Contig ID	19919_1.R1010
5'-most EST	LIB24-039-Q1-E1-B4
Method	BLASTN
NCBI GI	g619748
BLAST score	75
E value	6.0e-34
Match length	99
% identity	94
NCBI Description	Arabidopsis thaliana phosphoribosylanthranilate isomerase (PAI3) gene, complete cds

Seq. No.	126162
Contig ID	19921_1.R1010
5'-most EST	jC-atX24039Q1E1B06b1

Seq. No.	126163
Contig ID	19922_1.R1010
5'-most EST	LIB24-039-Q1-E1-B7
Method	BLASTX
NCBI GI	g1800223
BLAST score	211
E value	8.0e-17
Match length	109
% identity	42
NCBI Description	(U65018) mannosyltransferase [Dictyostelium discoideum]

Seq. No.	126164
Contig ID	19923_1.R1010
5'-most EST	jC-atXLIB327402P3e10b1
Method	BLASTX
NCBI GI	g2317904
BLAST score	415
E value	1.0e-40
Match length	123
% identity	71
NCBI Description	(U89959) Similar to rice chalcone synthase homolog, gp_U90341_2507617 and anther specific protein, gp_Y14507_2326772 [Arabidopsis thaliana]

Seq. No.	126165
Contig ID	19925_1.R1010
5'-most EST	LIB24-039-Q1-E1-C10

Seq. No.	126166
Contig ID	19928_1.R1010
5'-most EST	jC-atXLIB327407P4a01b1
Method	BLASTN
NCBI GI	g2564051
BLAST score	618
E value	0.0e+00
Match length	793
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	126167
Contig ID	19928_2.R1010
5'-most EST	jC-atX24020Q1E1B09b1
Method	BLASTN
NCBI GI	g2564051
BLAST score	405
E value	0.0e+00
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	126168
Contig ID	19935_1.R1010
5'-most EST	LIB3177-087-P1-K1-G5
Method	BLASTN
NCBI GI	g4757407
BLAST score	291
E value	1.0e-163
Match length	299
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	126169
Contig ID	19936_1.R1010
5'-most EST	jC-atXLIB327402P4f06b1

Seq. No.	126170
Contig ID	19938_1.R1010
5'-most EST	LIB24-039-Q1-E1-E5
Method	BLASTN
NCBI GI	g2656024
BLAST score	518
E value	0.0e+00
Match length	542
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	126171
Contig ID	19939_1.R1010
5'-most EST	jC-atXLIB327402P4f04b1
Method	BLASTN
NCBI GI	g2760164

BLAST score 85
E value 7.0e-40
Match length 271
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No. 126172
Contig ID 19941_1.R1010
5'-most EST jC-atX24039Q1E1E08b1
Method BLASTX
NCBI GI g4038034
BLAST score 243
E value 6.0e-41
Match length 90
% identity 94
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 126173
Contig ID 19945_1.R1010
5'-most EST jC-atXLIB327402P1g01b1
Method BLASTX
NCBI GI g4091117
BLAST score 450
E value 1.0e-44
Match length 132
% identity 61
NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No. 126174
Contig ID 19949_1.R1010
5'-most EST jC-atXLIB327402P3f10b1
Method BLASTX
NCBI GI g4490731
BLAST score 519
E value 8.0e-53
Match length 120
% identity 93
NCBI Description (AL035709) hypothetical protein [Arabidopsis thaliana]

Seq. No. 126175
Contig ID 19958_1.R1010
5'-most EST LIB25-047-Q1-E1-G10
Method BLASTX
NCBI GI g4006932
BLAST score 145
E value 7.0e-09
Match length 100
% identity 40
NCBI Description (AJ011400) NADH:ubiquinone oxidoreductase b17.2 subunit [Bos taurus]

Seq. No. 126176
Contig ID 19958_2.R1010
5'-most EST g2722504

Seq. No. 126177

Contig ID	19960_1.R1010
5'-most EST	jC-atXLIB327426P2f05b1
Method	BLASTX
NCBI GI	g2864610
BLAST score	632
E value	6.0e-66
Match length	176
% identity	74
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	126178
Contig ID	19961_1.R1010
5'-most EST	LIB24-039-Q1-E1-H10

Seq. No.	126179
Contig ID	19962_1.R1010
5'-most EST	g1269417
Method	BLASTX
NCBI GI	g3549679
BLAST score	214
E value	5.0e-17
Match length	111
% identity	50
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	126180
Contig ID	19965_1.R1010
5'-most EST	jC-atX24103Q1E2B09b1
Method	BLASTX
NCBI GI	g586858
BLAST score	278
E value	1.0e-24
Match length	122
% identity	47
NCBI Description	HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION >gi_2127020_pir__S66042 hypothetical protein - Bacillus subtilis >gi_467402_dbj_BAA05248_ (D26185) unknown [Bacillus subtilis] >gi_2632279_emb_CAB11788_ (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	126181
Contig ID	19977_1.R1010
5'-most EST	jC-atXLIB327402P1f06b1
Method	BLASTN
NCBI GI	g2264314
BLAST score	555
E value	0.0e+00
Match length	575
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	126182
Contig ID	19977_2.R1010
5'-most EST	jC-atXP104CE10F8T7b1

Method	BLASTN
NCBI GI	g2264314
BLAST score	498
E value	0.0e+00
Match length	498
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	126183
Contig ID	19977_3.R1010
5'-most EST	g2597776
Method	BLASTN
NCBI GI	g2264314
BLAST score	405
E value	0.0e+00
Match length	492
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	126184
Contig ID	19981_1.R1010
5'-most EST	LIB24-040-Q1-E1-D9
Method	BLASTX
NCBI GI	g2160185
BLAST score	361
E value	3.0e-34
Match length	151
% identity	47
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	126185
Contig ID	19982_1.R1010
5'-most EST	g3449715

Seq. No.	126186
Contig ID	19982_2.R1010
5'-most EST	LIB35-019-Q1-E1-E12
Method	BLASTX
NCBI GI	g3269293
BLAST score	571
E value	2.0e-58
Match length	173
% identity	65
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	126187
Contig ID	19983_1.R1010
5'-most EST	jC-atXP66C210J7T7d1

Seq. No.	126188
Contig ID	19983_2.R1010
5'-most EST	jC-atXLIB327401P3b04b2

Seq. No.	126189

Contig ID	19985_1.R1010
5'-most EST	jC-atXLIB327402P4f11b1
Method	BLASTX
NCBI GI	g4454033
BLAST score	166
E value	4.0e-37
Match length	137
% identity	57
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	126190
Contig ID	19991_1.R1010
5'-most EST	LIB24-041-Q1-E1-A11

Seq. No.	126191
Contig ID	19994_1.R1010
5'-most EST	jC-atXLIB327402P1e12b1
Method	BLASTN
NCBI GI	g3608126
BLAST score	331
E value	0.0e+00
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126192
Contig ID	19995_1.R1010
5'-most EST	jC-atXLIB327402P4e01b1
Method	BLASTN
NCBI GI	g2342673
BLAST score	576
E value	0.0e+00
Match length	608
% identity	99
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	126193
Contig ID	19999_1.R1010
5'-most EST	LIB25-041-Q1-E1-D8

Seq. No.	126194
Contig ID	20004_1.R1010
5'-most EST	jC-atXLIB327401P3b01b2
Method	BLASTX
NCBI GI	g2618705
BLAST score	701
E value	4.0e-74
Match length	137
% identity	99
NCBI Description	(AC002510) putative ABC transporter, 5' partial [Arabidopsis thaliana]

Seq. No.	126195
Contig ID	20007_1.R1010

5'-most EST	LIB24-041-Q1-E1-G2
Method	BLASTX
NCBI GI	g3063706
BLAST score	716
E value	5.0e-76
Match length	148
% identity	86
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	126196
Contig ID	20011_1.R1010
5'-most EST	jC-atXLIB327440P1h09a1
Method	BLASTN
NCBI GI	g4220468
BLAST score	297
E value	1.0e-166
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126197
Contig ID	20017_1.R1010
5'-most EST	jC-atX25070Q1E1H05b1
Method	BLASTX
NCBI GI	g1731181
BLAST score	195
E value	7.0e-15
Match length	67
% identity	57
NCBI Description	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi_3874230_emb_CAA90107_ (Z49909) weak similarity with a B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	126198
Contig ID	20018_1.R1010
5'-most EST	LIB24-041-Q1-E1-F5
Method	BLASTX
NCBI GI	g2459435
BLAST score	438
E value	2.0e-58
Match length	133
% identity	82
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	126199
Contig ID	20024_1.R1010
5'-most EST	jC-atXLIB327402P1f12b1
Method	BLASTN
NCBI GI	g3367500
BLAST score	200
E value	1.0e-108
Match length	372
% identity	100

NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	126200
Contig ID	20028_1.R1010
5'-most EST	jC-atXLIB327426P1e08b1
Method	BLASTX
NCBI GI	g2832681
BLAST score	582
E value	6.0e-60
Match length	108
% identity	100
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	126201
Contig ID	20029_1.R1010
5'-most EST	g2062910
Method	BLASTX
NCBI GI	g2213584
BLAST score	231
E value	6.0e-19
Match length	84
% identity	55
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	126202
Contig ID	20030_1.R1010
5'-most EST	jC-atXLIB327402P3f09b1
Method	BLASTN
NCBI GI	g4512690
BLAST score	470
E value	0.0e+00
Match length	474
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	126203
Contig ID	20032_1.R1010
5'-most EST	jC-atXLIB327402P4f08b1
Method	BLASTX
NCBI GI	g2801701
BLAST score	259
E value	3.0e-22
Match length	131
% identity	40
NCBI Description	(AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]

Seq. No.	126204
Contig ID	20034_1.R1010
5'-most EST	LIB24-041-Q1-E1-F8
Method	BLASTX
NCBI GI	g3522938
BLAST score	191
E value	3.0e-36
Match length	126

% identity	69
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	126205
Contig ID	20041_1.R1010
5'-most EST	LIB3177-006-P1-K2-D11
Method	BLASTN
NCBI GI	g4519183
BLAST score	240
E value	1.0e-132
Match length	323
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	126206
Contig ID	20042_1.R1010
5'-most EST	jC-atXLIB327402P1g03b1
Method	BLASTX
NCBI GI	g4263791
BLAST score	256
E value	5.0e-22
Match length	89
% identity	56
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	126207
Contig ID	20052_1.R1010
5'-most EST	LIB24-041-Q1-E1-H9
Method	BLASTX
NCBI GI	g629692
BLAST score	541
E value	1.0e-55
Match length	110
% identity	90
NCBI Description	hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No.	126208
Contig ID	20053_1.R1010
5'-most EST	jC-atXLIB327402P4e03b1
Method	BLASTX
NCBI GI	g3600058
BLAST score	787
E value	5.0e-84
Match length	228
% identity	69
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	126209
Contig ID	20054_1.R1010
5'-most EST	LIB24-042-Q1-E1-A11
Method	BLASTN
NCBI GI	g1402874

BLAST score	358
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	126210
Contig ID	20055_1.R1010
5'-most EST	LIB24-042-Q1-E1-A6
Method	BLASTN
NCBI GI	g531828
BLAST score	40
E value	7.0e-13
Match length	63
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	126211
Contig ID	20056_1.R1010
5'-most EST	jC-alXLIB327434P4g11b1
Method	BLASTX
NCBI GI	g4432856
BLAST score	1906
E value	0.0e+00
Match length	359
% identity	100
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	126212
Contig ID	20060_1.R1010
5'-most EST	LIB3175-015-P1-K1-B8
Method	BLASTX
NCBI GI	g2462935
BLAST score	641
E value	6.0e-67
Match length	164
% identity	71
NCBI Description	(Y12321) open reading frame 1 [Brassica oleracea]

Seq. No.	126213
Contig ID	20065_1.R1010
5'-most EST	LIB24-042-Q1-E1-B2
Method	BLASTX
NCBI GI	g953179
BLAST score	324
E value	4.0e-30
Match length	128
% identity	53
NCBI Description	(Z37980) ORF14 [Escherichia coli]

Seq. No.	126214
Contig ID	20066_1.R1010
5'-most EST	jC-atXLIB327402P4e09b1
Method	BLASTN
NCBI GI	g2264312
BLAST score	278
E value	1.0e-155

Match length	380
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	126215
Contig ID	20067_1.R1010
5'-most EST	jC-atXLIB327402P4e07b1

Seq. No.	126216
Contig ID	20068_1.R1010
5'-most EST	jC-alXLIB327436P3g11b1
Method	BLASTX
NCBI GI	g4586265
BLAST score	716
E value	2.0e-75
Match length	180
% identity	77
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	126217
Contig ID	20069_1.R1010
5'-most EST	jC-atXLIB327402P1f01b1
Method	BLASTX
NCBI GI	g1065515
BLAST score	261
E value	1.0e-22
Match length	141
% identity	43
NCBI Description	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]

Seq. No.	126218
Contig ID	20072_1.R1010
5'-most EST	LIB24-042-Q1-E1-C2
Method	BLASTN
NCBI GI	g4512690
BLAST score	308
E value	1.0e-173
Match length	378
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	126219
Contig ID	20073_1.R1010
5'-most EST	jC-atXLIB327401P4b01b1
Method	BLASTN
NCBI GI	g2191126
BLAST score	179
E value	6.0e-96
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	126220
Contig ID	20074_1.R1010

5'-most EST	jC-atXLIB327402P1f04b1
Method	BLASTN
NCBI GI	g527624
BLAST score	81
E value	2.0e-37
Match length	81
% identity	100
NCBI Description	Arabidopsis thaliana clone HAT14 homeobox protein mRNA, partial cds

Seq. No.	126221
Contig ID	20078_1.R1010
5'-most EST	jC-atXL1045Q1E1C08b1
Method	BLASTN
NCBI GI	g4757396
BLAST score	61
E value	1.0e-25
Match length	216
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8A10, complete sequence

Seq. No.	126222
Contig ID	20079_1.R1010
5'-most EST	LIB24-042-Q1-E1-F1
Method	BLASTN
NCBI GI	g2979540
BLAST score	167
E value	8.0e-89
Match length	427
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126223
Contig ID	20085_1.R1010
5'-most EST	jC-atXLIB327402P1f08b1
Method	BLASTX
NCBI GI	g1176658
BLAST score	329
E value	2.0e-30
Match length	145
% identity	47
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	126224
Contig ID	20086_1.R1010
5'-most EST	LIB24-042-Q1-E1-D7
Method	BLASTX
NCBI GI	g3882183
BLAST score	207
E value	1.0e-15
Match length	244
% identity	33
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]

Seq. No.	126225
Contig ID	20086_2.R1010
5'-most EST	LIB3176-033-P1-K1-G1
Method	BLASTX
NCBI GI	g3882183
BLAST score	496
E value	6.0e-50
Match length	228
% identity	46
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]

Seq. No.	126226
Contig ID	20094_1.R1010
5'-most EST	jC-atXP86CG8E8T7b1
Method	BLASTX
NCBI GI	g3885511
BLAST score	420
E value	6.0e-41
Match length	103
% identity	82
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	126227
Contig ID	20094_2.R1010
5'-most EST	jC-atXLIB327431P3c04a1
Method	BLASTX
NCBI GI	g3885511
BLAST score	143
E value	2.0e-30
Match length	96
% identity	77
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	126228
Contig ID	20098_1.R1010
5'-most EST	LIB24-042-Q1-E1-E7
Method	BLASTN
NCBI GI	g3885325
BLAST score	379
E value	0.0e+00
Match length	973
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126229
Contig ID	20098_2.R1010
5'-most EST	g2393295
Method	BLASTN
NCBI GI	g3885325
BLAST score	345
E value	0.0e+00
Match length	365
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	126230
Contig ID	20100_1.R1010
5'-most EST	jC-atXLIB327401P4b03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	1.0e-27
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	126231
Contig ID	20103_1.R1010
5'-most EST	jC-atXLIB327424P3c05b1
Method	BLASTN
NCBI GI	g2924730
BLAST score	79
E value	3.0e-36
Match length	328
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]
Seq. No.	126232
Contig ID	20103_2.R1010
5'-most EST	LIB25-023-Q1-E1-C6
Method	BLASTN
NCBI GI	g2924730
BLAST score	324
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]
Seq. No.	126233
Contig ID	20107_1.R1010
5'-most EST	jC-atXLIB327402P4f09b1
Seq. No.	126234
Contig ID	20109_1.R1010
5'-most EST	jC-atXLIB327423P4g01b1
Method	BLASTN
NCBI GI	g3600062
BLAST score	371
E value	0.0e+00
Match length	630
% identity	100
NCBI Description	Arabidopsis thaliana BAC T25C13
Seq. No.	126235
Contig ID	20111_1.R1010
5'-most EST	jC-atXP117C141P22T7a1

Method	BLASTX
NCBI GI	g2252844
BLAST score	511
E value	1.0e-51
Match length	116
% identity	84
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	126236
Contig ID	20111_3.R1010
5'-most EST	LIB3234-013-P1-K1-F1
Method	BLASTX
NCBI GI	g2252844
BLAST score	898
E value	3.0e-97
Match length	172
% identity	100
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	126237
Contig ID	20113_1.R1010
5'-most EST	LIB24-042-Q1-E1-G12
Method	BLASTX
NCBI GI	g2494041
BLAST score	274
E value	4.0e-24
Match length	66
% identity	76
NCBI Description	DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No.	126238
Contig ID	20115_1.R1010
5'-most EST	jC-atXLIB327402P1g04b1
Method	BLASTN
NCBI GI	g2244991
BLAST score	226
E value	1.0e-124
Match length	436
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126239
Contig ID	20117_1.R1010
5'-most EST	jC-atXLIB327402P1g02b1

Seq. No.	126240
Contig ID	20118_1.R1010
5'-most EST	LIB25-041-Q1-E1-D12
Method	BLASTN
NCBI GI	g4741184
BLAST score	138
E value	1.0e-71
Match length	414

% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	126241
Contig ID	20130_1.R1010
5'-most EST	jC-atXLIB327409P2e12b1
Method	BLASTX
NCBI GI	g3080393
BLAST score	272
E value	7.0e-24
Match length	71
% identity	72
NCBI Description	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	126242
Contig ID	20131_1.R1010
5'-most EST	LIB24-043-Q1-E1-A9

Seq. No.	126243
Contig ID	20132_1.R1010
5'-most EST	LIB3175-028-P1-K1-B7
Method	BLASTX
NCBI GI	g2132124
BLAST score	348
E value	2.0e-47
Match length	175
% identity	61
NCBI Description	hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae) >gi_1420671_emb_CAA99622_ (Z75212) ORF YOR304w [Saccharomyces cerevisiae]

Seq. No.	126244
Contig ID	20133_1.R1010
5'-most EST	jC-atXLIB327402P1h02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126245
Contig ID	20134_1.R1010
5'-most EST	jC-atXLIB327408P4d11b1
Method	BLASTN
NCBI GI	g2618601
BLAST score	657
E value	0.0e+00
Match length	717
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	126246
Contig ID	20137_1.R1010
5'-most EST	g2747938
Method	BLASTN
NCBI GI	g2335089
BLAST score	309
E value	1.0e-173
Match length	417
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126247
Contig ID	20137_2.R1010
5'-most EST	LIB24-043-Q1-E1-B4
Method	BLASTX
NCBI GI	g4490735
BLAST score	392
E value	1.0e-68
Match length	177
% identity	83
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	126248
Contig ID	20138_1.R1010
5'-most EST	jC-alXLIB327436P4h04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	117
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	126249
Contig ID	20138_2.R1010
5'-most EST	jC-atXLIB327408P1c12b1
Method	BLASTX
NCBI GI	g3875451
BLAST score	262
E value	3.0e-22
Match length	175
% identity	35
NCBI Description	(Z66496) cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA EST EMBL:D76330 comes from this gene; cDNA EST EMBL:D65192 comes from this gene; cDNA EST EMBL:D68540 comes from this gene; cDN

Seq. No.	126250
Contig ID	20143_1.R1010
5'-most EST	jC-atX22035Q1E1C05b1
Method	BLASTN
NCBI GI	g3894179
BLAST score	37
E value	3.0e-11
Match length	160
% identity	50

NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126251
Contig ID	20145_1.R1010
5'-most EST	jC-atX22087Q1E1D06b1
Method	BLASTX
NCBI GI	g1518540
BLAST score	617
E value	2.0e-64
Match length	136
% identity	88
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	126252
Contig ID	20156_1.R1010
5'-most EST	jC-atXLIB327402P4f05b1
Method	BLASTX
NCBI GI	g3935157
BLAST score	533
E value	3.0e-54
Match length	126
% identity	78
NCBI Description	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No.	126253
Contig ID	20157_1.R1010
5'-most EST	g550272
Method	BLASTX
NCBI GI	g4725941
BLAST score	465
E value	1.0e-46
Match length	127
% identity	76
NCBI Description	(AL049730) putative pollen-specific protein [Arabidopsis thaliana]

Seq. No.	126254
Contig ID	20161_1.R1010
5'-most EST	LIB24-043-Q1-E1-E4
Method	BLASTX
NCBI GI	g1653186
BLAST score	200
E value	3.0e-15
Match length	145
% identity	34
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	126255
Contig ID	20162_2.R1010
5'-most EST	jC-atXLIB327403P3e08b1
Method	BLASTX
NCBI GI	g2695861
BLAST score	433
E value	8.0e-43
Match length	99
% identity	84

NCBI Description	(Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]
Seq. No.	126256
Contig ID	20163_1.R1010
5'-most EST	LIB24-043-Q1-E1-E7
Method	BLASTX
NCBI GI	g4559358
BLAST score	484
E value	1.0e-48
Match length	93
% identity	100
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]
Seq. No.	126257
Contig ID	20166_1.R1010
5'-most EST	jC-alX24069Q1E1G01b1
Seq. No.	126258
Contig ID	20166_2.R1010
5'-most EST	LIB3175-058-P1-K1-H4
Seq. No.	126259
Contig ID	20173_1.R1010
5'-most EST	jC-atX24043Q1E1G11b1
Method	BLASTN
NCBI GI	g2351068
BLAST score	197
E value	1.0e-107
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.	126260
Contig ID	20181_1.R1010
5'-most EST	LIB24-069-Q1-E1-D1
Method	BLASTX
NCBI GI	g2832649
BLAST score	674
E value	5.0e-71
Match length	132
% identity	100
NCBI Description	(AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]
Seq. No.	126261
Contig ID	20185_1.R1010
5'-most EST	g430401
Method	BLASTX
NCBI GI	g4506223
BLAST score	282
E value	7.0e-25
Match length	188

% identity	33
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 >gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]

Seq. No.	126262
Contig ID	20187_1.R1010
5'-most EST	jC-atX24043Q1E1H07b1
Method	BLASTX
NCBI GI	g3785988
BLAST score	413
E value	6.0e-40
Match length	176
% identity	59
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	126263
Contig ID	20187_2.R1010
5'-most EST	g2722545
Method	BLASTN
NCBI GI	g3785968
BLAST score	231
E value	1.0e-127
Match length	394
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126264
Contig ID	20191_1.R1010
5'-most EST	jC-atX25073Q1E1H12b1
Method	BLASTN
NCBI GI	g4757413
BLAST score	218
E value	1.0e-119
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	126265
Contig ID	20193_1.R1010
5'-most EST	jC-atXLIB327402P4g08b1
Method	BLASTX
NCBI GI	g2388577
BLAST score	163
E value	4.0e-39
Match length	108
% identity	86
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No.	126266
Contig ID	20196_1.R1010
5'-most EST	jC-atX24044Q1E1A06b1
Method	BLASTN
NCBI GI	g4415928

BLAST score 144
E value 4.0e-75
Match length 416
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126267
Contig ID 20197_1.R1010
5'-most EST jC-atXP80C240I16T7s1
Method BLASTX
NCBI GI g960291
BLAST score 186
E value 2.0e-41
Match length 108
% identity 80
NCBI Description (L34344) anthranilate synthase alpha subunit [Ruta graveolens]

Seq. No. 126268
Contig ID 20200_1.R1010
5'-most EST g2749040
Method BLASTN
NCBI GI g4027862
BLAST score 357
E value 0.0e+00
Match length 440
% identity 95
NCBI Description Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126269
Contig ID 20204_1.R1010
5'-most EST jC-atXLIB327402P3g11b1
Method BLASTX
NCBI GI g4164473
BLAST score 170
E value 8.0e-12
Match length 71
% identity 56
NCBI Description (AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No. 126270
Contig ID 20212_1.R1010
5'-most EST LIB3234-015-P1-K1-D7
Method BLASTN
NCBI GI g2618604
BLAST score 281
E value 1.0e-156
Match length 955
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 126271
Contig ID 20212_2.R1010

5'-most EST	jC-atXLIB327423P2b07b1
Method	BLASTN
NCBI GI	g2618604
BLAST score	125
E value	9.0e-64
Match length	426
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No.	126272
Contig ID	20219_1.R1010
5'-most EST	jC-atX24044Q1E1D01b1
Method	BLASTX
NCBI GI	g2827700
BLAST score	737
E value	2.0e-78
Match length	142
% identity	99
NCBI Description	(AL021684) DEAD box ATP dependent helicase protein [Arabidopsis thaliana]

Seq. No.	126273
Contig ID	20235_1.R1010
5'-most EST	jC-atX24044Q1E1E07b1
Method	BLASTN
NCBI GI	g3451055
BLAST score	40
E value	4.0e-13
Match length	56
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	126274
Contig ID	20237_1.R1010
5'-most EST	jC-atX24116Q1E1E08b1

Seq. No.	126275
Contig ID	20239_1.R1010
5'-most EST	LIB3177-087-P1-K1-D7
Method	BLASTN
NCBI GI	g3212846
BLAST score	466
E value	0.0e+00
Match length	1209
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126276
Contig ID	20240_1.R1010
5'-most EST	LIB24-044-Q1-E1-F12
Method	BLASTN
NCBI GI	g4159699
BLAST score	303
E value	1.0e-170

Match length	362
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence

Seq. No.	126277
Contig ID	20243_1.R1010
5'-most EST	g957569
Method	BLASTX
NCBI GI	g2500959
BLAST score	84
E value	1.0e-36
Match length	184
% identity	45
NCBI Description	ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	126278
Contig ID	20244_1.R1010
5'-most EST	jC-atX24044Q1E1F05b1
Method	BLASTX
NCBI GI	g3668086
BLAST score	484
E value	1.0e-48
Match length	170
% identity	63
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	126279
Contig ID	20262_1.R1010
5'-most EST	jC-atXLIB327403P3a03b2
Method	BLASTX
NCBI GI	g3402711
BLAST score	164
E value	6.0e-11
Match length	87
% identity	48
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	126280
Contig ID	20263_1.R1010
5'-most EST	jC-alX24075Q1E1A02b1
Method	BLASTX
NCBI GI	g2494320
BLAST score	492
E value	1.0e-49
Match length	116
% identity	81
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	126281
Contig ID	20265_1.R1010
5'-most EST	jC-atXLIB327403P3a01b2

Method	BLASTX
NCBI GI	g134646
BLAST score	372
E value	1.0e-35
Match length	86
% identity	71
NCBI Description	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >gi_169955 (M64267) Fe-superoxide dismutase [Glycine max] >gi_228415_prf__1803527A Fe superoxide dismutase [Glycine max]

Seq. No.	126282
Contig ID	20266_1.R1010
5'-most EST	jC-atXLIB327403P3a02b2
Method	BLASTX
NCBI GI	g4581205
BLAST score	671
E value	1.0e-70
Match length	150
% identity	85
NCBI Description	(Y17913) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	126283
Contig ID	20276_1.R1010
5'-most EST	LIB24-045-Q1-E1-B11
Method	BLASTX
NCBI GI	g4335729
BLAST score	165
E value	2.0e-11
Match length	127
% identity	5
NCBI Description	(AC006248) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No.	126284
Contig ID	20277_1.R1010
5'-most EST	g2749230
Method	BLASTN
NCBI GI	g540252
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	126285
Contig ID	20277_2.R1010
5'-most EST	LIB35-032-Q1-E1-F9

Seq. No.	126286
Contig ID	20279_1.R1010
5'-most EST	jC-atXLIB327421P1h09b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	69
E value	3.0e-30

Match length 135
% identity 55
NCBI Description Mus musculus Pontin52 mRNA, complete cds

Seq. No. 126287
Contig ID 20279_2.R1010
5'-most EST LIB35-016-Q1-E1-A1
Method BLASTX
NCBI GI g3738285
BLAST score 267
E value 7.0e-23
Match length 162
% identity 35
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 126288
Contig ID 20279_3.R1010
5'-most EST g2762377

Seq. No. 126289
Contig ID 20279_4.R1010
5'-most EST jC-alX35051Q1E1E03b1
Method BLASTN
NCBI GI g4106527
BLAST score 77
E value 4.0e-35
Match length 109
% identity 66
NCBI Description Mus musculus Pontin52 mRNA, complete cds

Seq. No. 126290
Contig ID 20282_1.R1010
5'-most EST g936704
Method BLASTX
NCBI GI g3342552
BLAST score 646
E value 1.0e-67
Match length 128
% identity 95
NCBI Description (AF076979) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No. 126291
Contig ID 20283_1.R1010
5'-most EST jC-atXLIB327402P1h06b1
Method BLASTX
NCBI GI g2632254
BLAST score 191
E value 2.0e-14
Match length 57
% identity 67
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 126292
Contig ID 20290_1.R1010
5'-most EST jC-atXLIB327402P1h05b1
Method BLASTN

NCBI GI	g3608126
BLAST score	440
E value	0.0e+00
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126293
Contig ID	20291_1.R1010
5'-most EST	jC-alX24095Q1E1C12b1

Seq. No.	126294
Contig ID	20291_2.R1010
5'-most EST	LIB3168-083-P1-K1-G1

Seq. No.	126295
Contig ID	20293_1.R1010
5'-most EST	jC-atX24045Q1E1D01b1
Method	BLASTN
NCBI GI	g4589439
BLAST score	354
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	126296
Contig ID	20295_1.R1010
5'-most EST	jC-alXLIB327434P1h06b1
Method	BLASTX
NCBI GI	g2245108
BLAST score	66
E value	4.0e-64
Match length	194
% identity	80
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	126297
Contig ID	20296_1.R1010
5'-most EST	LIB24-045-Q1-E1-D3

Seq. No.	126298
Contig ID	20298_1.R1010
5'-most EST	jC-atX24045Q1E1D05b1

Seq. No.	126299
Contig ID	20300_1.R1010
5'-most EST	jC-atXLIB327402P1h12b1
Method	BLASTX
NCBI GI	g2462841
BLAST score	703
E value	2.0e-74
Match length	134
% identity	100
NCBI Description	(AF000657) similar to selenium-binding protein

gp_Z97335_2244760 [Arabidopsis thaliana]

Seq. No.	126300
Contig ID	20305_1.R1010
5'-most EST	LIB35-012-Q1-E1-C1
Method	BLASTX
NCBI GI	g4467116
BLAST score	231
E value	9.0e-53
Match length	129
% identity	88
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126301
Contig ID	20306_1.R1010
5'-most EST	jC-atXLIB327408P4h01b1
Method	BLASTX
NCBI GI	g2190187
BLAST score	580
E value	9.0e-60
Match length	213
% identity	53
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	126302
Contig ID	20312_1.R1010
5'-most EST	jC-atXP37C157O24T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	9.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126303
Contig ID	20312_2.R1010
5'-most EST	jC-atXP69C218M13T7074d1
Method	BLASTX
NCBI GI	g339878
BLAST score	195
E value	2.0e-14
Match length	237
% identity	26
NCBI Description	(M55169) tripeptidyl peptidase II [Homo sapiens]

Seq. No.	126304
Contig ID	20312_3.R1010
5'-most EST	g2749005

Seq. No.	126305
Contig ID	20321_1.R1010
5'-most EST	jC-atXLIB327407P3b04b1
Method	BLASTX
NCBI GI	g4539359
BLAST score	172

E value 7.0e-13
Match length 131
% identity 36
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 126306
Contig ID 20323_1.R1010
5'-most EST jC-atXLIB327418P3c08b1
Method BLASTN
NCBI GI g2582640
BLAST score 59
E value 2.0e-24
Match length 63
% identity 98
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 126307
Contig ID 20323_2.R1010
5'-most EST LIB24-045-Q1-E1-G11

Seq. No. 126308
Contig ID 20327_1.R1010
5'-most EST jC-atX22035Q1E1G01b1
Method BLASTX
NCBI GI g4454033
BLAST score 837
E value 4.0e-90
Match length 158
% identity 99
NCBI Description (AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No. 126309
Contig ID 20333_1.R1010
5'-most EST LIB24-045-Q1-E1-H12
Method BLASTX
NCBI GI g2827699
BLAST score 374
E value 6.0e-36
Match length 100
% identity 74
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 126310
Contig ID 20335_1.R1010
5'-most EST jC-atX24045Q1E1H03b1
Method BLASTN
NCBI GI g3135250
BLAST score 85
E value 1.0e-39
Match length 321
% identity 82
NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126311

Contig ID	20336_1.R1010
5'-most EST	jC-atX24045Q1E1H04b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	312
E value	1.0e-175
Match length	345
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	126312
Contig ID	20342_1.R1010
5'-most EST	jC-atXLIB327414P3a03a1
Method	BLASTN
NCBI GI	g4455168
BLAST score	154
E value	6.0e-81
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	126313
Contig ID	20342_2.R1010
5'-most EST	g1216814
Method	BLASTN
NCBI GI	g4455168
BLAST score	167
E value	1.0e-88
Match length	499
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	126314
Contig ID	20344_1.R1010
5'-most EST	LIB3234-003-P1-K1-E6
Method	BLASTX
NCBI GI	g4001805
BLAST score	230
E value	7.0e-19
Match length	118
% identity	41
NCBI Description	(AF041476) BAF53a [Mus musculus]

Seq. No.	126315
Contig ID	20345_1.R1010
5'-most EST	LIB24-046-Q1-E1-A4
Method	BLASTX
NCBI GI	g3450842
BLAST score	372
E value	9.0e-36
Match length	94
% identity	68
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	126316
Contig ID	20347_1.R1010
5'-most EST	LIB24-046-Q1-E1-A6
Method	BLASTX
NCBI GI	g4309734
BLAST score	593
E value	1.0e-61
Match length	118
% identity	100
NCBI Description	(AC006439) putative 26S proteosome regulatory subunit 8 [Arabidopsis thaliana]

Seq. No.	126317
Contig ID	20348_1.R1010
5'-most EST	jC-atXLIB327402P4g02b1
Method	BLASTX
NCBI GI	g3738331
BLAST score	420
E value	3.0e-41
Match length	75
% identity	100
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	126318
Contig ID	20350_1.R1010
5'-most EST	jC-atXP38C158J22T7d1

Seq. No.	126319
Contig ID	20359_1.R1010
5'-most EST	jC-atXP98CH2H7T7061d1

Seq. No.	126320
Contig ID	20359_2.R1010
5'-most EST	jC-atXLIB327432P4a10b1

Seq. No.	126321
Contig ID	20362_1.R1010
5'-most EST	LIB24-046-Q1-E1-C10
Method	BLASTN
NCBI GI	g3449322
BLAST score	122
E value	5.0e-62
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	126322
Contig ID	20366_1.R1010
5'-most EST	g2733894

Seq. No.	126323
Contig ID	20369_1.R1010
5'-most EST	LIB24-046-Q1-E1-C6
Method	BLASTX
NCBI GI	g3915196

BLAST score	152
E value	7.0e-10
Match length	78
% identity	42
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-C (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_1493838 (U52949) cyclin-specific ubiquitin carrier protein E2-C [Spisula solidissima]

Seq. No.	126324
Contig ID	20371_1.R1010
5'-most EST	ARABL1-037-Q1-E1-H10
Method	BLASTN
NCBI GI	g2477521
BLAST score	353
E value	0.0e+00
Match length	353
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126325
Contig ID	20382_1.R1010
5'-most EST	LIB24-046-Q1-E1-E3
Method	BLASTX
NCBI GI	g4115360
BLAST score	577
E value	8.0e-60
Match length	108
% identity	100
NCBI Description	(AC005957) putative lipid transfer protein [Arabidopsis thaliana]

Seq. No.	126326
Contig ID	20386_1.R1010
5'-most EST	LIB24-046-Q1-E1-E7
Method	BLASTX
NCBI GI	g4544445
BLAST score	221
E value	7.0e-18
Match length	110
% identity	45
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	126327
Contig ID	20387_1.R1010
5'-most EST	jC-atXLIB327424P1d05a1
Method	BLASTX
NCBI GI	g3776023
BLAST score	331
E value	8.0e-31
Match length	108
% identity	63
NCBI Description	(AJ010473) RNA helicase [Arabidopsis thaliana]

Seq. No. 126328

Contig ID	20389_1.R1010
5'-most EST	LIB24-128-Q1-E1-E10

Seq. No.	126329
Contig ID	20390_1.R1010
5'-most EST	jC-atXLIB327431P2f08a1
Method	BLASTN
NCBI GI	g836895
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	126330
Contig ID	20392_1.R1010
5'-most EST	jC-atXLIB327401P3e05b2
Method	BLASTX
NCBI GI	g541858
BLAST score	381
E value	1.0e-36
Match length	122
% identity	55
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	126331
Contig ID	20397_1.R1010
5'-most EST	jC-alXLIB327436P1e12b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	282
E value	1.0e-157
Match length	1177
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126332
Contig ID	20397_3.R1010
5'-most EST	jC-atXP73C224C7T7b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	288
E value	1.0e-161
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126333
Contig ID	20398_1.R1010
5'-most EST	jC-atXLIB327416P2d01a1
Method	BLASTN
NCBI GI	g3510339

BLAST score	301
E value	1.0e-169
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	126334
Contig ID	20415_1.R1010
5'-most EST	jC-atXmonuni10Dc05a1
Method	BLASTX
NCBI GI	g2335099
BLAST score	349
E value	8.0e-33
Match length	114
% identity	60
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	126335
Contig ID	20416_1.R1010
5'-most EST	jC-atXLIB327438P3b11a2

Seq. No.	126336
Contig ID	20417_1.R1010
5'-most EST	jC-atX24047Q1E1A01b1

Seq. No.	126337
Contig ID	20427_1.R1010
5'-most EST	jC-alXLIB327434P4g04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	78
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126338
Contig ID	20428_1.R1010
5'-most EST	jC-atXLIB327403P1d04b1
Method	BLASTN
NCBI GI	g2924729
BLAST score	82
E value	5.0e-38
Match length	341
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	126339
Contig ID	20434_1.R1010
5'-most EST	jC-atX24047Q1E1B03b1
Method	BLASTN
NCBI GI	g4757415
BLAST score	293
E value	1.0e-164

Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	126340
Contig ID	20435_1.R1010
5'-most EST	jC-atX24047Q1E1B04b1
Method	BLASTX
NCBI GI	g730502
BLAST score	497
E value	3.0e-50
Match length	145
% identity	66
NCBI Description	ACTIVATOR 1 41 KD SUBUNIT (REPLICATION FACTOR C 41 KD SUBUNIT) >gi_626873_pir__S45531 replication factor C chain RFC2 - yeast (Saccharomyces cerevisiae) >gi_498463_dbj_BAA05858_ (D28499) Rfc2 protein [Saccharomyces cerevisiae] >gi_841464 (U26028) Rfc2p [Saccharomyces cerevisiae] >gi_1015747_emb_CAA89596_ (Z49568) ORF YJR068w [Saccharomyces cerevisiae] >gi_1019690 (L47993) ORF YJR068w [Saccharomyces cerevisiae]

Seq. No.	126341
Contig ID	20440_1.R1010
5'-most EST	jC-atXLIB327403P3d10b2
Method	BLASTN
NCBI GI	g3242700
BLAST score	110
E value	1.0e-54
Match length	118
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126342
Contig ID	20448_1.R1010
5'-most EST	jC-atXP71C222I11T7057d1
Method	BLASTX
NCBI GI	g4678333
BLAST score	639
E value	7.0e-84
Match length	194
% identity	84
NCBI Description	(AL049658) H+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	126343
Contig ID	20449_1.R1010
5'-most EST	jC-atXLIB327403P1e06b1

Seq. No.	126344
Contig ID	20457_1.R1010
5'-most EST	LIB24-047-Q1-E1-D9
Method	BLASTX
NCBI GI	g3540198
BLAST score	869

E value	2.0e-93
Match length	180
% identity	93
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	126345
Contig ID	20460_1.R1010
5'-most EST	jC-atX24047Q1E1E11b1
Method	BLASTN
NCBI GI	g4309719
BLAST score	198
E value	1.0e-107
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126346
Contig ID	20462_1.R1010
5'-most EST	LIB24-047-Q1-E1-E2
Method	BLASTX
NCBI GI	g3025299
BLAST score	363
E value	1.0e-34
Match length	73
% identity	96
NCBI Description	HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660 (AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No.	126347
Contig ID	20463_1.R1010
5'-most EST	jC-atXLIB327403P3e07b2
Method	BLASTN
NCBI GI	g4406790
BLAST score	196
E value	1.0e-106
Match length	297
% identity	67
NCBI Description	Arabidopsis thaliana chromosome II BAC T1016 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126348
Contig ID	20469_1.R1010
5'-most EST	LIB3175-027-P1-K1-F7
Method	BLASTN
NCBI GI	g4757395
BLAST score	185
E value	1.0e-99
Match length	502
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	126349
Contig ID	20471_1.R1010
5'-most EST	LIB3168-072-P1-K1-F7
Method	BLASTX

NCBI GI	g3193331
BLAST score	298
E value	1.0e-26
Match length	104
% identity	96
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	126350
Contig ID	20472_1.R1010
5'-most EST	LIB24-047-Q1-E1-H1
Method	BLASTX
NCBI GI	g4835230
BLAST score	225
E value	2.0e-18
Match length	121
% identity	38
NCBI Description	(AL049862) putative LEA protein [Arabidopsis thaliana]

Seq. No.	126351
Contig ID	20473_1.R1010
5'-most EST	LIB3168-054-P1-K1-H10

Seq. No.	126352
Contig ID	20476_1.R1010
5'-most EST	jC-atXLIB327430P1g04b1
Method	BLASTX
NCBI GI	g3980403
BLAST score	701
E value	4.0e-74
Match length	146
% identity	93
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	126353
Contig ID	20483_2.R1010
5'-most EST	jC-atXLIB327411P3f03b1
Method	BLASTX
NCBI GI	g2827559
BLAST score	265
E value	1.0e-22
Match length	67
% identity	79
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	126354
Contig ID	20483_3.R1010
5'-most EST	jC-alX24077Q1E1H05b1
Method	BLASTX
NCBI GI	g2827559
BLAST score	122
E value	4.0e-17
Match length	59
% identity	75
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

>gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	126355
Contig ID	20483_4.R1010
5'-most EST	jC-alX24077Q1E1H05a1
Method	BLASTX
NCBI GI	g4586109
BLAST score	281
E value	7.0e-25
Match length	67
% identity	75
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	126356
Contig ID	20483_6.R1010
5'-most EST	g2704851
Method	BLASTX
NCBI GI	g4586109
BLAST score	259
E value	2.0e-22
Match length	62
% identity	77
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	126357
Contig ID	20485_1.R1010
5'-most EST	jC-atXLIB327431P1d03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	35
E value	5.0e-10
Match length	50
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	126358
Contig ID	20486_1.R1010
5'-most EST	LIB24-047-Q1-E1-G3

Seq. No.	126359
Contig ID	20491_1.R1010
5'-most EST	jC-atXLIB327403P1f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	2.0e-09
Match length	46
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126360
Contig ID	20501_1.R1010
5'-most EST	jC-atX24047Q1E1H07b1
Method	BLASTN

NCBI GI g3702734
BLAST score 178
E value 3.0e-95
Match length 412
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No. 126361
Contig ID 20506_1.R1010
5'-most EST LIB24-048-Q1-E2-A6
Method BLASTX
NCBI GI g4455367
BLAST score 697
E value 8.0e-74
Match length 134
% identity 99
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 126362
Contig ID 20508_1.R1010
5'-most EST jC-atXLIB327403P3d01b2
Method BLASTX
NCBI GI g2501850
BLAST score 326
E value 2.0e-58
Match length 133
% identity 84
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No. 126363
Contig ID 20516_1.R1010
5'-most EST g936572
Method BLASTN
NCBI GI g2980757
BLAST score 420
E value 0.0e+00
Match length 934
% identity 97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No. 126364
Contig ID 20517_1.R1010
5'-most EST jC-alXLIB327436P2h01b1
Method BLASTX
NCBI GI g4468813
BLAST score 614
E value 2.0e-65
Match length 142
% identity 92
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 126365
Contig ID 20519_1.R1010
5'-most EST jC-atXLIB327403P3e01b2
Method BLASTN

NCBI GI g2656028
BLAST score 440
E value 0.0e+00
Match length 444
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No. 126366
Contig ID 20523_1.R1010
5'-most EST jC-atXP39C162A23T7d1
Method BLASTX
NCBI GI g4678226
BLAST score 602
E value 2.0e-62
Match length 139
% identity 88
NCBI Description (AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No. 126367
Contig ID 20529_1.R1010
5'-most EST LIB24-048-Q1-E2-F8

Seq. No. 126368
Contig ID 20533_1.R1010
5'-most EST jC-atXLIB327403P1f11b1
Method BLASTN
NCBI GI g2244788
BLAST score 321
E value 0.0e+00
Match length 420
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 126369
Contig ID 20536_1.R1010
5'-most EST g958206

Seq. No. 126370
Contig ID 20537_1.R1010
5'-most EST LIB24-048-Q1-E1-G8
Method BLASTX
NCBI GI g1001478
BLAST score 283
E value 2.0e-25
Match length 109
% identity 45
NCBI Description (D63999) hypothetical protein [Synechocystis sp.]

Seq. No. 126371
Contig ID 20539_1.R1010
5'-most EST LIB24-048-Q1-E1-H2
Method BLASTX
NCBI GI g4056453
BLAST score 321

E value	2.0e-29
Match length	111
% identity	59
NCBI Description	(AC005990) EST gb_AA597511 comes from this gene. [Arabidopsis thaliana]

Seq. No.	126372
Contig ID	20540_2.R1010
5'-most EST	jC-atXLIB327421P2d10b1
Method	BLASTN
NCBI GI	g2914688
BLAST score	225
E value	1.0e-123
Match length	607
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126373
Contig ID	20540_3.R1010
5'-most EST	jC-atXLIB327401P4c09b2
Method	BLASTN
NCBI GI	g2914688
BLAST score	224
E value	1.0e-122
Match length	521
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126374
Contig ID	20540_4.R1010
5'-most EST	jC-atX24048Q1E1H03b1
Method	BLASTN
NCBI GI	g2914688
BLAST score	98
E value	1.0e-47
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126375
Contig ID	20540_5.R1010
5'-most EST	g1159502
Method	BLASTX
NCBI GI	g4586044
BLAST score	283
E value	5.0e-25
Match length	54
% identity	96
NCBI Description	(AC007020) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	126376
Contig ID	20543_1.R1010
5'-most EST	LIB25-080-Q1-E1-A2

Seq. No.	126377
Contig ID	20544_1.R1010
5'-most EST	LIB3168-078-P1-K1-H2
Method	BLASTX
NCBI GI	g3434971
BLAST score	313
E value	8.0e-29
Match length	102
% identity	64
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	126378
Contig ID	20547_1.R1010
5'-most EST	jC-atXP73C224B2T7b1
Method	BLASTN
NCBI GI	g4584841
BLAST score	495
E value	0.0e+00
Match length	531
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	126379
Contig ID	20548_1.R1010
5'-most EST	jC-atXLIB327403P1d03b1
Method	BLASTX
NCBI GI	g2496879
BLAST score	198
E value	6.0e-15
Match length	203
% identity	28
NCBI Description	HYPOTHETICAL 93.8 KD PROTEIN C05D11.2 IN CHROMOSOME III >gi_485089 (U00048) weakly similar to S. cerevisiae VPS16 protein [Caenorhabditis elegans]

Seq. No.	126380
Contig ID	20551_1.R1010
5'-most EST	LIB35-038-Q1-E1-G9
Method	BLASTX
NCBI GI	g2565275
BLAST score	571
E value	7.0e-66
Match length	142
% identity	79
NCBI Description	(AF023611) Dim1p homolog [Homo sapiens]

Seq. No.	126381
Contig ID	20564_1.R1010
5'-most EST	g934670
Method	BLASTX
NCBI GI	g4512678
BLAST score	254
E value	3.0e-21
Match length	282

% identity	32
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	126382
Contig ID	20567_2.R1010
5'-most EST	jC-atX24048Q1E2D04b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	189
E value	1.0e-102
Match length	367
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	126383
Contig ID	20570_1.R1010
5'-most EST	jC-alX24077Q1E1D04b1

Seq. No.	126384
Contig ID	20592_1.R1010
5'-most EST	LIB25-049-Q1-E1-B3
Method	BLASTN
NCBI GI	g2244788
BLAST score	401
E value	0.0e+00
Match length	479
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126385
Contig ID	20594_1.R1010
5'-most EST	jC-alXLIB327434P4a06b1
Method	BLASTX
NCBI GI	g4582441
BLAST score	376
E value	7.0e-36
Match length	142
% identity	44
NCBI Description	(AC007142) unknown protein [Arabidopsis thaliana]

Seq. No.	126386
Contig ID	20598_1.R1010
5'-most EST	jC-atX24049Q1E2B01b1
Method	BLASTX
NCBI GI	g3047125
BLAST score	411
E value	2.0e-44
Match length	126
% identity	78
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	126387
Contig ID	20599_1.R1010
5'-most EST	jC-atX24049Q1E2B02b1
Method	BLASTX

NCBI GI	g3024583
BLAST score	547
E value	3.0e-56
Match length	129
% identity	86
NCBI Description	RT14 PROTEIN HOMOLOG >gi_2347196 (AC002338) RT14 protein isolog [Arabidopsis thaliana]

Seq. No.	126388
Contig ID	20602_1.R1010
5'-most EST	LIB35-045-Q1-E1-B5
Method	BLASTN
NCBI GI	g3869069
BLAST score	149
E value	4.0e-78
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	126389
Contig ID	20605_1.R1010
5'-most EST	LIB24-049-Q1-E2-B9
Method	BLASTN
NCBI GI	g1769892
BLAST score	76
E value	1.0e-34
Match length	260
% identity	97
NCBI Description	A.thaliana bas1 gene

Seq. No.	126390
Contig ID	20609_1.R1010
5'-most EST	jC-atX24049Q1E2C04b1
Method	BLASTN
NCBI GI	g2244829
BLAST score	275
E value	1.0e-153
Match length	453
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126391
Contig ID	20611_1.R1010
5'-most EST	g1215904

Seq. No.	126392
Contig ID	20612_1.R1010
5'-most EST	jC-atX24049Q1E1C07b1
Method	BLASTX
NCBI GI	g3420050
BLAST score	608
E value	2.0e-63
Match length	119
% identity	92
NCBI Description	(AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126393
Contig ID	20618_1.R1010
5'-most EST	jC-alX24078Q1E1D10b1
Method	BLASTN
NCBI GI	g2244829
BLAST score	80
E value	5.0e-37
Match length	397
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126394
Contig ID	20620_1.R1010
5'-most EST	LIB3168-030-P1-K1-H12

Seq. No.	126395
Contig ID	20622_1.R1010
5'-most EST	LIB24-049-Q1-E1-D7

Seq. No.	126396
Contig ID	20628_1.R1010
5'-most EST	LIB24-049-Q1-E1-E3
Method	BLASTN
NCBI GI	g3702315
BLAST score	125
E value	5.0e-64
Match length	258
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126397
Contig ID	20631_1.R1010
5'-most EST	jC-atXLIB327408P4g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	5.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126398
Contig ID	20635_1.R1010
5'-most EST	LIB24-049-Q1-E2-F11
Method	BLASTX
NCBI GI	g2331036
BLAST score	224
E value	2.0e-18
Match length	138
% identity	38
NCBI Description	(AF012822) cleavage and polyadenylation specificity factor [Mus musculus]

Seq. No.	126399
Contig ID	20636_1.R1010
5'-most EST	LIB24-049-Q1-E2-F2
Method	BLASTX
NCBI GI	g3201626
BLAST score	502
E value	4.0e-51
Match length	101
% identity	94
NCBI Description	(AC004669) putative protein kinase MAP3K [Arabidopsis thaliana]

Seq. No.	126400
Contig ID	20642_1.R1010
5'-most EST	jC-atX24049Q1E2F08b1

Seq. No.	126401
Contig ID	20645_1.R1010
5'-most EST	LIB3234-077-P1-K1-E8
Method	BLASTN
NCBI GI	g4581138
BLAST score	368
E value	0.0e+00
Match length	525
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	126402
Contig ID	20649_1.R1010
5'-most EST	LIB25-004-Q1-E1-H1
Method	BLASTN
NCBI GI	g3805839
BLAST score	220
E value	1.0e-120
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	126403
Contig ID	20658_1.R1010
5'-most EST	LIB24-049-Q1-E2-H3
Method	BLASTN
NCBI GI	g4757404
BLAST score	83
E value	2.0e-38
Match length	317
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	126404
Contig ID	20660_1.R1010
5'-most EST	LIB24-049-Q1-E2-H5
Method	BLASTX
NCBI GI	g4467147

BLAST score	372
E value	1.0e-35
Match length	161
% identity	53
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	126405
Contig ID	20661_1.R1010
5'-most EST	LIB24-049-Q1-E2-H6
Method	BLASTN
NCBI GI	g2351061
BLAST score	255
E value	1.0e-141
Match length	319
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	126406
Contig ID	20662_1.R1010
5'-most EST	LIB24-049-Q1-E1-H7

Seq. No.	126407
Contig ID	20673_1.R1010
5'-most EST	g2048544
Method	BLASTX
NCBI GI	g4056456
BLAST score	545
E value	8.0e-56
Match length	106
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	126408
Contig ID	20673_2.R1010
5'-most EST	g1054257
Method	BLASTX
NCBI GI	g4056456
BLAST score	721
E value	1.0e-76
Match length	148
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	126409
Contig ID	20674_1.R1010
5'-most EST	jC-atXLIB327403P1d10a1
Method	BLASTN
NCBI GI	g4558521
BLAST score	195
E value	1.0e-105

Match length	195
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	126410
Contig ID	20683_1.R1010
5'-most EST	jC-atXLIB327403P3d05b2
Method	BLASTX
NCBI GI	g2130442
BLAST score	184
E value	2.0e-13
Match length	149
% identity	30
NCBI Description	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment) >gi_1052534_emb_CAA91511_ (Z66569) unknown [Schizosaccharomyces pombe]

Seq. No.	126411
Contig ID	20685_1.R1010
5'-most EST	jC-atXLIB327438P4g11a2
Method	BLASTX
NCBI GI	g3386597
BLAST score	582
E value	3.0e-60
Match length	109
% identity	100
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi_3702347 (AC005397) putative permease [Arabidopsis thaliana]

Seq. No.	126412
Contig ID	20706_1.R1010
5'-most EST	jC-atXLIB327406P2a12b1
Method	BLASTN
NCBI GI	g2815404
BLAST score	160
E value	1.0e-84
Match length	445
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	126413
Contig ID	20748_1.R1010
5'-most EST	jC-atXLIB327403P3c12b2
Method	BLASTN
NCBI GI	g2924651
BLAST score	176
E value	4.0e-94
Match length	462
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 126414

Contig ID	20753_1.R1010
5'-most EST	jC-atX24050Q1E1B05b1
Method	BLASTN
NCBI GI	g3046850
BLAST score	164
E value	5.0e-87
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	126415
Contig ID	20755_1.R1010
5'-most EST	LIB3175-003-P1-K1-C3
Method	BLASTN
NCBI GI	g4063735
BLAST score	125
E value	8.0e-64
Match length	391
% identity	99
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	126416
Contig ID	20772_1.R1010
5'-most EST	jC-atX24050Q1E1E05b1
Method	BLASTX
NCBI GI	g3046696
BLAST score	411
E value	3.0e-40
Match length	118
% identity	72
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	126417
Contig ID	20773_1.R1010
5'-most EST	jC-atXLIB327403P1e09b1
Method	BLASTN
NCBI GI	g1931636
BLAST score	282
E value	1.0e-157
Match length	463
% identity	99
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	126418
Contig ID	20774_1.R1010
5'-most EST	LIB24-050-Q1-E1-E7
Method	BLASTX
NCBI GI	g4325367
BLAST score	210
E value	3.0e-16
Match length	193
% identity	35
NCBI Description	(AF128396) contains similarity to Nicotiana tabacum B-type cyclin (GB:D50737) [Arabidopsis thaliana]

Seq. No.	126419
Contig ID	20780_1.R1010
5'-most EST	LIB24-050-Q1-E1-F5
Method	BLASTN
NCBI GI	g3297806
BLAST score	270
E value	1.0e-150
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	126420
Contig ID	20781_1.R1010
5'-most EST	jC-atXLIB327406P1f05b1
Method	BLASTX
NCBI GI	g1362009
BLAST score	610
E value	2.0e-63
Match length	141
% identity	58
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	126421
Contig ID	20784_1.R1010
5'-most EST	LIB25-078-Q1-E1-B10
Method	BLASTX
NCBI GI	g3335333
BLAST score	597
E value	6.0e-62
Match length	144
% identity	85
NCBI Description	(AC004512) Similar to chloroplast membrane-associated 30KD protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this gene. [Arabidopsis thaliana]

Seq. No.	126422
Contig ID	20785_1.R1010
5'-most EST	jC-atXLIB327422P1h06b1
Method	BLASTX
NCBI GI	g4558591
BLAST score	623
E value	6.0e-65
Match length	125
% identity	100
NCBI Description	(AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana] >gi_4662638_gb_AAD26909.1_AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	126423
Contig ID	20799_1.R1010
5'-most EST	jC-atX24050Q1E1H08b1
Method	BLASTX
NCBI GI	g1256509
BLAST score	464
E value	2.0e-46

Match length	119
% identity	67
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	126424
Contig ID	20801_1.R1010
5'-most EST	g2757621
Method	BLASTX
NCBI GI	g3033398
BLAST score	843
E value	8.0e-91
Match length	160
% identity	99
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	126425
Contig ID	20804_1.R1010
5'-most EST	LIB25-036-Q1-E1-F3
Method	BLASTN
NCBI GI	g3746057
BLAST score	181
E value	3.0e-97
Match length	439
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126426
Contig ID	20807_1.R1010
5'-most EST	LIB24-051-Q1-E1-C1
Method	BLASTX
NCBI GI	g2344901
BLAST score	606
E value	3.0e-63
Match length	127
% identity	91
NCBI Description	(AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]

Seq. No.	126427
Contig ID	20811_1.R1010
5'-most EST	jC-atX24051Q1E1C03b1
Method	BLASTX
NCBI GI	g728868
BLAST score	239
E value	5.0e-20
Match length	78
% identity	54
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) >gi_99824_pir__S16748 proline-rich protein - rape (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich protein [Brassica napus]

Seq. No.	126428
Contig ID	20813_1.R1010
5'-most EST	LIB24-051-Q1-E1-C8

Method	BLASTX
NCBI GI	g2245004
BLAST score	651
E value	2.0e-68
Match length	151
% identity	87
NCBI Description	(Z97341) similarity to membrane transport protein [Arabidopsis thaliana]

Seq. No.	126429
Contig ID	20823_1.R1010
5'-most EST	g934866
Method	BLASTX
NCBI GI	g3386615
BLAST score	618
E value	4.0e-66
Match length	136
% identity	90
NCBI Description	(AC004665) putative phosphomannomutase [Arabidopsis thaliana]

Seq. No.	126430
Contig ID	20830_1.R1010
5'-most EST	LIB24-051-Q1-E1-F10
Method	BLASTN
NCBI GI	g3242700
BLAST score	657
E value	0.0e+00
Match length	759
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126431
Contig ID	20838_1.R1010
5'-most EST	jC-atXP69C217P10T7084d1
Method	BLASTX
NCBI GI	g1350930
BLAST score	761
E value	6.0e-81
Match length	150
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	126432
Contig ID	20838_3.R1010
5'-most EST	g3449655
Method	BLASTX
NCBI GI	g1350930
BLAST score	327
E value	2.0e-30
Match length	70
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	126433
Contig ID	20841_1.R1010

5'-most EST	jC-atXLIB327430P3e09b1
Method	BLASTX
NCBI GI	g4417304
BLAST score	458
E value	1.0e-45
Match length	155
% identity	54
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	126434
Contig ID	20845_2.R1010
5'-most EST	jC-alX24087Q1E1B08b1

Seq. No.	126435
Contig ID	20848_1.R1010
5'-most EST	LIB3176-037-P1-K1-F7
Method	BLASTX
NCBI GI	g3341679
BLAST score	1051
E value	1.0e-115
Match length	254
% identity	75
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	126436
Contig ID	20854_1.R1010
5'-most EST	LIB24-052-Q1-E1-A11

Seq. No.	126437
Contig ID	20855_1.R1010
5'-most EST	jC-atXLIB327403P3f07b2
Method	BLASTN
NCBI GI	g3869075
BLAST score	403
E value	0.0e+00
Match length	448
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	126438
Contig ID	20858_1.R1010
5'-most EST	jC-atXP78CF4F5T7b1
Method	BLASTX
NCBI GI	g3540181
BLAST score	208
E value	5.0e-16
Match length	147
% identity	35
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	126439
Contig ID	20860_1.R1010
5'-most EST	LIB24-052-Q1-E2-B1

Method	BLASTN
NCBI GI	g2828184
BLAST score	107
E value	3.0e-53
Match length	263
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	126440
Contig ID	20861_1.R1010
5'-most EST	jC-atXLIB327427P1c10b1
Method	BLASTN
NCBI GI	g2477521
BLAST score	321
E value	1.0e-180
Match length	475
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126441
Contig ID	20862_1.R1010
5'-most EST	LIB3234-041-P1-K1-E2
Method	BLASTX
NCBI GI	g2494842
BLAST score	281
E value	9.0e-25
Match length	137
% identity	46
NCBI Description	GLUCOSYLTRANSFERASE ALG6 >gi_2131171_pir__S61985 ALG6 protein - yeast (Saccharomyces cerevisiae) >gi_1150997 (U43491) hypothetical protein UNA544 [Saccharomyces cerevisiae] >gi_1420090_emb_CAA99190_ (Z74910) ORF YOR002w [Saccharomyces cerevisiae]

Seq. No.	126442
Contig ID	20864_1.R1010
5'-most EST	jC-atXLIB327409P4d03b1
Method	BLASTN
NCBI GI	g2828278
BLAST score	166
E value	4.0e-88
Match length	142
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	126443
Contig ID	20864_3.R1010
5'-most EST	jC-atXLIB327403P1g04b1
Method	BLASTN
NCBI GI	g2828278
BLAST score	269
E value	1.0e-149
Match length	427
% identity	100

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)
Seq. No.	126444
Contig ID	20868_1.R1010
5'-most EST	LIB24-052-Q1-E1-B8
Method	BLASTX
NCBI GI	g4678339
BLAST score	338
E value	7.0e-32
Match length	104
% identity	66
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]
Seq. No.	126445
Contig ID	20869_1.R1010
5'-most EST	LIB25-026-Q1-E1-A2
Method	BLASTN
NCBI GI	g4580454
BLAST score	357
E value	0.0e+00
Match length	734
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence
Seq. No.	126446
Contig ID	20870_1.R1010
5'-most EST	jC-atXLIB327403P1g11b1
Method	BLASTN
NCBI GI	g3449322
BLAST score	179
E value	5.0e-96
Match length	375
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]
Seq. No.	126447
Contig ID	20881_1.R1010
5'-most EST	LIB24-052-Q1-E2-D2
Method	BLASTN
NCBI GI	g4587641
BLAST score	263
E value	1.0e-146
Match length	267
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence
Seq. No.	126448
Contig ID	20886_1.R1010
5'-most EST	jC-atXLIB327403P3g06b2
Method	BLASTX
NCBI GI	g3478637
BLAST score	328
E value	1.0e-34

Match length	129
% identity	57
NCBI Description	(AC005546) R29425_1 [Homo sapiens]

Seq. No.	126449
Contig ID	20891_1.R1010
5'-most EST	LIB24-052-Q1-E1-E2
Method	BLASTN
NCBI GI	g2739359
BLAST score	170
E value	7.0e-91
Match length	285
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126450
Contig ID	20893_1.R1010
5'-most EST	LIB24-082-Q1-E1-G4
Method	BLASTX
NCBI GI	g2623956
BLAST score	158
E value	1.0e-10
Match length	121
% identity	34
NCBI Description	(AJ002477) Ananain precursor [Ananas comosus]

Seq. No.	126451
Contig ID	20894_1.R1010
5'-most EST	LIB24-052-Q1-E1-E5
Method	BLASTX
NCBI GI	g2749982
BLAST score	325
E value	3.0e-30
Match length	107
% identity	62
NCBI Description	(AF036705) Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans cDNA yk257d4.5;

Seq. No.	126452
Contig ID	20902_1.R1010
5'-most EST	LIB3176-032-P1-K1-D4
Method	BLASTN
NCBI GI	g2264310
BLAST score	274
E value	1.0e-152
Match length	1052
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	126453
Contig ID	20905_1.R1010
5'-most EST	jC-a1X24086Q1E1A11b1

Method	BLASTX
NCBI GI	g2665890
BLAST score	736
E value	4.0e-78
Match length	157
% identity	87
NCBI Description	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No.	126454
Contig ID	20908_1.R1010
5'-most EST	jC-atX24052Q1E1G02b1
Method	BLASTX
NCBI GI	g3540208
BLAST score	1125
E value	1.0e-123
Match length	213
% identity	99
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	126455
Contig ID	20909_1.R1010
5'-most EST	jC-atXLIB327403P3h01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	55
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126456
Contig ID	20910_1.R1010
5'-most EST	LIB3234-016-P1-K1-F9
Method	BLASTN
NCBI GI	g4589410
BLAST score	325
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	126457
Contig ID	20917_1.R1010
5'-most EST	LIB24-052-Q1-E1-H3
Method	BLASTN
NCBI GI	g4371278
BLAST score	216
E value	1.0e-118
Match length	228
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126458

Contig ID	20919_1.R1010
5'-most EST	LIB24-052-Q1-E1-H5
Method	BLASTN
NCBI GI	g2564049
BLAST score	185
E value	1.0e-100
Match length	287
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	126459
Contig ID	20920_1.R1010
5'-most EST	jC-alXLIB327435P4f06b1
Method	BLASTX
NCBI GI	g2245061
BLAST score	920
E value	1.0e-99
Match length	200
% identity	91
NCBI Description	(Z97342) Clp proteinase homolog [Arabidopsis thaliana]

Seq. No.	126460
Contig ID	20920_2.R1010
5'-most EST	jC-atXP52C181M9T7d2
Method	BLASTX
NCBI GI	g2245061
BLAST score	608
E value	3.0e-63
Match length	165
% identity	76
NCBI Description	(Z97342) Clp proteinase homolog [Arabidopsis thaliana]

Seq. No.	126461
Contig ID	20934_1.R1010
5'-most EST	jC-alX24074Q1E1F10b1
Method	BLASTX
NCBI GI	g1730560
BLAST score	439
E value	2.0e-43
Match length	123
% identity	69
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]

Seq. No.	126462
Contig ID	20952_1.R1010
5'-most EST	jC-atXP38C160H19T7d1
Method	BLASTX
NCBI GI	g2983347
BLAST score	342
E value	9.0e-32
Match length	190
% identity	44
NCBI Description	(AE000707) hemolysin [Aquifex aeolicus]

Seq. No.	126463
Contig ID	20968_1.R1010
5'-most EST	jC-atXP46C172G16T7052d1
Method	BLASTX
NCBI GI	g4539452
BLAST score	685
E value	8.0e-75
Match length	219
% identity	64
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	126464
Contig ID	20999_1.R1010
5'-most EST	LIB24-053-Q1-E2-B4
Method	BLASTX
NCBI GI	g4586116
BLAST score	797
E value	7.0e-88
Match length	229
% identity	67
NCBI Description	(AL049638) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	126465
Contig ID	21004_1.R1010
5'-most EST	LIB24-053-Q1-E2-F10

Seq. No.	126466
Contig ID	21008_1.R1010
5'-most EST	LIB24-053-Q1-E2-C5
Method	BLASTX
NCBI GI	g4587553
BLAST score	300
E value	3.0e-27
Match length	60
% identity	100
NCBI Description	(AC006577) F15I1.20 [Arabidopsis thaliana]

Seq. No.	126467
Contig ID	21011_1.R1010
5'-most EST	jC-atXLIB327403P1g06b1
Method	BLASTN
NCBI GI	g4220510
BLAST score	309
E value	1.0e-173
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	126468
Contig ID	21016_1.R1010
5'-most EST	LIB24-053-Q1-E2-D5
Method	BLASTN
NCBI GI	g2264315
BLAST score	324

E value	0.0e+00
Match length	369
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	126469
Contig ID	21022_1.R1010
5'-most EST	jC-atX24053Q1E1E02b1

Seq. No.	126470
Contig ID	21023_1.R1010
5'-most EST	LIB24-053-Q1-E2-E3
Method	BLASTN
NCBI GI	g4220643
BLAST score	153
E value	2.0e-80
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	126471
Contig ID	21030_1.R1010
5'-most EST	LIB24-053-Q1-E2-F3
Method	BLASTX
NCBI GI	g1169451
BLAST score	437
E value	2.0e-43
Match length	119
% identity	71
NCBI Description	PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir__S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana >gi_22677_emb_CAA49853_ (X70409) A6 [Arabidopsis thaliana] >gi_2244764_emb_CAB10187_ (Z97335) AMP-binding protein [Arabidopsis thaliana]

Seq. No.	126472
Contig ID	21033_1.R1010
5'-most EST	g937650
Method	BLASTX
NCBI GI	g3193330
BLAST score	265
E value	8.0e-23
Match length	93
% identity	60
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	126473
Contig ID	21039_1.R1010
5'-most EST	LIB24-053-Q1-E1-G2
Method	BLASTX
NCBI GI	g320553
BLAST score	275

E value	1.0e-24
Match length	74
% identity	80
NCBI Description	anthranilate synthase (EC 4.1.3.27) alpha-2 chain - Arabidopsis thaliana

Seq. No.	126474
Contig ID	21043_1.R1010
5'-most EST	jC-atXLIB327403P1h10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	1.0e-17
Match length	60
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126475
Contig ID	21050_1.R1010
5'-most EST	LIB3234-047-P1-K1-F5
Method	BLASTX
NCBI GI	g2586125
BLAST score	625
E value	5.0e-65
Match length	136
% identity	95
NCBI Description	(U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No.	126476
Contig ID	21051_1.R1010
5'-most EST	jC-atXLIB327403P3h05b2

Seq. No.	126477
Contig ID	21054_1.R1010
5'-most EST	jC-atX24053Q1E1H06b1
Method	BLASTN
NCBI GI	g2245073
BLAST score	344
E value	0.0e+00
Match length	742
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126478
Contig ID	21055_1.R1010
5'-most EST	g2748496
Method	BLASTN
NCBI GI	g2828183
BLAST score	358
E value	0.0e+00
Match length	412
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	126479
Contig ID	21056_1.R1010
5'-most EST	LIB24-053-Q1-E1-H8
Method	BLASTX
NCBI GI	g4586038
BLAST score	180
E value	3.0e-13
Match length	118
% identity	40
NCBI Description	(AC007109) putative heat shock protein [Arabidopsis thaliana]

Seq. No.	126480
Contig ID	21064_1.R1010
5'-most EST	jC-atXLIB327403P3f10b2
Method	BLASTN
NCBI GI	g3249094
BLAST score	201
E value	1.0e-109
Match length	649
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126481
Contig ID	21092_1.R1010
5'-most EST	jC-atXP26C128B15T7d1

Seq. No.	126482
Contig ID	21094_1.R1010
5'-most EST	LIB24-127-Q1-E1-D4
Method	BLASTN
NCBI GI	g4757391
BLAST score	275
E value	1.0e-153
Match length	275
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2C19, complete sequence

Seq. No.	126483
Contig ID	21100_1.R1010
5'-most EST	jC-atX24053Q1E2E08b1
Method	BLASTX
NCBI GI	g2129932
BLAST score	639
E value	6.0e-67
Match length	114
% identity	97
NCBI Description	myb-related transcription factor TMH1 - tomato >gi_1167486_emb_CAA64615_ (X95297) transcription factor [Lycopersicon esculentum]

Seq. No.	126484
Contig ID	21125_1.R1010
5'-most EST	jC-atXLIB327403P3f06b2
Method	BLASTN

NCBI GI	g3327922
BLAST score	157
E value	8.0e-83
Match length	379
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126485
Contig ID	21133_1.R1010
5'-most EST	jC-atXP32C147K13T7d2

Seq. No.	126486
Contig ID	21133_2.R1010
5'-most EST	g906576
Method	BLASTX
NCBI GI	g1350625
BLAST score	138
E value	2.0e-45
Match length	114
% identity	85
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L1 PRECURSOR >gi_577089_emb_CAA58020_ (X82776) chloroplast ribosomal protein L1 [Pisum sativum]

Seq. No.	126487
Contig ID	21133_3.R1010
5'-most EST	g1520543
Method	BLASTX
NCBI GI	g3602937
BLAST score	376
E value	7.0e-43
Match length	160
% identity	53
NCBI Description	(AF041468) ribosomal protein L1 [Guillardia theta]

Seq. No.	126488
Contig ID	21133_4.R1010
5'-most EST	jC-atXLIB327403P3f08b2
Method	BLASTX
NCBI GI	g3602937
BLAST score	207
E value	9.0e-16
Match length	86
% identity	49
NCBI Description	(AF041468) ribosomal protein L1 [Guillardia theta]

Seq. No.	126489
Contig ID	21133_5.R1010
5'-most EST	jC-atXLIB327424P3d04a1

Seq. No.	126490
Contig ID	21133_6.R1010
5'-most EST	LIB25-024-Q1-E1-E5

Seq. No.	126491
Contig ID	21135_1.R1010

5'-most EST	LIB24-062-Q1-E1-H5
Method	BLASTX
NCBI GI	g728867
BLAST score	1368
E value	1.0e-152
Match length	268
% identity	99
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi_99694_pir__S21961 proline-rich protein APG - Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana]

Seq. No.	126492
Contig ID	21136_1.R1010
5'-most EST	jC-atXLIB327401P4c11b2

Seq. No.	126493
Contig ID	21137_1.R1010
5'-most EST	jC-atXLIB327401P4f07b1

Seq. No.	126494
Contig ID	21137_2.R1010
5'-most EST	jC-atX24107Q1E1G11b1
Method	BLASTX
NCBI GI	g4309732
BLAST score	252
E value	1.0e-21
Match length	55
% identity	80
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126495
Contig ID	21147_1.R1010
5'-most EST	g2758024
Method	BLASTX
NCBI GI	g3128199
BLAST score	147
E value	5.0e-11
Match length	88
% identity	50
NCBI Description	(AC004521) putative proteinase [Arabidopsis thaliana]

Seq. No.	126496
Contig ID	21148_1.R1010
5'-most EST	LIB25-038-Q1-E1-H10
Method	BLASTN
NCBI GI	g4580386
BLAST score	183
E value	2.0e-98
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	126497
Contig ID	21150_1.R1010
5'-most EST	jC-atX24054Q1E1C04b1

Seq. No.	126498
Contig ID	21152_1.R1010
5'-most EST	LIB24-054-Q1-E1-C6
Method	BLASTX
NCBI GI	g4510342
BLAST score	142
E value	1.0e-08
Match length	56
% identity	62
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	126499
Contig ID	21155_1.R1010
5'-most EST	jC-atXLIB327403P3g04b2
Method	BLASTN
NCBI GI	g4165340
BLAST score	443
E value	0.0e+00
Match length	455
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126500
Contig ID	21161_1.R1010
5'-most EST	LIB24-054-Q1-E1-D6
Method	BLASTN
NCBI GI	g4584519
BLAST score	40
E value	4.0e-13
Match length	110
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)

Seq. No.	126501
Contig ID	21168_1.R1010
5'-most EST	jC-atXLIB327402P4b08b1
Method	BLASTN
NCBI GI	g4490324
BLAST score	252
E value	1.0e-139
Match length	467
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	126502
Contig ID	21168_2.R1010
5'-most EST	LIB3175-004-P1-K1-E2
Method	BLASTX
NCBI GI	g4490331
BLAST score	588
E value	6.0e-61
Match length	131

% identity	88
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.	126503
Contig ID	21174_1.R1010
5'-most EST	LIB3177-096-P1-K1-G3
Method	BLASTN
NCBI GI	g4757405
BLAST score	131
E value	2.0e-67
Match length	398
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence
Seq. No.	126504
Contig ID	21181_1.R1010
5'-most EST	jC-alX24087Q1E1B05b1
Seq. No.	126505
Contig ID	21184_1.R1010
5'-most EST	jC-alXLIB327436P1b10b1
Method	BLASTX
NCBI GI	g3461845
BLAST score	431
E value	2.0e-42
Match length	120
% identity	78
NCBI Description	(AC005315) hypothetical protein [Arabidopsis thaliana]
Seq. No.	126506
Contig ID	21187_1.R1010
5'-most EST	jC-atX24054Q1E1H04b2
Seq. No.	126507
Contig ID	21189_1.R1010
5'-most EST	jC-atX24055Q1E1A06b1
Method	BLASTX
NCBI GI	g4056552
BLAST score	381
E value	9.0e-37
Match length	104
% identity	64
NCBI Description	(AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]
Seq. No.	126508
Contig ID	21190_1.R1010
5'-most EST	LIB24-055-Q1-E1-B3
Method	BLASTN
NCBI GI	g2832689
BLAST score	435
E value	0.0e+00
Match length	435
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	126509
Contig ID	21193_1.R1010
5'-most EST	LIB3176-061-P1-K1-D11
Method	BLASTX
NCBI GI	g1362093
BLAST score	164
E value	3.0e-11
Match length	80
% identity	47
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	126510
Contig ID	21194_1.R1010
5'-most EST	LIB24-055-Q1-E1-F6
Method	BLASTN
NCBI GI	g4585896
BLAST score	344
E value	0.0e+00
Match length	424
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F13I13 genomic sequence, complete sequence

Seq. No.	126511
Contig ID	21195_1.R1010
5'-most EST	jC-atXLIB327421P3f01b1
Method	BLASTX
NCBI GI	g2253411
BLAST score	473
E value	6.0e-47
Match length	203
% identity	46
NCBI Description	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]

Seq. No.	126512
Contig ID	21196_1.R1010
5'-most EST	LIB3168-013-P1-K1-H8
Method	BLASTN
NCBI GI	g4185128
BLAST score	227
E value	1.0e-124
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126513
Contig ID	21200_1.R1010
5'-most EST	jC-atXLIB327404P2a01b1

Seq. No.	126514
Contig ID	21204_1.R1010
5'-most EST	LIB24-085-Q1-E1-B9
Method	BLASTN
NCBI GI	g3046851

BLAST score	212
E value	1.0e-116
Match length	377
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	126515
Contig ID	21207_1.R1010
5'-most EST	jC-atXLIB327406P4b05b2

Seq. No.	126516
Contig ID	21207_2.R1010
5'-most EST	LIB24-056-Q1-E2-B2

Seq. No.	126517
Contig ID	21211_1.R1010
5'-most EST	LIB24-056-Q1-E2-B7
Method	BLASTN
NCBI GI	g4454587
BLAST score	136
E value	2.0e-70
Match length	475
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	126518
Contig ID	21212_1.R1010
5'-most EST	LIB24-056-Q1-E2-B8
Method	BLASTX
NCBI GI	g417073
BLAST score	324
E value	5.0e-30
Match length	103
% identity	60
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	126519
Contig ID	21216_1.R1010
5'-most EST	jC-atXLIB327404P4b11b1

Seq. No.	126520
Contig ID	21216_2.R1010
5'-most EST	LIB24-056-Q1-E2-C5

Seq. No.	126521
Contig ID	21226_1.R1010
5'-most EST	LIB35-047-Q1-E1-F6

Seq. No.	126522
Contig ID	21229_1.R1010
5'-most EST	LIB24-056-Q1-E2-E3
Method	BLASTN

NCBI GI	g2264318
BLAST score	234
E value	1.0e-129
Match length	339
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	126523
Contig ID	21237_1.R1010
5'-most EST	LIB24-056-Q1-E2-F4
Method	BLASTX
NCBI GI	g3176690
BLAST score	1441
E value	1.0e-160
Match length	294
% identity	97
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	126524
Contig ID	21241_1.R1010
5'-most EST	LIB3177-045-P1-K2-D1
Method	BLASTX
NCBI GI	g627469
BLAST score	233
E value	3.0e-19
Match length	169
% identity	8
NCBI Description	hypothetical protein 2 - human (fragment)

Seq. No.	126525
Contig ID	21243_1.R1010
5'-most EST	jC-atX24056Q1E1G06b1
Method	BLASTX
NCBI GI	g3236241
BLAST score	700
E value	5.0e-74
Match length	166
% identity	80
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	126526
Contig ID	21261_1.R1010
5'-most EST	LIB24-058-Q1-E1-B8
Method	BLASTX
NCBI GI	g4406764
BLAST score	219
E value	2.0e-56
Match length	119
% identity	98
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No. 126527

Contig ID	21267_1.R1010
5'-most EST	jC-atXLIB327404P2b09b1
Method	BLASTN
NCBI GI	g3176693
BLAST score	386
E value	0.0e+00
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126528
Contig ID	21273_1.R1010
5'-most EST	LIB24-097-Q1-E1-G8
Method	BLASTX
NCBI GI	g3451071
BLAST score	297
E value	2.0e-26
Match length	142
% identity	89
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	126529
Contig ID	21282_1.R1010
5'-most EST	LIB24-058-Q1-E1-E11
Method	BLASTN
NCBI GI	g2244991
BLAST score	384
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126530
Contig ID	21284_1.R1010
5'-most EST	jC-atX24008Q1E1G05b1
Method	BLASTX
NCBI GI	g3819099
BLAST score	351
E value	3.0e-33
Match length	103
% identity	57
NCBI Description	(AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No.	126531
Contig ID	21285_2.R1010
5'-most EST	jC-atXLIB327404P1c09b1
Method	BLASTN
NCBI GI	g3402695
BLAST score	402
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126532
Contig ID	21288_1.R1010
5'-most EST	jC-atXLIB327404P2c05b1
Method	BLASTX
NCBI GI	g4455359
BLAST score	608
E value	3.0e-63
Match length	132
% identity	89
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	126533
Contig ID	21290_1.R1010
5'-most EST	jC-atX24058Q1E1F01b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	368
E value	0.0e+00
Match length	390
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	126534
Contig ID	21292_1.R1010
5'-most EST	jC-atXLIB327404P4c05a1
Method	BLASTN
NCBI GI	g4757678
BLAST score	250
E value	1.0e-138
Match length	290
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	126535
Contig ID	21292_2.R1010
5'-most EST	jC-atXLIB327404P4c05b1
Method	BLASTN
NCBI GI	g4757678
BLAST score	311
E value	1.0e-174
Match length	399
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	126536
Contig ID	21293_1.R1010
5'-most EST	g937329

Seq. No.	126537
Contig ID	21300_1.R1010
5'-most EST	LIB24-059-Q1-E1-F9

Seq. No.	126538

Contig ID	21315_1.R1010
5'-most EST	LIB25-007-Q1-E1-G1

Seq. No.	126539
Contig ID	21320_1.R1010
5'-most EST	jC-atXLIB327404P4a06b1
Method	BLASTX
NCBI GI	g4510412
BLAST score	156
E value	4.0e-10
Match length	156
% identity	28
NCBI Description	(AC006929) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	126540
Contig ID	21326_1.R1010
5'-most EST	jC-atXLIB327404P4a05b1
Method	BLASTX
NCBI GI	g4262143
BLAST score	930
E value	1.0e-100
Match length	183
% identity	100
NCBI Description	(AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126541
Contig ID	21331_1.R1010
5'-most EST	jC-alX24075Q1E1C09b1
Method	BLASTN
NCBI GI	g4589435
BLAST score	369
E value	0.0e+00
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	126542
Contig ID	21332_1.R1010
5'-most EST	LIB24-059-Q1-E1-B5

Seq. No.	126543
Contig ID	21340_1.R1010
5'-most EST	jC-atXLIB327404P1b09b1
Method	BLASTN
NCBI GI	g2656027
BLAST score	304
E value	1.0e-170
Match length	384
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJH22

Seq. No.	126544
Contig ID	21342_1.R1010
5'-most EST	g1216702

Method	BLASTX
NCBI GI	g2924785
BLAST score	598
E value	1.0e-61
Match length	314
% identity	10
NCBI Description	(AC002334) similar to disease resistance protein [Arabidopsis thaliana]

Seq. No.	126545
Contig ID	21346_1.R1010
5'-most EST	jC-atX24059Q1E1D01b1
Method	BLASTX
NCBI GI	g3643600
BLAST score	271
E value	9.0e-24
Match length	158
% identity	63
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126546
Contig ID	21347_1.R1010
5'-most EST	LIB24-059-Q1-E1-D10
Method	BLASTN
NCBI GI	g2275194
BLAST score	374
E value	0.0e+00
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126547
Contig ID	21353_1.R1010
5'-most EST	g2748087
Method	BLASTX
NCBI GI	g4503515
BLAST score	191
E value	4.0e-14
Match length	101
% identity	38
NCBI Description	UNKNOWN >gi_2351380 (U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens]

Seq. No.	126548
Contig ID	21355_1.R1010
5'-most EST	LIB3168-040-P1-K1-C12
Method	BLASTX
NCBI GI	g4490331
BLAST score	584
E value	3.0e-60
Match length	142
% identity	81
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126549
Contig ID	21361_1.R1010

5'-most EST	jC-atXLIB327404P2c07b1
Method	BLASTX
NCBI GI	g3785977
BLAST score	138
E value	2.0e-20
Match length	110
% identity	47
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	126550
Contig ID	21365_1.R1010
5'-most EST	jC-atXLIB327404P1c05b1
Method	BLASTX
NCBI GI	g3335372
BLAST score	650
E value	4.0e-68
Match length	120
% identity	99
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	126551
Contig ID	21366_1.R1010
5'-most EST	jC-atXLIB327404P1c06b1
Method	BLASTX
NCBI GI	g3970880
BLAST score	290
E value	5.0e-26
Match length	117
% identity	50
NCBI Description	(AB015724) nuclear receptor binding factor-1 [Rattus norvegicus]

Seq. No.	126552
Contig ID	21378_1.R1010
5'-most EST	LIB24-059-Q1-E1-G10
Method	BLASTN
NCBI GI	g3894179
BLAST score	344
E value	0.0e+00
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126553
Contig ID	21381_1.R1010
5'-most EST	jC-atXLIB327404P2d01b1
Method	BLASTX
NCBI GI	g4510395
BLAST score	293
E value	7.0e-70
Match length	140
% identity	99
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	126554
Contig ID	21382_1.R1010
5'-most EST	jC-atXP102CE4F3T7b1
Method	BLASTX
NCBI GI	g1255951
BLAST score	498
E value	4.0e-50
Match length	108
% identity	82
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	126555
Contig ID	21382_2.R1010
5'-most EST	jC-atXLIB327404P1d02b1
Method	BLASTX
NCBI GI	g1255951
BLAST score	602
E value	3.0e-62
Match length	135
% identity	80
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	126556
Contig ID	21382_3.R1010
5'-most EST	g2723110

Seq. No.	126557
Contig ID	21385_1.R1010
5'-most EST	jC-atXLIB327423P1g12b1
Method	BLASTX
NCBI GI	g2129578
BLAST score	477
E value	2.0e-47
Match length	218
% identity	50
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	126558
Contig ID	21389_1.R1010
5'-most EST	jC-atXLIB327416P3h12b1
Method	BLASTN
NCBI GI	g2760173
BLAST score	508
E value	0.0e+00
Match length	529
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	126559
Contig ID	21396_1.R1010
5'-most EST	jC-atX24060Q1E1A06b2
Method	BLASTX

NCBI GI	g3036807
BLAST score	407
E value	8.0e-40
Match length	125
% identity	70
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	126560
Contig ID	21400_1.R1010
5'-most EST	LIB25-080-Q1-E1-H10
Method	BLASTN
NCBI GI	g2351070
BLAST score	145
E value	8.0e-76
Match length	338
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	126561
Contig ID	21403_1.R1010
5'-most EST	LIB24-060-Q1-E1-A6

Seq. No.	126562
Contig ID	21405_1.R1010
5'-most EST	jC-alXLIB327436P3h12b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	8.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126563
Contig ID	21406_1.R1010
5'-most EST	LIB24-060-Q1-E1-A9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	48
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	126564
Contig ID	21407_1.R1010
5'-most EST	jC-atXLIB327404P4a09b1

Seq. No.	126565
Contig ID	21414_1.R1010
5'-most EST	jC-atXLIB327404P4a07b1
Method	BLASTX
NCBI GI	g1653089
BLAST score	313
E value	1.0e-28
Match length	122

% identity	53
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	126566
Contig ID	21416_1.R1010
5'-most EST	jC-atXP100CE1C2T7b1
Method	BLASTX
NCBI GI	g4204285
BLAST score	658
E value	8.0e-69
Match length	201
% identity	63
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	126567
Contig ID	21416_2.R1010
5'-most EST	jC-atXP31C147C2T7d2
Method	BLASTX
NCBI GI	g4204285
BLAST score	742
E value	1.0e-78
Match length	173
% identity	76
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	126568
Contig ID	21416_3.R1010
5'-most EST	g2763766
Method	BLASTN
NCBI GI	g2351068
BLAST score	249
E value	1.0e-138
Match length	269
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	126569
Contig ID	21416_5.R1010
5'-most EST	g1217371
Method	BLASTX
NCBI GI	g4204285
BLAST score	286
E value	2.0e-25
Match length	182
% identity	40
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	126570
Contig ID	21417_1.R1010
5'-most EST	jC-atXLIB327404P2b04b1
Method	BLASTX
NCBI GI	g3334144
BLAST score	204

E value	3.0e-35
Match length	127
% identity	63
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	126571
Contig ID	21418_1.R1010
5'-most EST	LIB25-096-Q1-E1-F4

Seq. No.	126572
Contig ID	21420_1.R1010
5'-most EST	jC-atXLIB327427P3c01b2
Method	BLASTX
NCBI GI	g4585875
BLAST score	170
E value	1.0e-108
Match length	203
% identity	92
NCBI Description	(AC005850) Unknown protein [Arabidopsis thaliana]

Seq. No.	126573
Contig ID	21421_1.R1010
5'-most EST	jC-atXLIB327404P2b06b1

Seq. No.	126574
Contig ID	21423_1.R1010
5'-most EST	jC-atXLIB327401P3g12b2
Method	BLASTX
NCBI GI	g4455159
BLAST score	1148
E value	1.0e-126
Match length	282
% identity	73
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	126575
Contig ID	21428_1.R1010
5'-most EST	LIB24-060-Q1-E1-D10
Method	BLASTN
NCBI GI	g4756963
BLAST score	235
E value	1.0e-129
Match length	679
% identity	74
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	126576
Contig ID	21431_1.R1010
5'-most EST	LIB24-060-Q1-E1-D4
Method	BLASTX
NCBI GI	g3819164
BLAST score	354
E value	1.0e-33
Match length	96
% identity	77

NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	126577
Contig ID	21432_1.R1010
5'-most EST	jC-atXLIB327404P1b10b1
Method	BLASTN
NCBI GI	g4589444
BLAST score	341
E value	0.0e+00
Match length	480
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence

Seq. No.	126578
Contig ID	21433_1.R1010
5'-most EST	jC-atXLIB327404P2b10b1
Method	BLASTX
NCBI GI	g4263515
BLAST score	921
E value	1.0e-99
Match length	218
% identity	88
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126579
Contig ID	21434_1.R1010
5'-most EST	jC-atXLIB327404P2b11b1
Method	BLASTN
NCBI GI	g2760168
BLAST score	121
E value	3.0e-61
Match length	433
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	126580
Contig ID	21435_1.R1010
5'-most EST	jC-atXLIB327409P1e04b1
Method	BLASTX
NCBI GI	g4467126
BLAST score	356
E value	3.0e-46
Match length	199
% identity	49
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	126581
Contig ID	21437_1.R1010
5'-most EST	jC-atXLIB327404P1c02b1
Method	BLASTX
NCBI GI	g1723239
BLAST score	213
E value	4.0e-25

Match length	154
% identity	47
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	126582
Contig ID	21439_1.R1010
5'-most EST	LIB24-060-Q1-E1-E3
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	6.0e-20
Match length	64
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	126583
Contig ID	21439_2.R1010
5'-most EST	g2393252

Seq. No.	126584
Contig ID	21440_1.R1010
5'-most EST	jC-atXLIB327404P2c04b1
Method	BLASTN
NCBI GI	g4589443
BLAST score	426
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	126585
Contig ID	21441_1.R1010
5'-most EST	LIB24-060-Q1-E1-E5
Method	BLASTX
NCBI GI	g4454484
BLAST score	532
E value	2.0e-54
Match length	132
% identity	79
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	126586
Contig ID	21447_1.R1010
5'-most EST	LIB3175-060-P1-K1-G4

Seq. No.	126587
Contig ID	21450_1.R1010
5'-most EST	LIB25-009-Q1-E1-D9
Method	BLASTX
NCBI GI	g3688174
BLAST score	892
E value	2.0e-96

Match length	167
% identity	100
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	126588
Contig ID	21453_1.R1010
5'-most EST	jC-atXLIB327404P1c10b1
Method	BLASTX
NCBI GI	g3243234
BLAST score	60
E value	4.0e-38
Match length	148
% identity	66
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	126589
Contig ID	21456_1.R1010
5'-most EST	jC-atXLIB327404P1c11b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	264
E value	1.0e-146
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	126590
Contig ID	21459_1.R1010
5'-most EST	jC-atXLIB327431P2f11a1
Method	BLASTN
NCBI GI	g836895
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	126591
Contig ID	21462_1.R1010
5'-most EST	jC-atXLIB327404P4c09b1
Method	BLASTX
NCBI GI	g3769472
BLAST score	395
E value	3.0e-38
Match length	86
% identity	78
NCBI Description	(AF064732) putative phospholipase A2 [Dianthus caryophyllus]

Seq. No.	126592
Contig ID	21465_1.R1010
5'-most EST	jC-atXLIB327418P4e12b1
Method	BLASTN
NCBI GI	g2618677
BLAST score	441

E value	0.0e+00
Match length	483
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	126593
Contig ID	21465_2.R1010
5'-most EST	g2733571
Method	BLASTN
NCBI GI	g2618677
BLAST score	578
E value	0.0e+00
Match length	698
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	126594
Contig ID	21466_1.R1010
5'-most EST	jC-atXLIB327404P1d03b1
Method	BLASTX
NCBI GI	g2149254
BLAST score	270
E value	1.0e-23
Match length	112
% identity	53
NCBI Description	(U83914) eukaryotic initiation factor eIF-2B beta subunit [Rattus norvegicus]

Seq. No.	126595
Contig ID	21468_1.R1010
5'-most EST	jC-atXLIB327404P2d03b1

Seq. No.	126596
Contig ID	21472_1.R1010
5'-most EST	g315918
Method	BLASTN
NCBI GI	g2245031
BLAST score	380
E value	0.0e+00
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126597
Contig ID	21477_1.R1010
5'-most EST	jC-atXLIB327421P2h04b1
Method	BLASTX
NCBI GI	g4544428
BLAST score	768
E value	1.0e-81
Match length	163
% identity	93
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	126598
Contig ID	21477_2.R1010
5'-most EST	jC-atXLIB327423P2d06b1
Method	BLASTX
NCBI GI	g4544428
BLAST score	463
E value	7.0e-46
Match length	163
% identity	48
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	126599
Contig ID	21477_3.R1010
5'-most EST	g2581599
Method	BLASTN
NCBI GI	g4544405
BLAST score	160
E value	1.0e-84
Match length	390
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	126600
Contig ID	21477_4.R1010
5'-most EST	LIB24-061-Q1-E1-A5
Method	BLASTX
NCBI GI	g4544428
BLAST score	612
E value	1.0e-63
Match length	137
% identity	88
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	126601
Contig ID	21483_1.R1010
5'-most EST	jC-alX24075Q1E1E09b1
Method	BLASTN
NCBI GI	g4539415
BLAST score	144
E value	4.0e-75
Match length	429
% identity	75
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	126602
Contig ID	21485_1.R1010
5'-most EST	jC-atX24061Q1E1B03b1
Method	BLASTX
NCBI GI	g2894599
BLAST score	665
E value	1.0e-69
Match length	208
% identity	68
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	126603
Contig ID	21485_2.R1010
5'-most EST	jC-atXP11C98B15T7040d1
Method	BLASTX
NCBI GI	g2894599
BLAST score	490
E value	5.0e-49
Match length	181
% identity	62
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	126604
Contig ID	21486_1.R1010
5'-most EST	jC-atXLIB327404P4a10b1
Method	BLASTX
NCBI GI	g3941424
BLAST score	678
E value	2.0e-71
Match length	146
% identity	88
NCBI Description	(AF062866) putative transcription factor [Arabidopsis thaliana]

Seq. No.	126605
Contig ID	21490_1.R1010
5'-most EST	jC-atXP98CH8C8T7087d1
Method	BLASTN
NCBI GI	g3193305
BLAST score	652
E value	0.0e+00
Match length	715
% identity	98
NCBI Description	Arabidopsis thaliana BAC F3D13

Seq. No.	126606
Contig ID	21490_2.R1010
5'-most EST	jC-atXP94CG11A4T7013d1
Method	BLASTN
NCBI GI	g3193305
BLAST score	421
E value	0.0e+00
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana BAC F3D13

Seq. No.	126607
Contig ID	21492_1.R1010
5'-most EST	LIB24-061-Q1-E1-C10

Seq. No.	126608
Contig ID	21494_1.R1010
5'-most EST	jC-atXLIB327404P2b05b1
Method	BLASTX
NCBI GI	g4567263
BLAST score	534
E value	2.0e-54
Match length	103

% identity	100
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	126609
Contig ID	21497_1.R1010
5'-most EST	jC-atXLIB327404P1b02b1

Seq. No.	126610
Contig ID	21503_1.R1010
5'-most EST	LIB24-061-Q1-E1-D12
Method	BLASTN
NCBI GI	g1707006
BLAST score	54
E value	3.0e-21
Match length	170
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126611
Contig ID	21512_1.R1010
5'-most EST	g435188

Seq. No.	126612
Contig ID	21512_2.R1010
5'-most EST	jC-atXLIB327404P4b10b1

Seq. No.	126613
Contig ID	21521_1.R1010
5'-most EST	jC-atXLIB327404P1c01b1
Method	BLASTX
NCBI GI	g2655008
BLAST score	316
E value	5.0e-29
Match length	99
% identity	58
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	126614
Contig ID	21524_1.R1010
5'-most EST	jC-atXLIB327404P2c12b1
Method	BLASTX
NCBI GI	g3482929
BLAST score	424
E value	2.0e-46
Match length	111
% identity	72
NCBI Description	(AC003970) Putative transcription factor [Arabidopsis thaliana]

Seq. No.	126615
Contig ID	21526_1.R1010
5'-most EST	jC-atXmonuni25Da08a1
Method	BLASTX
NCBI GI	g2827548

BLAST score	436
E value	4.0e-43
Match length	116
% identity	67
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	126616
Contig ID	21527_1.R1010
5'-most EST	LIB24-061-Q1-E1-F5
Method	BLASTX
NCBI GI	g1330401
BLAST score	214
E value	5.0e-17
Match length	112
% identity	40
NCBI Description	(U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No.	126617
Contig ID	21550_1.R1010
5'-most EST	jC-alX35056Q1E2D09b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	146
E value	4.0e-76
Match length	660
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	126618
Contig ID	21553_1.R1010
5'-most EST	g2413790

Seq. No.	126619
Contig ID	21553_2.R1010
5'-most EST	jC-atXLIB327405P2g07b2

Seq. No.	126620
Contig ID	21558_1.R1010
5'-most EST	jC-atXLIB327421P1d12b1
Method	BLASTX
NCBI GI	g132964
BLAST score	201
E value	2.0e-15
Match length	52
% identity	69
NCBI Description	60S RIBOSOMAL PROTEIN L29 (P23) >gi_71376_pir__R6RT43 ribosomal protein RL43 - rat >gi_57145_emb_CAA43146_ (X60744) ribosomal protein [Rattus norvegicus] >gi_312208_emb_CAA48344_ (X68283) rat ribosomal protein L29 [Rattus norvegicus]

Seq. No.	126621
Contig ID	21559_1.R1010
5'-most EST	jC-atX24062Q1E1B11b1
Method	BLASTN

NCBI GI	g3492855
BLAST score	118
E value	1.0e-59
Match length	419
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	126622
Contig ID	21561_1.R1010
5'-most EST	LIB3175-019-P1-K1-E1
Method	BLASTX
NCBI GI	g3309170
BLAST score	449
E value	3.0e-44
Match length	200
% identity	48
NCBI Description	(AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No.	126623
Contig ID	21564_1.R1010
5'-most EST	LIB25-106-Q1-E1-E2
Method	BLASTN
NCBI GI	g3510342
BLAST score	344
E value	0.0e+00
Match length	541
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No.	126624
Contig ID	21565_1.R1010
5'-most EST	jC-alXLIB327434P4a11b1
Method	BLASTX
NCBI GI	g1350956
BLAST score	591
E value	5.0e-61
Match length	117
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	126625
Contig ID	21565_2.R1010
5'-most EST	jC-atXP20C113H20T7035a1
Method	BLASTX
NCBI GI	g1350956
BLAST score	469
E value	6.0e-55
Match length	118
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	126626
Contig ID	21565_3.R1010
5'-most EST	LIB3176-050-P1-K1-E9
Method	BLASTX

NCBI GI	g1350956
BLAST score	47
E value	8.0e-46
Match length	119
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	126627
Contig ID	21567_1.R1010
5'-most EST	g2723041
Method	BLASTX
NCBI GI	g3242714
BLAST score	219
E value	1.0e-17
Match length	96
% identity	47
NCBI Description	(AC003040) hypersensitivity-related protein [Arabidopsis thaliana]

Seq. No.	126628
Contig ID	21578_2.R1010
5'-most EST	jC-atX24062Q1E1C09b1

Seq. No.	126629
Contig ID	21582_1.R1010
5'-most EST	jC-atXLIB327404P1e03b1
Method	BLASTX
NCBI GI	g4539460
BLAST score	84
E value	7.0e-16
Match length	188
% identity	6
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	126630
Contig ID	21586_1.R1010
5'-most EST	jC-atXLIB327404P2e01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	6.0e-19
Match length	69
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126631
Contig ID	21590_1.R1010
5'-most EST	jC-atXLIB327404P1e10b1
Method	BLASTN
NCBI GI	g2252848
BLAST score	34
E value	2.0e-09
Match length	190
% identity	84
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	126632
Contig ID	21593_1.R1010
5'-most EST	jC-atXLIB327404P2e10b1
Method	BLASTN
NCBI GI	g2673901
BLAST score	255
E value	1.0e-141
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126633
Contig ID	21595_1.R1010
5'-most EST	jC-atXLIB327404P2e11b1

Seq. No.	126634
Contig ID	21598_1.R1010
5'-most EST	LIB24-091-Q1-E1-F5
Method	BLASTX
NCBI GI	g3617742
BLAST score	967
E value	1.0e-105
Match length	192
% identity	94
NCBI Description	(AC005687) RAP2.6 [Arabidopsis thaliana]

Seq. No.	126635
Contig ID	21599_1.R1010
5'-most EST	jC-atXLIB327404P1e08b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	34
E value	3.0e-09
Match length	197
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	126636
Contig ID	21608_1.R1010
5'-most EST	ARABL1-07-Q1-B1-A1
Method	BLASTX
NCBI GI	g2760327
BLAST score	748
E value	1.0e-79
Match length	140
% identity	52
NCBI Description	(AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No.	126637
Contig ID	21612_1.R1010
5'-most EST	jC-atXP121C117G16T7088d1
Method	BLASTX
NCBI GI	g3757514
BLAST score	824
E value	2.0e-88

Match length	201
% identity	82
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana] >gi_4581129_gb_AAD24619.1_AC005825_26 (AC005825) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	126638
Contig ID	21612_2.R1010
5'-most EST	jC-atXLIB327404P4e08b1
Method	BLASTX
NCBI GI	g3757514
BLAST score	600
E value	4.0e-64
Match length	124
% identity	96
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana] >gi_4581129_gb_AAD24619.1_AC005825_26 (AC005825) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	126639
Contig ID	21613_1.R1010
5'-most EST	LIB24-062-Q1-E1-G4
Method	BLASTN
NCBI GI	g3080430
BLAST score	367
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	126640
Contig ID	21630_1.R1010
5'-most EST	jC-atXLIB327404P2d09b1
Method	BLASTX
NCBI GI	g2982452
BLAST score	593
E value	3.0e-61
Match length	182
% identity	12
NCBI Description	(AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	126641
Contig ID	21632_1.R1010
5'-most EST	jC-atXLIB327404P2d10b1
Method	BLASTX
NCBI GI	g114974
BLAST score	332
E value	6.0e-41
Match length	124
% identity	65
NCBI Description	NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21) precursor (clone TRE361) - white clover

>gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase [Trifolium repens]

Seq. No.	126642
Contig ID	21633_1.R1010
5'-most EST	jC-atXP28C133P19T7d1
Method	BLASTN
NCBI GI	g4159706
BLAST score	477
E value	0.0e+00
Match length	641
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	126643
Contig ID	21635_1.R1010
5'-most EST	jC-atXLIB327404P1d09b1

Seq. No.	126644
Contig ID	21640_1.R1010
5'-most EST	g936122
Method	BLASTX
NCBI GI	g2894596
BLAST score	330
E value	2.0e-66
Match length	181
% identity	73
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	126645
Contig ID	21641_1.R1010
5'-most EST	LIB24-111-Q1-E1-G6
Method	BLASTX
NCBI GI	g4558591
BLAST score	711
E value	2.0e-75
Match length	138
% identity	100
NCBI Description	(AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana] >gi_4662638_gb_AAD26909.1_AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	126646
Contig ID	21651_1.R1010
5'-most EST	jC-atXmonuni27Cd07b1
Method	BLASTX
NCBI GI	g1001678
BLAST score	148
E value	2.0e-09
Match length	71
% identity	44
NCBI Description	(D64002) ribose 5-phosphate isomerase [Synechocystis sp.]

Seq. No.	126647
Contig ID	21663_1.R1010
5'-most EST	LIB24-063-Q1-E1-D5

Method	BLASTX
NCBI GI	g3033392
BLAST score	650
E value	3.0e-68
Match length	134
% identity	95
NCBI Description	(AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No.	126648
Contig ID	21668_1.R1010
5'-most EST	g3450091
Method	BLASTN
NCBI GI	g2924730
BLAST score	374
E value	0.0e+00
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	126649
Contig ID	21671_1.R1010
5'-most EST	LIB24-063-Q1-E1-E2
Method	BLASTX
NCBI GI	g2244776
BLAST score	732
E value	7.0e-78
Match length	149
% identity	99
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126650
Contig ID	21672_1.R1010
5'-most EST	LIB25-087-Q1-E1-F12
Method	BLASTN
NCBI GI	g4589450
BLAST score	272
E value	1.0e-151
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T31K7, complete sequence

Seq. No.	126651
Contig ID	21673_1.R1010
5'-most EST	jC-atXLIB327404P1e12b1

Seq. No.	126652
Contig ID	21677_1.R1010
5'-most EST	jC-atXLIB327404P2e08b1

Seq. No.	126653
Contig ID	21680_1.R1010
5'-most EST	LIB3234-038-P1-K1-G5
Method	BLASTX
NCBI GI	g3021336

BLAST score	257
E value	6.0e-22
Match length	98
% identity	62
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	126654
Contig ID	21686_1.R1010
5'-most EST	jC-atX24048Q1E1E07b1
Method	BLASTX
NCBI GI	g4204095
BLAST score	374
E value	1.0e-35
Match length	157
% identity	48
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No.	126655
Contig ID	21697_1.R1010
5'-most EST	LIB24-063-Q1-E1-G8
Method	BLASTX
NCBI GI	g4587551
BLAST score	167
E value	3.0e-11
Match length	74
% identity	46
NCBI Description	(AC006577) F15I1.18 [Arabidopsis thaliana]

Seq. No.	126656
Contig ID	21702_1.R1010
5'-most EST	jC-atX24063Q1E1H01b1
Method	BLASTX
NCBI GI	g3702328
BLAST score	595
E value	9.0e-62
Match length	109
% identity	100
NCBI Description	(AC005397) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No.	126657
Contig ID	21704_1.R1010
5'-most EST	jC-atXLIB327404P1e04b1
Method	BLASTX
NCBI GI	g3785996
BLAST score	257
E value	2.0e-69
Match length	142
% identity	94
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]

Seq. No.	126658
Contig ID	21715_1.R1010
5'-most EST	jC-atXLIB327404P2d06b1
Method	BLASTX
NCBI GI	g2388971
BLAST score	290
E value	1.0e-25

Match length	161
% identity	40
NCBI Description	(Z98979) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	126659
Contig ID	21716_1.R1010
5'-most EST	jC-atXLIB327416P3h07b1
Method	BLASTX
NCBI GI	g1168529
BLAST score	407
E value	1.0e-39
Match length	86
% identity	92
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir__S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	126660
Contig ID	21716_2.R1010
5'-most EST	g2756821

Seq. No.	126661
Contig ID	21719_1.R1010
5'-most EST	jC-atXLIB327404P4d11b1
Method	BLASTX
NCBI GI	g2244763
BLAST score	243
E value	2.0e-20
Match length	72
% identity	71
NCBI Description	(Z97335) A6 anther-specific protein [Arabidopsis thaliana]

Seq. No.	126662
Contig ID	21720_1.R1010
5'-most EST	jC-atXLIB327404P1d12b1

Seq. No.	126663
Contig ID	21725_1.R1010
5'-most EST	jC-atXLIB327404P1d11b1
Method	BLASTX
NCBI GI	g4467134
BLAST score	315
E value	1.0e-112
Match length	311
% identity	72
NCBI Description	(AL035540) protein kinase like protein [Arabidopsis thaliana]

Seq. No.	126664
Contig ID	21726_1.R1010
5'-most EST	jC-atXLIB327404P2d11b1
Method	BLASTX
NCBI GI	g4510356
BLAST score	706
E value	1.0e-74

Match length	143
% identity	98
NCBI Description	(AC006921) putative kinesin-related protein TKRP125 [Arabidopsis thaliana]

Seq. No.	126665
Contig ID	21728_1.R1010
5'-most EST	jC-atXLIB327420P3b04b1
Method	BLASTX
NCBI GI	g4567231
BLAST score	411
E value	4.0e-40
Match length	80
% identity	99
NCBI Description	(AC007119) putative glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	126666
Contig ID	21729_1.R1010
5'-most EST	LIB3234-011-P1-K1-C3

Seq. No.	126667
Contig ID	21730_1.R1010
5'-most EST	jC-atXLIB327401P2b09a1
Method	BLASTN
NCBI GI	g4757404
BLAST score	312
E value	1.0e-175
Match length	389
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	126668
Contig ID	21730_2.R1010
5'-most EST	jC-atXLIB327404P4d04b1
Method	BLASTN
NCBI GI	g4757404
BLAST score	346
E value	0.0e+00
Match length	354
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	126669
Contig ID	21734_1.R1010
5'-most EST	jC-atXLIB327408P4f02b1
Method	BLASTX
NCBI GI	g4468980
BLAST score	802
E value	7.0e-86
Match length	148
% identity	100
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No. 126670

Contig ID	21734_3.R1010
5'-most EST	LIB35-032-Q1-E1-H7
Method	BLASTX
NCBI GI	g4468980
BLAST score	361
E value	3.0e-53
Match length	110
% identity	96
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	126671
Contig ID	21737_1.R1010
5'-most EST	LIB3234-070-P1-K1-A2
Method	BLASTX
NCBI GI	g629528
BLAST score	545
E value	6.0e-56
Match length	116
% identity	99
NCBI Description	hypothetical protein - Arabidopsis thaliana >gi_1076335_pir__S51580 hypothetical protein 1 - Arabidopsis thaliana >gi_499167_emb_CAA56144_ (X79707) ORF [Arabidopsis thaliana]

Seq. No.	126672
Contig ID	21737_2.R1010
5'-most EST	jC-atXLIB327404P4d05b1
Method	BLASTX
NCBI GI	g629528
BLAST score	487
E value	5.0e-49
Match length	111
% identity	88
NCBI Description	hypothetical protein - Arabidopsis thaliana >gi_1076335_pir__S51580 hypothetical protein 1 - Arabidopsis thaliana >gi_499167_emb_CAA56144_ (X79707) ORF [Arabidopsis thaliana]

Seq. No.	126673
Contig ID	21745_1.R1010
5'-most EST	jC-atX24064Q1E1D07b1
Method	BLASTN
NCBI GI	g3985949
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	126674
Contig ID	21753_1.R1010
5'-most EST	jC-atXLIB327404P2e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26

Match length	78
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126675
Contig ID	21754_1.R1010
5'-most EST	jC-alXLIB327435P2h05a1
Method	BLASTX
NCBI GI	g2827076
BLAST score	794
E value	7.0e-85
Match length	183
% identity	85
NCBI Description	(AF020269) malate dehydrogenase precursor [Medicago sativa]

Seq. No.	126676
Contig ID	21754_2.R1010
5'-most EST	jC-atXLIB327408P2c06b1
Method	BLASTX
NCBI GI	g2827076
BLAST score	891
E value	4.0e-96
Match length	212
% identity	84
NCBI Description	(AF020269) malate dehydrogenase precursor [Medicago sativa]

Seq. No.	126677
Contig ID	21755_1.R1010
5'-most EST	jC-atXLIB327404P2e03b1

Seq. No.	126678
Contig ID	21756_1.R1010
5'-most EST	g634454
Method	BLASTN
NCBI GI	g3859658
BLAST score	162
E value	9.0e-86
Match length	516
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	126679
Contig ID	21759_2.R1010
5'-most EST	LIB3175-062-P1-K1-E9
Method	BLASTX
NCBI GI	g4249410
BLAST score	629
E value	1.0e-65
Match length	169
% identity	93
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	126680
Contig ID	21763_1.R1010
5'-most EST	g1053360

Seq. No.	126681
Contig ID	21763_2.R1010
5'-most EST	g2739594

Seq. No.	126682
Contig ID	21763_3.R1010
5'-most EST	jC-alXLIB327435P3a01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	8.0e-22
Match length	59
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	126683
Contig ID	21764_1.R1010
5'-most EST	LIB24-064-Q1-E1-F4
Method	BLASTX
NCBI GI	g134025
BLAST score	572
E value	1.0e-58
Match length	134
% identity	84
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8 ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No.	126684
Contig ID	21765_1.R1010
5'-most EST	LIB3168-036-P1-K1-E9

Seq. No.	126685
Contig ID	21766_1.R1010
5'-most EST	jC-atXLIB327422P1g11b1
Method	BLASTX
NCBI GI	g3273755
BLAST score	859
E value	2.0e-92
Match length	162
% identity	100
NCBI Description	(AF061520) copper/zinc superoxide dismutase [Arabidopsis thaliana]

Seq. No.	126686
Contig ID	21771_1.R1010
5'-most EST	LIB24-064-Q1-E1-G12
Method	BLASTX
NCBI GI	g4467096
BLAST score	540
E value	2.0e-55
Match length	112
% identity	55

NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	126687
Contig ID	21776_1.R1010
5'-most EST	jC-atXLIB327405P3d06b1
Method	BLASTX
NCBI GI	g4056433
BLAST score	531
E value	5.0e-54
Match length	204
% identity	53
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	126688
Contig ID	21777_1.R1010
5'-most EST	jC-atXLIB327404P4e06b1
Method	BLASTX
NCBI GI	g4191780
BLAST score	240
E value	4.0e-20
Match length	89
% identity	49
NCBI Description	(AC005917) putative cytokinin oxidase [Arabidopsis thaliana]

Seq. No.	126689
Contig ID	21781_1.R1010
5'-most EST	LIB24-064-Q1-E1-H3

Seq. No.	126690
Contig ID	21788_1.R1010
5'-most EST	jC-atXLIB327404P1d07b1
Method	BLASTX
NCBI GI	g4567232
BLAST score	354
E value	3.0e-33
Match length	72
% identity	100
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	126691
Contig ID	21794_1.R1010
5'-most EST	jC-atX24065Q1E1B04b1

Seq. No.	126692
Contig ID	21795_1.R1010
5'-most EST	LIB25-012-Q1-E1-C10
Method	BLASTX
NCBI GI	g3451473
BLAST score	227
E value	7.0e-19
Match length	96
% identity	45
NCBI Description	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]

Seq. No.	126693
Contig ID	21800_1.R1010
5'-most EST	jC-atX24065Q1E1C04b1
Method	BLASTN
NCBI GI	g4558586
BLAST score	195
E value	1.0e-105
Match length	318
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	126694
Contig ID	21805_1.R1010
5'-most EST	jC-atX24065Q1E1D11b1
Method	BLASTX
NCBI GI	g1402878
BLAST score	269
E value	7.0e-24
Match length	92
% identity	48
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	126695
Contig ID	21806_1.R1010
5'-most EST	jC-atXLIB327405P3g07b1

Seq. No.	126696
Contig ID	21808_1.R1010
5'-most EST	jC-atXLIB327404P4d12b1
Method	BLASTN
NCBI GI	g2351061
BLAST score	327
E value	0.0e+00
Match length	564
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	126697
Contig ID	21810_1.R1010
5'-most EST	LIB3234-049-P1-K1-B10

Seq. No.	126698
Contig ID	21813_1.R1010
5'-most EST	LIB24-065-Q1-E1-E10
Method	BLASTN
NCBI GI	g4056476
BLAST score	513
E value	0.0e+00
Match length	996
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126699

Contig ID	21814_1.R1010
5'-most EST	LIB24-065-Q1-E1-E11

Seq. No.	126700
Contig ID	21820_1.R1010
5'-most EST	LIB3176-049-P1-K1-A3
Method	BLASTN
NCBI GI	g2160155
BLAST score	48
E value	8.0e-18
Match length	112
% identity	93
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	126701
Contig ID	21824_1.R1010
5'-most EST	g2733903
Method	BLASTN
NCBI GI	g4454447
BLAST score	212
E value	1.0e-115
Match length	492
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126702
Contig ID	21824_2.R1010
5'-most EST	jC-atXLIB327403P3c07b2
Method	BLASTN
NCBI GI	g4454447
BLAST score	232
E value	1.0e-127
Match length	510
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126703
Contig ID	21824_3.R1010
5'-most EST	g2048926
Method	BLASTN
NCBI GI	g4454447
BLAST score	287
E value	1.0e-160
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126704
Contig ID	21830_1.R1010
5'-most EST	jC-atXLIB327404P4e11b1
Method	BLASTX
NCBI GI	g2244763
BLAST score	303

E value	8.0e-28
Match length	82
% identity	73
NCBI Description	(Z97335) A6 anther-specific protein [Arabidopsis thaliana]

Seq. No.	126705
Contig ID	21833_1.R1010
5'-most EST	jC-atXLIB327403P3e09b2
Method	BLASTX
NCBI GI	g4432840
BLAST score	284
E value	7.0e-25
Match length	155
% identity	41
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	126706
Contig ID	21835_1.R1010
5'-most EST	jC-atXLIB327404P2f05b1
Method	BLASTX
NCBI GI	g4028155
BLAST score	169
E value	2.0e-19
Match length	136
% identity	40
NCBI Description	(AF083221) YDR140w homolog [Fugu rubripes]

Seq. No.	126707
Contig ID	21839_1.R1010
5'-most EST	g2048239
Method	BLASTN
NCBI GI	g3128166
BLAST score	263
E value	1.0e-146
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126708
Contig ID	21839_2.R1010
5'-most EST	jC-atXLIB327404P2f06b1
Method	BLASTN
NCBI GI	g3128166
BLAST score	234
E value	1.0e-128
Match length	529
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126709
Contig ID	21840_1.R1010
5'-most EST	jC-atXLIB327404P2f07b1
Method	BLASTX
NCBI GI	g2894378
BLAST score	377

E value	6.0e-36
Match length	169
% identity	46
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	126710
Contig ID	21845_1.R1010
5'-most EST	jC-atXLIB327404P1f08b1
Method	BLASTX
NCBI GI	g2129742
BLAST score	327
E value	4.0e-30
Match length	78
% identity	76
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	126711
Contig ID	21846_1.R1010
5'-most EST	jC-atXLIB327404P2f08b1
Method	BLASTN
NCBI GI	g3241926
BLAST score	424
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	126712
Contig ID	21847_1.R1010
5'-most EST	LIB24-066-Q1-E1-B11
Method	BLASTN
NCBI GI	g3445196
BLAST score	368
E value	0.0e+00
Match length	380
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126713
Contig ID	21849_1.R1010
5'-most EST	jC-atXLIB327404P1f10b1
Method	BLASTX
NCBI GI	g4105782
BLAST score	422
E value	3.0e-41
Match length	93
% identity	86
NCBI Description	(AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 126714

Contig ID	21852_1.R1010
5'-most EST	LIB24-066-Q1-E1-B7
Method	BLASTX
NCBI GI	g2642450
BLAST score	867
E value	2.0e-93
Match length	208
% identity	78
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	126715
Contig ID	21855_1.R1010
5'-most EST	LIB24-085-Q1-E1-H4
Method	BLASTX
NCBI GI	g1806140
BLAST score	690
E value	8.0e-73
Match length	153
% identity	87
NCBI Description	(X97314) cdc2MsC [Medicago sativa]

Seq. No.	126716
Contig ID	21856_1.R1010
5'-most EST	jC-atX24066Q1E1C11b1
Method	BLASTX
NCBI GI	g4512620
BLAST score	719
E value	1.0e-96
Match length	189
% identity	96
NCBI Description	(AC004793) Identical to gb_X71364 gene for aspartate kinase homoserine dehydrogenase from Arabidopsis thaliana

Seq. No.	126717
Contig ID	21857_1.R1010
5'-most EST	LIB3175-024-P1-K1-E9
Method	BLASTX
NCBI GI	g3047101
BLAST score	310
E value	2.0e-28
Match length	140
% identity	51
NCBI Description	(AF058919) Similar to protein kinase; coded for by A. thaliana cDNA H36947; coded for by A. thaliana cDNA H37158 [Arabidopsis thaliana]

Seq. No.	126718
Contig ID	21862_1.R1010
5'-most EST	g398648
Method	BLASTX
NCBI GI	g4582455
BLAST score	270
E value	1.0e-23
Match length	111
% identity	47

NCBI Description	(AC007071) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	126719
Contig ID	21866_1.R1010
5'-most EST	LIB24-066-Q1-E1-D1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	69
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	126720
Contig ID	21867_1.R1010
5'-most EST	LIB24-066-Q1-E1-D10
Method	BLASTX
NCBI GI	g2244833
BLAST score	166
E value	2.0e-11
Match length	166
% identity	30
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	126721
Contig ID	21870_1.R1010
5'-most EST	jC-alXLIB327434P1f09b1
Method	BLASTN
NCBI GI	g3985934
BLAST score	232
E value	1.0e-127
Match length	812
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	126722
Contig ID	21872_1.R1010
5'-most EST	g502089
Method	BLASTX
NCBI GI	g4522004
BLAST score	1004
E value	1.0e-110
Match length	219
% identity	95
NCBI Description	(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No.	126723
Contig ID	21873_1.R1010
5'-most EST	jC-atX24066Q1E1D06b1
Method	BLASTN
NCBI GI	g3600045
BLAST score	440
E value	0.0e+00

Match length 493
% identity 100
NCBI Description Arabidopsis thaliana BAC F2P3

Seq. No. 126724
Contig ID 21876_1.R1010
5'-most EST jC-atXLIB327440P1f12b1
Method BLASTX
NCBI GI g2317905
BLAST score 339
E value 1.0e-31
Match length 78
% identity 86
NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 126725
Contig ID 21879_1.R1010
5'-most EST jC-atX24066Q1E1E11b1
Method BLASTN
NCBI GI g4220640
BLAST score 219
E value 1.0e-120
Match length 477
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 126726
Contig ID 21887_1.R1010
5'-most EST jC-atXLIB327404P4f09b1
Method BLASTX
NCBI GI g4758918
BLAST score 275
E value 3.0e-24
Match length 100
% identity 47
NCBI Description phosphatidylinositol glycan, class B >gi_1552169_dbj_BAA07709_ (D42138) PIG-B [Homo sapiens]

Seq. No. 126727
Contig ID 21888_1.R1010
5'-most EST LIB24-066-Q1-E1-E9
Method BLASTN
NCBI GI g3449330
BLAST score 710
E value 0.0e+00
Match length 730
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No. 126728
Contig ID 21889_1.R1010
5'-most EST g17653

Seq. No. 126729
Contig ID 21891_1.R1010

5'-most EST	jC-atXLIB327404P2g01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	6.0e-28
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126730
Contig ID	21894_1.R1010
5'-most EST	jC-atXLIB327404P2g02b1

Seq. No.	126731
Contig ID	21901_1.R1010
5'-most EST	jC-atXP108C142C7T7025d1
Method	BLASTN
NCBI GI	g3133272
BLAST score	292
E value	1.0e-163
Match length	292
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No.	126732
Contig ID	21905_1.R1010
5'-most EST	jC-atXLIB327404P2g04b1
Method	BLASTX
NCBI GI	g3426039
BLAST score	231
E value	5.0e-19
Match length	90
% identity	63
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	126733
Contig ID	21905_2.R1010
5'-most EST	LIB3175-070-P1-K-E12
Method	BLASTX
NCBI GI	g3426039
BLAST score	253
E value	9.0e-22
Match length	76
% identity	66
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	126734
Contig ID	21916_1.R1010
5'-most EST	LIB24-066-Q1-E1-H6
Method	BLASTX
NCBI GI	g2274862
BLAST score	411
E value	2.0e-40
Match length	114
% identity	74

NCBI Description	(AJ000497) Starch branching enzyme II [Arabidopsis thaliana] >gi_4581160_gb_AAD24644.1_AC006919_22 (AC006919) starch branching enzyme II [Arabidopsis thaliana]

Seq. No.	126735
Contig ID	21917_2.R1010
5'-most EST	LIB24-066-Q1-E1-H7
Method	BLASTX
NCBI GI	g2244886
BLAST score	481
E value	4.0e-48
Match length	208
% identity	51
NCBI Description	(Z97338) strong similarity to UTP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	126736
Contig ID	21920_1.R1010
5'-most EST	jC-atXLIB327404P1f05b1
Method	BLASTN
NCBI GI	g4589408
BLAST score	37
E value	3.0e-11
Match length	210
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F14A1, complete sequence

Seq. No.	126737
Contig ID	21923_1.R1010
5'-most EST	LIB24-067-Q1-E1-A4

Seq. No.	126738
Contig ID	21937_1.R1010
5'-most EST	LIB3175-081-P1-K1-G6
Method	BLASTN
NCBI GI	g3046854
BLAST score	126
E value	2.0e-64
Match length	402
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	126739
Contig ID	21939_1.R1010
5'-most EST	LIB24-067-Q1-E1-C6
Method	BLASTX
NCBI GI	g1931645
BLAST score	342
E value	4.0e-32
Match length	94
% identity	71
NCBI Description	(U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No.	126740
Contig ID	21941_1.R1010

5'-most EST	LIB24-067-Q1-E1-C9
Method	BLASTX
NCBI GI	g3702333
BLAST score	205
E value	3.0e-17
Match length	95
% identity	55
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126741
Contig ID	21960_1.R1010
5'-most EST	jC-atXLIB327404P2f09b1
Method	BLASTX
NCBI GI	g4585973
BLAST score	578
E value	2.0e-59
Match length	113
% identity	100
NCBI Description	(AC005287) translation initiation factor [Arabidopsis thaliana]

Seq. No.	126742
Contig ID	21960_2.R1010
5'-most EST	jC-atXLIB327414P2h08a1
Method	BLASTX
NCBI GI	g4585973
BLAST score	523
E value	3.0e-53
Match length	103
% identity	100
NCBI Description	(AC005287) translation initiation factor [Arabidopsis thaliana]

Seq. No.	126743
Contig ID	21961_1.R1010
5'-most EST	jC-atXLIB327407P2h01b1
Method	BLASTX
NCBI GI	g2253583
BLAST score	169
E value	1.0e-13
Match length	76
% identity	61
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126744
Contig ID	21962_1.R1010
5'-most EST	g905707
Method	BLASTX
NCBI GI	g3337361
BLAST score	82
E value	1.0e-50
Match length	142
% identity	66
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	126745
Contig ID	21962_2.R1010

5'-most EST	ARABL1-031-Q1-E1-F3
Method	BLASTN
NCBI GI	g2618601
BLAST score	332
E value	0.0e+00
Match length	380
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	126746
Contig ID	21965_1.R1010
5'-most EST	jC-atXLIB327404P1g03b1
Method	BLASTX
NCBI GI	g1707412
BLAST score	348
E value	9.0e-33
Match length	147
% identity	48
NCBI Description	(X95906) Cleavage and Polyadenylation Specifity Factor protein [Bos taurus]

Seq. No.	126747
Contig ID	21968_1.R1010
5'-most EST	jC-atXLIB327426P1d05b1
Method	BLASTX
NCBI GI	g3036805
BLAST score	381
E value	1.0e-36
Match length	70
% identity	100
NCBI Description	(AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	126748
Contig ID	21972_1.R1010
5'-most EST	jC-atXLIB327404P1g05b1
Method	BLASTN
NCBI GI	g3228389
BLAST score	379
E value	0.0e+00
Match length	484
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	126749
Contig ID	21979_1.R1010
5'-most EST	jC-atXLIB327404P1g08b1
Method	BLASTN
NCBI GI	g3341671
BLAST score	442
E value	0.0e+00
Match length	467
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126750
Contig ID	21983_1.R1010
5'-most EST	jC-atXP118C145G11T7076d2
Method	BLASTX
NCBI GI	g3287944
BLAST score	240
E value	8.0e-20
Match length	73
% identity	62
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN C3D6.08C IN CHROMOSOME II >gi_2117304_emb_CAB09117.1_ (Z95620) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	126751
Contig ID	21983_3.R1010
5'-most EST	jC-atXLIB327404P1g06b1
Method	BLASTX
NCBI GI	g3287944
BLAST score	165
E value	9.0e-14
Match length	76
% identity	52
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN C3D6.08C IN CHROMOSOME II >gi_2117304_emb_CAB09117.1_ (Z95620) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	126752
Contig ID	21986_1.R1010
5'-most EST	jC-atXLIB327404P1g10b1

Seq. No.	126753
Contig ID	21992_1.R1010
5'-most EST	jC-alXLIB327436P3b02b1
Method	BLASTX
NCBI GI	g2811029
BLAST score	330
E value	1.0e-30
Match length	82
% identity	73
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	126754
Contig ID	22002_1.R1010
5'-most EST	LIB24-069-Q1-E1-B9
Method	BLASTX
NCBI GI	g2462732
BLAST score	245
E value	8.0e-21
Match length	96
% identity	46
NCBI Description	(AC002292) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	126755
Contig ID	22005_1.R1010

5'-most EST	jC-atXLIB327422P3e12b2
Method	BLASTX
NCBI GI	g1771162
BLAST score	847
E value	8.0e-91
Match length	299
% identity	61
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	126756
Contig ID	22005_2.R1010
5'-most EST	jC-atXLIB327418P2d09b2
Method	BLASTN
NCBI GI	g2760170
BLAST score	218
E value	1.0e-119
Match length	326
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	126757
Contig ID	22008_1.R1010
5'-most EST	jC-atXLIB327405P2b10b2
Method	BLASTN
NCBI GI	g3513725
BLAST score	416
E value	0.0e+00
Match length	465
% identity	100
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	126758
Contig ID	22009_1.R1010
5'-most EST	LIB24-070-Q1-E1-B8
Method	BLASTX
NCBI GI	g3451474
BLAST score	751
E value	1.0e-79
Match length	320
% identity	47
NCBI Description	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	126759
Contig ID	22012_1.R1010
5'-most EST	jC-atXLIB327408P3a05b1
Method	BLASTN
NCBI GI	g3241919
BLAST score	277
E value	1.0e-154
Match length	804
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9B18, complete sequence [Arabidopsis thaliana]

Seq. No.	126760
Contig ID	22014_1.R1010
5'-most EST	jC-atXLIB327404P1h07b1
Method	BLASTN
NCBI GI	g2832667
BLAST score	275
E value	1.0e-153
Match length	391
% identity	64
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	126761
Contig ID	22018_1.R1010
5'-most EST	jC-atXLIB327404P2h08b1
Method	BLASTN
NCBI GI	g2656029
BLAST score	226
E value	1.0e-124
Match length	458
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	126762
Contig ID	22019_1.R1010
5'-most EST	LIB24-069-Q1-E1-D6
Method	BLASTN
NCBI GI	g3228389
BLAST score	162
E value	5.0e-86
Match length	347
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	126763
Contig ID	22022_1.R1010
5'-most EST	jC-atXP118C153M2T7078d2
Method	BLASTX
NCBI GI	g2708746
BLAST score	616
E value	7.0e-64
Match length	116
% identity	100
NCBI Description	(AC003952) putative DnaJ-like chaperonin [Arabidopsis thaliana]

Seq. No.	126764
Contig ID	22024_1.R1010
5'-most EST	jC-atX24059Q1E1D05b1

Seq. No.	126765
Contig ID	22037_1.R1010
5'-most EST	jC-atXLIB327405P2a08b2
Method	BLASTX

NCBI GI	g4567260
BLAST score	775
E value	9.0e-83
Match length	147
% identity	100
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	126766
Contig ID	22039_1.R1010
5'-most EST	jC-atXP112C127P3T7d2
Method	BLASTX
NCBI GI	g2739360
BLAST score	1000
E value	1.0e-109
Match length	234
% identity	87
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana] >gi_3075385 (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	126767
Contig ID	22047_1.R1010
5'-most EST	jC-atXP1C72B2T7d1
Method	BLASTX
NCBI GI	g1711513
BLAST score	1106
E value	1.0e-121
Match length	261
% identity	85
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54) >gi_515681 (U12127) signal recognition particle 54 kDa subunit [Arabidopsis thaliana]

Seq. No.	126768
Contig ID	22051_1.R1010
5'-most EST	jC-atXLIB327408P1h08b1
Method	BLASTX
NCBI GI	g4539376
BLAST score	155
E value	9.0e-10
Match length	113
% identity	39
NCBI Description	(AL049525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126769
Contig ID	22062_1.R1010
5'-most EST	jC-atXP102CE4E9T7b1
Method	BLASTN
NCBI GI	g3169654
BLAST score	52
E value	6.0e-20
Match length	82
% identity	99

NCBI Description	Cloning vector pSFI polylinker, complete polylinker sequence
Seq. No.	126770
Contig ID	22062_2.R1010
5'-most EST	jC-atXP73CF3D10T7b1
Seq. No.	126771
Contig ID	22068_1.R1010
5'-most EST	LIB3168-099-P1-K1-C7
Method	BLASTN
NCBI GI	g2656030
BLAST score	385
E value	0.0e+00
Match length	629
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
Seq. No.	126772
Contig ID	22069_1.R1010
5'-most EST	jC-atXLIB327404P2h01b1
Method	BLASTX
NCBI GI	g3608155
BLAST score	260
E value	2.0e-22
Match length	142
% identity	47
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]
Seq. No.	126773
Contig ID	22071_2.R1010
5'-most EST	jC-atX24015Q1E1H03b1
Seq. No.	126774
Contig ID	22076_1.R1010
5'-most EST	jC-atXLIB327404P1h06b1
Method	BLASTX
NCBI GI	g4582451
BLAST score	566
E value	2.0e-58
Match length	123
% identity	87
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana]
Seq. No.	126775
Contig ID	22077_1.R1010
5'-most EST	jC-atXLIB327404P2h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	68
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126776
Contig ID	22081_1.R1010
5'-most EST	jC-atXLIB327404P1h08b1
Method	BLASTN
NCBI GI	g4760411
BLAST score	266
E value	1.0e-148
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	126777
Contig ID	22083_1.R1010
5'-most EST	jC-atXLIB327408P3g03b1
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	8.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	126778
Contig ID	22083_2.R1010
5'-most EST	jC-atXP46C173N12T7054a1
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	8.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	126779
Contig ID	22083_3.R1010
5'-most EST	LIB24-121-Q1-E1-G6
Method	BLASTX
NCBI GI	g122106
BLAST score	392
E value	7.0e-38
Match length	82
% identity	95

NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	126780
Contig ID	22083_4.R1010
5'-most EST	LIB24-070-Q1-E1-F6
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	126781
Contig ID	22096_1.R1010
5'-most EST	jC-atX24060Q1E1D04b1

Seq. No.	126782
Contig ID	22126_1.R1010
5'-most EST	jC-alX24073Q1E1B07b1

Seq. No.	126783
Contig ID	22142_1.R1010
5'-most EST	g1217078
Method	BLASTN
NCBI GI	g3600062
BLAST score	184
E value	6.0e-99
Match length	511

% identity	98
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	126784
Contig ID	22161_1.R1010
5'-most EST	jC-atXLIB327408P2b09b1
Method	BLASTX
NCBI GI	g2244838
BLAST score	209
E value	2.0e-16
Match length	48
% identity	88
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126785
Contig ID	22162_1.R1010
5'-most EST	LIB24-071-Q1-E1-D8

Seq. No.	126786
Contig ID	22163_1.R1010
5'-most EST	jC-atXLIB327404P1h03b1
Method	BLASTX
NCBI GI	g1361311
BLAST score	225
E value	2.0e-18
Match length	86
% identity	51
NCBI Description	CMP-2-keto-3-deoxyoctulosonic acid synthetase homolog - Chlamydia trachomatis >gi_557478 (U15192) CMP-2-keto-3-deoxyoctulosonic acid synthetase [Chlamydia trachomatis]

Seq. No.	126787
Contig ID	22164_1.R1010
5'-most EST	jC-atXLIB327404P2h10b1
Method	BLASTX
NCBI GI	g4454051
BLAST score	248
E value	5.0e-21
Match length	100
% identity	55
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	126788
Contig ID	22165_1.R1010
5'-most EST	jC-atXLIB327428P1b08b2
Method	BLASTN
NCBI GI	g2351073
BLAST score	98
E value	1.0e-47
Match length	328
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 126789

Contig ID	22165_2.R1010
5'-most EST	jC-atXLIB327404P1h11b1
Method	BLASTN
NCBI GI	g2351073
BLAST score	416
E value	0.0e+00
Match length	437
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	126790
Contig ID	22168_1.R1010
5'-most EST	jC-atXLIB327404P2h12b1
Method	BLASTN
NCBI GI	g4589432
BLAST score	251
E value	1.0e-139
Match length	432
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMJ24, complete sequence

Seq. No.	126791
Contig ID	22170_1.R1010
5'-most EST	g2748299
Method	BLASTN
NCBI GI	g2351063
BLAST score	283
E value	1.0e-158
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	126792
Contig ID	22174_1.R1010
5'-most EST	LIB24-071-Q1-E1-F1
Method	BLASTN
NCBI GI	g3510345
BLAST score	165
E value	2.0e-87
Match length	739
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	126793
Contig ID	22178_1.R1010
5'-most EST	LIB24-134-Q1-E1-F11
Method	BLASTN
NCBI GI	g4544405
BLAST score	49
E value	2.0e-18
Match length	93
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic

sequence, complete sequence

Seq. No.	126794
Contig ID	22181_1.R1010
5'-most EST	g2733739

Seq. No.	126795
Contig ID	22182_1.R1010
5'-most EST	jC-atXP115C96C19T7047d1
Method	BLASTX
NCBI GI	g4454474
BLAST score	348
E value	1.0e-59
Match length	116
% identity	100
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126796
Contig ID	22196_1.R1010
5'-most EST	g695435
Method	BLASTX
NCBI GI	g400983
BLAST score	288
E value	1.0e-25
Match length	74
% identity	81
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	126797
Contig ID	22197_1.R1010
5'-most EST	jC-atXLIB327405P1a06b2
Method	BLASTN
NCBI GI	g4589445
BLAST score	289
E value	1.0e-161
Match length	490
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	126798
Contig ID	22198_1.R1010
5'-most EST	jC-alX24076Q1E1B02b1
Method	BLASTX
NCBI GI	g1770301
BLAST score	276
E value	4.0e-24
Match length	114
% identity	46
NCBI Description	(X95074) Translin [Gallus gallus]

Seq. No.	126799
Contig ID	22200_1.R1010
5'-most EST	LIB24-071-Q1-E1-H6

Method	BLASTN
NCBI GI	g3600062
BLAST score	410
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	126800
Contig ID	22201_1.R1010
5'-most EST	LIB24-083-Q1-E1-E2
Method	BLASTX
NCBI GI	g4163997
BLAST score	1224
E value	1.0e-138
Match length	273
% identity	87
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	126801
Contig ID	22201_2.R1010
5'-most EST	jC-alXLIB327434P4g02b1
Method	BLASTX
NCBI GI	g4163997
BLAST score	1441
E value	1.0e-160
Match length	281
% identity	99
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	126802
Contig ID	22201_3.R1010
5'-most EST	jC-alXLIB327435P4a07a1
Method	BLASTN
NCBI GI	g4163996
BLAST score	355
E value	0.0e+00
Match length	403
% identity	96
NCBI Description	Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No.	126803
Contig ID	22201_4.R1010
5'-most EST	jC-alXLIB327434P4g02a1
Method	BLASTN
NCBI GI	g4163996
BLAST score	449
E value	0.0e+00
Match length	533
% identity	95
NCBI Description	Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No.	126804

Contig ID	22201_5.R1010
5'-most EST	g2576716
Method	BLASTN
NCBI GI	g4163996
BLAST score	225
E value	1.0e-123
Match length	354
% identity	90
NCBI Description	Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No.	126805
Contig ID	22201_6.R1010
5'-most EST	g2749685
Method	BLASTN
NCBI GI	g4163996
BLAST score	335
E value	0.0e+00
Match length	411
% identity	95
NCBI Description	Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No.	126806
Contig ID	22204_1.R1010
5'-most EST	LIB3234-097-P1-K1-C4
Method	BLASTX
NCBI GI	g2911044
BLAST score	770
E value	6.0e-82
Match length	190
% identity	82
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	126807
Contig ID	22204_2.R1010
5'-most EST	LIB24-085-Q1-E1-H3
Method	BLASTX
NCBI GI	g2911044
BLAST score	208
E value	5.0e-39
Match length	129
% identity	72
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	126808
Contig ID	22205_1.R1010
5'-most EST	jC-atXLIB327409P4a11b1
Method	BLASTN
NCBI GI	g3805839
BLAST score	280
E value	1.0e-156
Match length	774
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	126809
Contig ID	22217_1.R1010
5'-most EST	jC-atX24072Q1E1B11b1
Method	BLASTN
NCBI GI	g3985950
BLAST score	351
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]

Seq. No.	126810
Contig ID	22218_1.R1010
5'-most EST	jC-atXLIB327404P2e04b1
Method	BLASTX
NCBI GI	g1076715
BLAST score	266
E value	8.0e-23
Match length	92
% identity	47
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	126811
Contig ID	22219_1.R1010
5'-most EST	g2704860

Seq. No.	126812
Contig ID	22221_1.R1010
5'-most EST	LIB24-072-Q1-E1-B4

Seq. No.	126813
Contig ID	22223_1.R1010
5'-most EST	LIB24-078-Q1-E1-C2

Seq. No.	126814
Contig ID	22225_1.R1010
5'-most EST	jC-atX24072Q1E1B08b1
Method	BLASTN
NCBI GI	g4510338
BLAST score	217
E value	1.0e-118
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	126815
Contig ID	22227_1.R1010
5'-most EST	LIB3177-013-P1-K2-A2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	9.0e-16
Match length	57
% identity	95

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126816
Contig ID	22227_2.R1010
5'-most EST	LIB3177-016-P1-K2-D8

Seq. No.	126817
Contig ID	22235_1.R1010
5'-most EST	LIB3176-086-P1-K1-F6
Method	BLASTN
NCBI GI	g4585952
BLAST score	407
E value	0.0e+00
Match length	448
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	126818
Contig ID	22250_1.R1010
5'-most EST	jC-atXLIB327421P1a06b1
Method	BLASTX
NCBI GI	g2245144
BLAST score	443
E value	7.0e-44
Match length	107
% identity	81
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	126819
Contig ID	22253_1.R1010
5'-most EST	LIB24-072-Q1-E1-E5

Seq. No.	126820
Contig ID	22255_1.R1010
5'-most EST	jC-atXLIB327404P2h09b1
Method	BLASTX
NCBI GI	g3790591
BLAST score	458
E value	7.0e-49
Match length	124
% identity	82
NCBI Description	(AF079184) RING-H2 finger protein RHX1a [Arabidopsis thaliana]

Seq. No.	126821
Contig ID	22257_1.R1010
5'-most EST	LIB24-072-Q1-E1-F1
Method	BLASTX
NCBI GI	g1653702
BLAST score	203
E value	9.0e-16
Match length	141
% identity	35
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	126822
Contig ID	22260_1.R1010
5'-most EST	jC-atXLIB327424P2h08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	59
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126823
Contig ID	22267_1.R1010
5'-most EST	jC-alXLIB327436P3e06b1
Method	BLASTX
NCBI GI	g3201633
BLAST score	898
E value	4.0e-97
Match length	183
% identity	100
NCBI Description	(AC004669) putative cell division protein [Arabidopsis thaliana]

Seq. No.	126824
Contig ID	22275_1.R1010
5'-most EST	jC-atXLIB327405P1a01b2
Method	BLASTX
NCBI GI	g2623307
BLAST score	850
E value	3.0e-91
Match length	157
% identity	100
NCBI Description	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]

Seq. No.	126825
Contig ID	22276_1.R1010
5'-most EST	LIB24-072-Q1-E1-H1
Method	BLASTX
NCBI GI	g4249391
BLAST score	668
E value	8.0e-79
Match length	210
% identity	66
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	126826
Contig ID	22278_1.R1010
5'-most EST	jC-atXLIB327420P2e01a2
Method	BLASTN
NCBI GI	g2351062
BLAST score	195
E value	1.0e-105
Match length	419

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	126827
Contig ID	22280_1.R1010
5'-most EST	jC-atXLIB327406P4e08b2

Seq. No.	126828
Contig ID	22281_1.R1010
5'-most EST	jC-atXP82CG1G3T7d3
Method	BLASTX
NCBI GI	g2829918
BLAST score	256
E value	1.0e-35
Match length	157
% identity	54
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	126829
Contig ID	22283_1.R1010
5'-most EST	jC-atXLIB327405P2a07b2

Seq. No.	126830
Contig ID	22289_1.R1010
5'-most EST	jC-atXLIB327408P4e03b1
Method	BLASTX
NCBI GI	g4454019
BLAST score	266
E value	4.0e-23
Match length	132
% identity	42
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	126831
Contig ID	22291_1.R1010
5'-most EST	LIB3176-002-Q1-K1-A11
Method	BLASTX
NCBI GI	g3036806
BLAST score	422
E value	7.0e-42
Match length	83
% identity	100
NCBI Description	(AL022373) glycine-rich protein [Arabidopsis thaliana]

Seq. No.	126832
Contig ID	22292_1.R1010
5'-most EST	jC-atXLIB327405P3a03a1
Method	BLASTN
NCBI GI	g2702261
BLAST score	202
E value	1.0e-109
Match length	341
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126833
Contig ID	22292_2.R1010
5'-most EST	jC-atXLIB327405P3a03b1
Method	BLASTN
NCBI GI	g2702261
BLAST score	185
E value	2.0e-99
Match length	576
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126834
Contig ID	22298_1.R1010
5'-most EST	LIB24-112-Q1-E1-A7
Method	BLASTN
NCBI GI	g2264302
BLAST score	424
E value	0.0e+00
Match length	451
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	126835
Contig ID	22299_1.R1010
5'-most EST	jC-atXLIB327405P3a08b1
Method	BLASTX
NCBI GI	g3695383
BLAST score	668
E value	4.0e-70
Match length	144
% identity	90
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	126836
Contig ID	22299_2.R1010
5'-most EST	jC-atXLIB327405P3a08a1
Method	BLASTX
NCBI GI	g3510259
BLAST score	110
E value	6.0e-36
Match length	95
% identity	86
NCBI Description	(AC005310) putative inorganic pyrophosphatase [Arabidopsis thaliana] >gi_3522960 (AC004411) putative inorganic pyrophosphatase [Arabidopsis thaliana]

Seq. No.	126837
Contig ID	22300_1.R1010
5'-most EST	g2048885
Method	BLASTN
NCBI GI	g3402671
BLAST score	402

E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126838
Contig ID	22300_2.R1010
5'-most EST	jC-atXP10C97B19T7d1
Method	BLASTN
NCBI GI	g3402671
BLAST score	603
E value	0.0e+00
Match length	630
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126839
Contig ID	22300_3.R1010
5'-most EST	jC-atXLIB327405P3a09b1
Method	BLASTN
NCBI GI	g3402671
BLAST score	245
E value	1.0e-135
Match length	282
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126840
Contig ID	22304_1.R1010
5'-most EST	jC-atXLIB327405P1b07b2
Method	BLASTX
NCBI GI	g728867
BLAST score	376
E value	5.0e-36
Match length	119
% identity	58
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi_99694_pir__S21961 proline-rich protein APG - Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana]

Seq. No.	126841
Contig ID	22306_2.R1010
5'-most EST	LIB24-073-Q1-E1-C6
Method	BLASTX
NCBI GI	g2828252
BLAST score	300
E value	3.0e-27
Match length	103
% identity	57
NCBI Description	(AJ003137) CYP1 [Lycopersicon esculentum]

Seq. No.	126842
Contig ID	22310_1.R1010

5'-most EST	g2757994
Method	BLASTX
NCBI GI	g4733891
BLAST score	323
E value	8.0e-30
Match length	110
% identity	62
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	126843
Contig ID	22310_2.R1010
5'-most EST	jC-alX24076Q1E1F04b1
Method	BLASTX
NCBI GI	g4733891
BLAST score	605
E value	2.0e-62
Match length	203
% identity	63
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	126844
Contig ID	22315_1.R1010
5'-most EST	jC-atXLIB327407P1a10b2
Method	BLASTX
NCBI GI	g2245020
BLAST score	173
E value	6.0e-12
Match length	151
% identity	40
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	126845
Contig ID	22323_1.R1010
5'-most EST	jC-atXLIB327405P3a05b1
Method	BLASTN
NCBI GI	g2264312
BLAST score	418
E value	0.0e+00
Match length	524
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	126846
Contig ID	22324_1.R1010
5'-most EST	LIB24-074-Q1-E1-A2
Method	BLASTX
NCBI GI	g3738297
BLAST score	294
E value	1.0e-26
Match length	115
% identity	20
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	126847
Contig ID	22327_1.R1010
5'-most EST	LIB3177-088-P1-K1-B2

Seq. No.	126848
Contig ID	22329_1.R1010
5'-most EST	jC-atXLIB327405P3a04b1
Method	BLASTX
NCBI GI	g3287693
BLAST score	541
E value	2.0e-57
Match length	150
% identity	72
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	126849
Contig ID	22331_1.R1010
5'-most EST	LIB24-074-Q1-E1-B1
Method	BLASTX
NCBI GI	g4097547
BLAST score	271
E value	3.0e-23
Match length	160
% identity	26
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	126850
Contig ID	22333_1.R1010
5'-most EST	LIB25-002-Q1-E1-F5
Method	BLASTX
NCBI GI	g3023512
BLAST score	352
E value	3.0e-33
Match length	98
% identity	66
NCBI Description	PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT PRECURSOR (ENDOPEPTIDASE CLP) >gi_2134793_pir__S68421 ATP-dependent Clp proteinase (EC 3.4.21.92) chain P homolog - human >gi_963048_emb_CAA90705_ (Z50853) CLPP [Homo sapiens]

Seq. No.	126851
Contig ID	22334_1.R1010
5'-most EST	LIB24-074-Q1-E1-B12
Method	BLASTN
NCBI GI	g3869062
BLAST score	169
E value	4.0e-90
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	126852
Contig ID	22336_1.R1010
5'-most EST	LIB24-074-Q1-E1-C4
Method	BLASTX
NCBI GI	g2191175

BLAST score	204
E value	5.0e-16
Match length	70
% identity	97
NCBI Description	(AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No.	126853
Contig ID	22339_1.R1010
5'-most EST	jC-atXLIB327422P3g06b2
Method	BLASTX
NCBI GI	g4704730
BLAST score	739
E value	2.0e-78
Match length	162
% identity	90
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	126854
Contig ID	22339_2.R1010
5'-most EST	jC-alXLIB327435P4c04b1
Method	BLASTX
NCBI GI	g4704730
BLAST score	590
E value	2.0e-82
Match length	162
% identity	90
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	126855
Contig ID	22339_3.R1010
5'-most EST	jC-alXLIB327434P1b08b1
Method	BLASTX
NCBI GI	g4704730
BLAST score	532
E value	5.0e-54
Match length	163
% identity	74
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	126856
Contig ID	22339_4.R1010
5'-most EST	jC-alXLIB327435P2f05a1
Method	BLASTX
NCBI GI	g4704730
BLAST score	434
E value	4.0e-50
Match length	140
% identity	74
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	126857
Contig ID	22340_1.R1010
5'-most EST	LIB24-074-Q1-E1-B7
Method	BLASTX
NCBI GI	g4585974
BLAST score	634

E value	2.0e-66
Match length	138
% identity	88
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	126858
Contig ID	22352_1.R1010
5'-most EST	jC-atXLIB327405P3b01b1
Method	BLASTX
NCBI GI	g2244975
BLAST score	1425
E value	1.0e-158
Match length	279
% identity	99
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126859
Contig ID	22353_1.R1010
5'-most EST	jC-atXLIB327405P2c04b2
Method	BLASTX
NCBI GI	g4262228
BLAST score	236
E value	1.0e-19
Match length	150
% identity	23
NCBI Description	(AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	126860
Contig ID	22354_1.R1010
5'-most EST	jC-alX24086Q1E1F07b1

Seq. No.	126861
Contig ID	22372_1.R1010
5'-most EST	jC-atXLIB327405P2c03b2
Method	BLASTN
NCBI GI	g4539309
BLAST score	537
E value	0.0e+00
Match length	582
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	126862
Contig ID	22374_1.R1010
5'-most EST	jC-alX24076Q1E1H04b1
Method	BLASTX
NCBI GI	g4455231
BLAST score	674
E value	4.0e-71
Match length	143
% identity	92
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	126863
Contig ID	22377_1.R1010

5'-most EST	jC-alX24075Q1E1H08b1
Method	BLASTX
NCBI GI	g2388580
BLAST score	181
E value	3.0e-13
Match length	134
% identity	35
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	126864
Contig ID	22380_1.R1010
5'-most EST	jC-atXLIB327405P1c02b1
Method	BLASTN
NCBI GI	g2827644
BLAST score	236
E value	1.0e-130
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	126865
Contig ID	22385_1.R1010
5'-most EST	jC-atXLIB327405P2c11b2

Seq. No.	126866
Contig ID	22389_1.R1010
5'-most EST	LIB24-074-Q1-E1-G7
Method	BLASTX
NCBI GI	g4455293
BLAST score	432
E value	1.0e-42
Match length	135
% identity	73
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	126867
Contig ID	22390_1.R1010
5'-most EST	LIB24-074-Q1-E1-G8

Seq. No.	126868
Contig ID	22397_1.R1010
5'-most EST	jC-alXLIB327436P3h11b1
Method	BLASTX
NCBI GI	g4567247
BLAST score	805
E value	3.0e-86
Match length	174
% identity	84
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	126869
Contig ID	22398_1.R1010
5'-most EST	jC-atXLIB327421P3d05b1
Method	BLASTX
NCBI GI	g4006848

BLAST score	493
E value	2.0e-49
Match length	175
% identity	53
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	126870
Contig ID	22402_1.R1010
5'-most EST	jC-atXLIB327405P1a10b2
Method	BLASTN
NCBI GI	g4757395
BLAST score	316
E value	1.0e-177
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	126871
Contig ID	22409_1.R1010
5'-most EST	jC-alX24073Q1E1B08b1
Method	BLASTN
NCBI GI	g3449325
BLAST score	367
E value	0.0e+00
Match length	367
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	126872
Contig ID	22412_1.R1010
5'-most EST	jC-atXLIB327408P4h06b1
Method	BLASTX
NCBI GI	g3650033
BLAST score	254
E value	1.0e-21
Match length	156
% identity	40
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	126873
Contig ID	22418_1.R1010
5'-most EST	jC-atXP69C219O17T7095d1
Method	BLASTX
NCBI GI	g1001629
BLAST score	258
E value	6.0e-22
Match length	93
% identity	55
NCBI Description	(D64002) hypothetical protein [Synechocystis sp.]

Seq. No.	126874
Contig ID	22419_1.R1010
5'-most EST	jC-atXLIB327416P2g02b1
Method	BLASTN

NCBI GI	g3046854
BLAST score	37
E value	3.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	126875
Contig ID	22424_1.R1010
5'-most EST	LIB24-075-Q1-E1-C10
Method	BLASTX
NCBI GI	g2924785
BLAST score	542
E value	1.0e-55
Match length	136
% identity	27
NCBI Description	(AC002334) similar to disease resistance protein [Arabidopsis thaliana]

Seq. No.	126876
Contig ID	22425_1.R1010
5'-most EST	LIB24-075-Q1-E1-C11

Seq. No.	126877
Contig ID	22426_1.R1010
5'-most EST	jC-atXLIB327408P4a07b1
Method	BLASTX
NCBI GI	g4567263
BLAST score	145
E value	3.0e-52
Match length	110
% identity	98
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	126878
Contig ID	22436_1.R1010
5'-most EST	jC-atXLIB327408P4h11b1
Method	BLASTX
NCBI GI	g4263526
BLAST score	640
E value	6.0e-67
Match length	124
% identity	100
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126879
Contig ID	22440_1.R1010
5'-most EST	jC-atXLIB327409P3a04b1
Method	BLASTN
NCBI GI	g3046848
BLAST score	885
E value	0.0e+00
Match length	954
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	126880
Contig ID	22441_1.R1010
5'-most EST	jC-atXLIB327405P2b07b2
Method	BLASTN
NCBI GI	g3250673
BLAST score	271
E value	1.0e-151
Match length	379
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	126881
Contig ID	22442_1.R1010
5'-most EST	LIB3177-086-P1-K1-H12
Method	BLASTN
NCBI GI	g3212846
BLAST score	161
E value	4.0e-85
Match length	495
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126882
Contig ID	22443_1.R1010
5'-most EST	jC-atXLIB327405P2b08b2

Seq. No.	126883
Contig ID	22454_1.R1010
5'-most EST	jC-atXP86CG9F9T7b1
Method	BLASTX
NCBI GI	g294845
BLAST score	259
E value	4.0e-22
Match length	82
% identity	51
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	126884
Contig ID	22454_2.R1010
5'-most EST	jC-atXP86CG9G9T7b1
Method	BLASTX
NCBI GI	g294845
BLAST score	411
E value	7.0e-40
Match length	147
% identity	52
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	126885
Contig ID	22454_3.R1010
5'-most EST	LIB24-075-Q1-E1-F12

Seq. No.	126886
Contig ID	22458_1.R1010
5'-most EST	jC-atXLIB327405P3b08b1
Method	BLASTX
NCBI GI	g2623298
BLAST score	1105
E value	1.0e-121
Match length	223
% identity	93
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	126887
Contig ID	22462_1.R1010
5'-most EST	jC-alX24078Q1E1A07b1
Method	BLASTX
NCBI GI	g4539419
BLAST score	466
E value	2.0e-46
Match length	113
% identity	84
NCBI Description	(AL049171) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	126888
Contig ID	22464_1.R1010
5'-most EST	jC-atX24075Q1E1G12b1
Method	BLASTX
NCBI GI	g4314359
BLAST score	442
E value	8.0e-44
Match length	98
% identity	90
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126889
Contig ID	22467_1.R1010
5'-most EST	LIB24-075-Q1-E1-G4
Method	BLASTN
NCBI GI	g2494106
BLAST score	368
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126890
Contig ID	22468_1.R1010
5'-most EST	jC-atXLIB327405P1c05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	77
% identity	95

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126891
Contig ID	22471_1.R1010
5'-most EST	LIB24-075-Q1-E1-H10
Method	BLASTN
NCBI GI	g2244901
BLAST score	224
E value	1.0e-123
Match length	487
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	126892
Contig ID	22472_1.R1010
5'-most EST	jC-atXP2C74E4T7018a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126893
Contig ID	22472_2.R1010
5'-most EST	jC-atXLIB327405P3c02b1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	126894
Contig ID	22474_1.R1010
5'-most EST	LIB24-075-Q1-E1-H2
Method	BLASTX
NCBI GI	g2827713
BLAST score	562
E value	5.0e-58
Match length	109
% identity	99
NCBI Description	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]

Seq. No.	126895
Contig ID	22475_1.R1010
5'-most EST	LIB35-018-Q1-E1-D8
Method	BLASTX
NCBI GI	g4490737
BLAST score	473
E value	3.0e-47
Match length	188

% identity	34
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	126896
Contig ID	22477_1.R1010
5'-most EST	jC-atXLIB327418P4d12b1
Method	BLASTX
NCBI GI	g2130003
BLAST score	312
E value	4.0e-28
Match length	78
% identity	72
NCBI Description	squamosa-promoter binding protein 1 - garden snapdragon >gi_1183866_emb_CAA63113_ (X92369) squamosa-promoter binding protein 1 [Antirrhinum majus]

Seq. No.	126897
Contig ID	22477_2.R1010
5'-most EST	jC-atXLIB327405P2c12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	4.0e-11
Match length	51
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	126898
Contig ID	22482_1.R1010
5'-most EST	LIB24-076-Q1-E1-A12
Method	BLASTX
NCBI GI	g2632252
BLAST score	129
E value	2.0e-20
Match length	132
% identity	45
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	126899
Contig ID	22484_1.R1010
5'-most EST	jC-atXLIB327405P3a02b1

Seq. No.	126900
Contig ID	22494_1.R1010
5'-most EST	jC-atXLIB327408P1g12b1
Method	BLASTN
NCBI GI	g3366536
BLAST score	76
E value	2.0e-34
Match length	268
% identity	87
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	126901
Contig ID	22496_1.R1010

5'-most EST	LIB3176-092-P1-K1-F4
Method	BLASTX
NCBI GI	g2500347
BLAST score	413
E value	4.0e-40
Match length	125
% identity	68
NCBI Description	NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127_ (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No.	126902
Contig ID	22496_2.R1010
5'-most EST	g2756878
Method	BLASTX
NCBI GI	g4826860
BLAST score	224
E value	3.0e-18
Match length	111
% identity	50
NCBI Description	non-histone chromosome protein 2 (S. cerevisiae)-like 1 >gi_2500345_sp_P55769_NHPX_HUMAN NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG) >gi_2618578_dbj_BAA23363_ (D50420) OTK27 [Homo sapiens] >gi_3859990 (AF091076) OTK27 [Homo sapiens] >gi_1589072_prf__2210268A nuclear protein-NHP2-like protein [Homo sapiens]

Seq. No.	126903
Contig ID	22496_3.R1010
5'-most EST	jC-atXP25C125O6T7072a1
Method	BLASTN
NCBI GI	g2832667
BLAST score	39
E value	3.0e-12
Match length	122
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	126904
Contig ID	22501_1.R1010
5'-most EST	LIB24-076-Q1-E1-C2

Seq. No.	126905
Contig ID	22502_1.R1010
5'-most EST	LIB24-123-Q1-E1-D7
Method	BLASTX
NCBI GI	g1771162
BLAST score	651
E value	4.0e-68
Match length	203
% identity	58
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum]

	>gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]
Seq. No.	126906
Contig ID	22508_1.R1010
5'-most EST	LIB3168-040-P1-K1-G6
Method	BLASTX
NCBI GI	g4630748
BLAST score	472
E value	2.0e-47
Match length	91
% identity	100
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]
Seq. No.	126907
Contig ID	22518_1.R1010
5'-most EST	jC-atXLIB327423P4h02b1
Method	BLASTX
NCBI GI	g4506717
BLAST score	224
E value	4.0e-18
Match length	54
% identity	72
NCBI Description	ribosomal protein S29 >gi_266972_sp_P30054_RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens]
Seq. No.	126908
Contig ID	22519_1.R1010
5'-most EST	LIB3176-106-P1-K1-F7
Method	BLASTX
NCBI GI	g4741956
BLAST score	1079
E value	1.0e-118
Match length	228
% identity	92
NCBI Description	(AF134128) Lhcb4:3 protein [Arabidopsis thaliana]
Seq. No.	126909
Contig ID	22522_1.R1010
5'-most EST	jC-atXLIB327401P3d10b2
Seq. No.	126910
Contig ID	22522_3.R1010
5'-most EST	jC-alX24076Q1E1E09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54

E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126911
Contig ID	22527_1.R1010
5'-most EST	jC-atXLIB327404P1g12b1
Method	BLASTX
NCBI GI	g4539443
BLAST score	293
E value	2.0e-34
Match length	121
% identity	71
NCBI Description	(AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	126912
Contig ID	22529_1.R1010
5'-most EST	jC-atXLIB327405P3b12b1
Method	BLASTX
NCBI GI	g3668082
BLAST score	1070
E value	1.0e-117
Match length	220
% identity	93
NCBI Description	(AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No.	126913
Contig ID	22532_1.R1010
5'-most EST	jC-alX24085Q1E1G05b1
Method	BLASTX
NCBI GI	g1421741
BLAST score	462
E value	3.0e-46
Match length	140
% identity	62
NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	126914
Contig ID	22535_1.R1010
5'-most EST	jC-atXLIB327408P1b07b1
Method	BLASTX
NCBI GI	g2492782
BLAST score	958
E value	1.0e-104
Match length	209
% identity	83
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992) alpha-galactosidase [Coffea arabica]

Seq. No.	126915
Contig ID	22538_1.R1010
5'-most EST	LIB24-082-Q1-E1-B2

Seq. No.	126916
Contig ID	22539_1.R1010

5'-most EST	jC-atXLIB327405P2c05b2
Method	BLASTN
NCBI GI	g2264310
BLAST score	193
E value	1.0e-104
Match length	416
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	126917
Contig ID	22540_1.R1010
5'-most EST	LIB24-076-Q1-E1-G8

Seq. No.	126918
Contig ID	22543_1.R1010
5'-most EST	jC-atXLIB327405P1c12b2

Seq. No.	126919
Contig ID	22561_1.R1010
5'-most EST	LIB25-023-Q1-E1-C4

Seq. No.	126920
Contig ID	22565_1.R1010
5'-most EST	LIB24-077-Q1-E1-B11
Method	BLASTX
NCBI GI	g4539005
BLAST score	326
E value	3.0e-30
Match length	123
% identity	49
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	126921
Contig ID	22566_1.R1010
5'-most EST	jC-atXLIB327405P3c06b1
Method	BLASTX
NCBI GI	g2980798
BLAST score	117
E value	4.0e-51
Match length	228
% identity	52
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	126922
Contig ID	22571_1.R1010
5'-most EST	jC-atXLIB327405P2d04b2
Method	BLASTN
NCBI GI	g3282170
BLAST score	462
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 126923

Contig ID	22572_1.R1010
5'-most EST	jC-atXmonuni25Ag12b1
Method	BLASTX
NCBI GI	g3335366
BLAST score	299
E value	4.0e-30
Match length	97
% identity	75
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	126924
Contig ID	22574_1.R1010
5'-most EST	jC-alX24078Q1E1C11b1

Seq. No.	126925
Contig ID	22581_1.R1010
5'-most EST	jC-atXP96C248B21T7b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	5.0e-24
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	126926
Contig ID	22581_2.R1010
5'-most EST	LIB3234-040-P1-K1-H4

Seq. No.	126927
Contig ID	22581_3.R1010
5'-most EST	LIB24-077-Q1-E1-C7

Seq. No.	126928
Contig ID	22583_1.R1010
5'-most EST	jC-atXLIB327405P3d04b1

Seq. No.	126929
Contig ID	22584_1.R1010
5'-most EST	LIB24-077-Q1-E1-D1
Method	BLASTN
NCBI GI	g3510340
BLAST score	193
E value	1.0e-104
Match length	402
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	126930
Contig ID	22587_1.R1010
5'-most EST	jC-atXLIB327405P1e04b1
Method	BLASTX
NCBI GI	g3510261
BLAST score	567
E value	3.0e-58
Match length	134

% identity	86
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126931
Contig ID	22599_1.R1010
5'-most EST	LIB3234-081-Q1-K1-F3
Method	BLASTX
NCBI GI	g2160189
BLAST score	1179
E value	1.0e-130
Match length	232
% identity	25
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	126932
Contig ID	22604_1.R1010
5'-most EST	LIB24-077-Q1-E1-E6
Method	BLASTX
NCBI GI	g4454014
BLAST score	325
E value	9.0e-30
Match length	184
% identity	38
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	126933
Contig ID	22613_1.R1010
5'-most EST	jC-atXLIB327405P4e10b1
Method	BLASTX
NCBI GI	g2565001
BLAST score	387
E value	3.0e-37
Match length	119
% identity	71
NCBI Description	(AC002983) putative lipid transfer protein [Arabidopsis thaliana]

Seq. No.	126934
Contig ID	22615_1.R1010
5'-most EST	LIB25-071-Q1-E1-C1

Seq. No.	126935
Contig ID	22620_1.R1010
5'-most EST	jC-atXLIB327405P2f02b2
Method	BLASTX
NCBI GI	g3688187
BLAST score	594
E value	1.0e-61
Match length	130
% identity	87
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	126936
Contig ID	22622_1.R1010
5'-most EST	jC-atXLIB327405P2f03b2

Method	BLASTX
NCBI GI	g3757527
BLAST score	597
E value	1.0e-61
Match length	113
% identity	100
NCBI Description	(AC005167) putative ribosomal protein L27 [Arabidopsis thaliana]

Seq. No.	126937
Contig ID	22622_2.R1010
5'-most EST	LIB24-077-Q1-E1-G2
Method	BLASTX
NCBI GI	g3757527
BLAST score	219
E value	8.0e-18
Match length	43
% identity	98
NCBI Description	(AC005167) putative ribosomal protein L27 [Arabidopsis thaliana]

Seq. No.	126938
Contig ID	22624_1.R1010
5'-most EST	jC-atXP118C155D9T7094d2
Method	BLASTX
NCBI GI	g3201969
BLAST score	689
E value	2.0e-72
Match length	179
% identity	65
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	126939
Contig ID	22627_1.R1010
5'-most EST	jC-atXLIB327405P1f01b2
Method	BLASTX
NCBI GI	g2224901
BLAST score	215
E value	4.0e-17
Match length	60
% identity	65
NCBI Description	(U67134) PcMYB1 protein [Petroselinum crispum]

Seq. No.	126940
Contig ID	22628_1.R1010
5'-most EST	g1159597
Method	BLASTX
NCBI GI	g4056467
BLAST score	1041
E value	1.0e-113
Match length	205
% identity	98
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No.	126941
Contig ID	22629_1.R1010
5'-most EST	jC-atXLIB327405P2f05b2
Method	BLASTX
NCBI GI	g2911049
BLAST score	434
E value	8.0e-43
Match length	118
% identity	73
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	126942
Contig ID	22631_1.R1010
5'-most EST	LIB24-077-Q1-E1-H11
Method	BLASTX
NCBI GI	g3142289
BLAST score	430
E value	2.0e-42
Match length	126
% identity	67
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	126943
Contig ID	22635_1.R1010
5'-most EST	jC-atXP112C129N17T7d2
Method	BLASTN
NCBI GI	g4741184
BLAST score	348
E value	0.0e+00
Match length	1025
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	126944
Contig ID	22639_1.R1010
5'-most EST	LIB24-077-Q1-E1-H9
Method	BLASTX
NCBI GI	g1362009
BLAST score	618
E value	2.0e-64
Match length	146
% identity	58
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	126945
Contig ID	22643_1.R1010
5'-most EST	jC-atXLIB327405P3c11b1
Method	BLASTX
NCBI GI	g2828290
BLAST score	466
E value	2.0e-46
Match length	156
% identity	68
NCBI Description	(AL021687) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	126946
Contig ID	22646_1.R1010
5'-most EST	jC-atXLIB327405P3c07b1
Method	BLASTX
NCBI GI	g4063743
BLAST score	284
E value	3.0e-25
Match length	103
% identity	54
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126947
Contig ID	22649_1.R1010
5'-most EST	jC-atXLIB327405P2d06b2
Method	BLASTN
NCBI GI	g4585890
BLAST score	90
E value	8.0e-43
Match length	396
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	126948
Contig ID	22658_1.R1010
5'-most EST	jC-atXP112C131G18T7a1
Method	BLASTN
NCBI GI	g3335356
BLAST score	394
E value	0.0e+00
Match length	446
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126949
Contig ID	22658_3.R1010
5'-most EST	jC-atXP112C131C21T7d2
Method	BLASTN
NCBI GI	g3335356
BLAST score	427
E value	0.0e+00
Match length	1106
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	126950
Contig ID	22658_6.R1010
5'-most EST	jC-atXLIB327405P2d05b2
Method	BLASTN
NCBI GI	g3335356
BLAST score	277
E value	1.0e-154
Match length	451
% identity	98

NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	126951
Contig ID	22660_1.R1010
5'-most EST	LIB24-078-Q1-E1-C11
Method	BLASTX
NCBI GI	g2529683
BLAST score	401
E value	4.0e-39
Match length	91
% identity	86
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.	126952
Contig ID	22664_1.R1010
5'-most EST	jC-atXLIB327421P1e01b1
Method	BLASTX
NCBI GI	g2780365
BLAST score	217
E value	2.0e-17
Match length	90
% identity	49
NCBI Description	(AB007693) Elongin C [Drosophila melanogaster]
Seq. No.	126953
Contig ID	22670_1.R1010
5'-most EST	jC-atXLIB327405P1e03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	76
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	126954
Contig ID	22673_1.R1010
5'-most EST	jC-atX24078Q1E1D03b1
Method	BLASTN
NCBI GI	g4760411
BLAST score	395
E value	0.0e+00
Match length	399
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence
Seq. No.	126955
Contig ID	22681_1.R1010
5'-most EST	jC-alXLIB327435P3e02b1
Method	BLASTN
NCBI GI	g3193282
BLAST score	300
E value	1.0e-168
Match length	472

% identity	52
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	126956
Contig ID	22681_2.R1010
5'-most EST	LIB3177-078-P1-K1-H6
Method	BLASTX
NCBI GI	g1173218
BLAST score	556
E value	6.0e-57
Match length	119
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	126957
Contig ID	22681_5.R1010
5'-most EST	LIB35-012-Q1-E1-F6
Method	BLASTX
NCBI GI	g1173218
BLAST score	533
E value	2.0e-54
Match length	106
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	126958
Contig ID	22684_2.R1010
5'-most EST	LIB24-078-Q1-E1-E2

Seq. No.	126959
Contig ID	22685_1.R1010
5'-most EST	jC-atXLIB327405P2e12b2
Method	BLASTX
NCBI GI	g136140
BLAST score	194
E value	1.0e-14
Match length	128
% identity	32
NCBI Description	PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable transposase - maize transposon Ac9

Seq. No.	126960
Contig ID	22690_1.R1010
5'-most EST	jC-atXLIB327405P2e10b2
Method	BLASTN
NCBI GI	g3063690
BLAST score	313
E value	1.0e-175
Match length	672
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	126961
Contig ID	22697_1.R1010
5'-most EST	jC-atXLIB327405P3e11b1
Seq. No.	126962
Contig ID	22701_1.R1010
5'-most EST	jC-atXLIB327405P4e08b1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	2.0e-19
Match length	59
% identity	97
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	126963
Contig ID	22701_2.R1010
5'-most EST	LIB3234-009-P1-K1-E12
Seq. No.	126964
Contig ID	22717_1.R1010
5'-most EST	jC-atXLIB327405P4e09b1
Seq. No.	126965
Contig ID	22718_1.R1010
5'-most EST	jC-alXLIB327435P3a07b1
Method	BLASTN
NCBI GI	g3894179
BLAST score	239
E value	1.0e-131
Match length	654
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	126966
Contig ID	22721_1.R1010
5'-most EST	LIB24-078-Q1-E1-H7
Method	BLASTX
NCBI GI	g1707012
BLAST score	507
E value	2.0e-51
Match length	97
% identity	100
NCBI Description	(U78721) tyrosyl-tRNA synthetase isolog [Arabidopsis thaliana]
Seq. No.	126967
Contig ID	22727_1.R1010
5'-most EST	LIB3177-069-P1-K1-D3
Seq. No.	126968
Contig ID	22728_1.R1010
5'-most EST	jC-atXLIB327421P2e12b1
Method	BLASTX
NCBI GI	g3142292
BLAST score	509

E value	1.0e-51
Match length	105
% identity	100
NCBI Description	(AC002411) Contains similarity to tetratricopeptide repeat protein gb_U46571 from home sapiens. EST gb_Z47802 and gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No.	126969
Contig ID	22730_1.R1010
5'-most EST	jC-atXLIB327405P3f05b1
Method	BLASTX
NCBI GI	g2245000
BLAST score	766
E value	2.0e-81
Match length	168
% identity	92
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	126970
Contig ID	22733_1.R1010
5'-most EST	LIB24-079-Q1-E1-A8
Method	BLASTN
NCBI GI	g2252848
BLAST score	192
E value	1.0e-103
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	126971
Contig ID	22734_1.R1010
5'-most EST	jC-atXLIB327405P3c05b1
Method	BLASTX
NCBI GI	g2245053
BLAST score	503
E value	9.0e-51
Match length	186
% identity	50
NCBI Description	(Z97342) resistance gene homolog [Arabidopsis thaliana]

Seq. No.	126972
Contig ID	22735_1.R1010
5'-most EST	jC-atXLIB327405P1d03b1
Method	BLASTN
NCBI GI	g2262155
BLAST score	311
E value	1.0e-174
Match length	441
% identity	100
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	126973
Contig ID	22736_1.R1010
5'-most EST	jC-atX24079Q1E1B10b1

Seq. No. 126974

Contig ID	22740_1.R1010
5'-most EST	ARABLI-15-Q1-B1-F5
Method	BLASTX
NCBI GI	g4432855
BLAST score	559
E value	3.0e-57
Match length	142
% identity	81
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	126975
Contig ID	22742_1.R1010
5'-most EST	jC-atXLIB327405P1d01b2
Method	BLASTN
NCBI GI	g3449322
BLAST score	292
E value	1.0e-163
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	126976
Contig ID	22743_1.R1010
5'-most EST	jC-atXLIB327405P2d01b2
Method	BLASTX
NCBI GI	g2213615
BLAST score	490
E value	4.0e-49
Match length	133
% identity	63
NCBI Description	(AC000103) F21J9.9 [Arabidopsis thaliana]

Seq. No.	126977
Contig ID	22746_1.R1010
5'-most EST	jC-atXP92C246N6T7018d1
Method	BLASTX
NCBI GI	g3763918
BLAST score	1283
E value	1.0e-142
Match length	251
% identity	100
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	126978
Contig ID	22747_1.R1010
5'-most EST	jC-atXLIB327405P3d01b1
Method	BLASTN
NCBI GI	g4581138
BLAST score	77
E value	5.0e-35
Match length	169
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	126979
Contig ID	22750_1.R1010
5'-most EST	jC-atXLIB327405P3d02b1
Method	BLASTN
NCBI GI	g4263373
BLAST score	40
E value	8.0e-13
Match length	232
% identity	89
NCBI Description	Arabidopsis thaliana BAC T15G18 from chromosome IV, near 25 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	126980
Contig ID	22753_1.R1010
5'-most EST	LIB3168-016-P1-K1-G6
Method	BLASTN
NCBI GI	g3128139
BLAST score	177
E value	8.0e-95
Match length	450
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	126981
Contig ID	22755_1.R1010
5'-most EST	g1158783
Method	BLASTX
NCBI GI	g3193331
BLAST score	182
E value	3.0e-13
Match length	45
% identity	69
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	126982
Contig ID	22756_1.R1010
5'-most EST	jC-atXLIB327421P3e06b1
Method	BLASTN
NCBI GI	g4455348
BLAST score	249
E value	1.0e-137
Match length	695
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	126983
Contig ID	22758_1.R1010
5'-most EST	jC-atXLIB327405P3d10b1
Method	BLASTX
NCBI GI	g4056441
BLAST score	651
E value	3.0e-76
Match length	141
% identity	100
NCBI Description	(AC005990) Similar to OBP32pep protein gb_U37698 from

Arabidopsis thaliana. [Arabidopsis thaliana]

Seq. No.	126984
Contig ID	22766_1.R1010
5'-most EST	jC-alX24089Q1E1F11b1
Method	BLASTX
NCBI GI	g3128168
BLAST score	620
E value	1.0e-64
Match length	160
% identity	69
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	126985
Contig ID	22767_1.R1010
5'-most EST	jC-atXLIB327405P4d07b1
Method	BLASTN
NCBI GI	g4678291
BLAST score	234
E value	1.0e-128
Match length	497
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	126986
Contig ID	22769_1.R1010
5'-most EST	LIB24-079-Q1-E1-D9
Method	BLASTX
NCBI GI	g1931647
BLAST score	712
E value	3.0e-75
Match length	187
% identity	74
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	126987
Contig ID	22771_1.R1010
5'-most EST	LIB24-079-Q1-E1-E10
Method	BLASTN
NCBI GI	g2564049
BLAST score	165
E value	1.0e-87
Match length	534
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	126988
Contig ID	22773_1.R1010
5'-most EST	jC-atXLIB327405P2e08b2
Method	BLASTX
NCBI GI	g2213584
BLAST score	192
E value	2.0e-14

Match length	70
% identity	49
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	126989
Contig ID	22774_1.R1010
5'-most EST	LIB24-079-Q1-E1-E2
Method	BLASTN
NCBI GI	g4589439
BLAST score	210
E value	1.0e-114
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	126990
Contig ID	22777_1.R1010
5'-most EST	jC-atXLIB327408P3a11b1

Seq. No.	126991
Contig ID	22779_1.R1010
5'-most EST	jC-atXLIB327405P2e06b2
Method	BLASTX
NCBI GI	g3287695
BLAST score	308
E value	5.0e-28
Match length	106
% identity	56
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	126992
Contig ID	22782_1.R1010
5'-most EST	LIB24-079-Q1-E1-F10
Method	BLASTX
NCBI GI	g3702332
BLAST score	353
E value	2.0e-33
Match length	99
% identity	74
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	126993
Contig ID	22783_1.R1010
5'-most EST	jC-atXLIB327405P3e05b1
Method	BLASTX
NCBI GI	g1888557
BLAST score	447
E value	5.0e-44
Match length	160
% identity	60
NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No. 126994

Contig ID	22789_1.R1010
5'-most EST	jC-atXLIB327405P3e02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	71
% identity	49
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	126995
Contig ID	22791_1.R1010
5'-most EST	jC-atXLIB327405P3e03b1
Method	BLASTX
NCBI GI	g2498329
BLAST score	274
E value	1.0e-26
Match length	125
% identity	54
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No.	126996
Contig ID	22793_1.R1010
5'-most EST	LIB3175-024-P1-K1-D12
Method	BLASTX
NCBI GI	g1304227
BLAST score	173
E value	3.0e-28
Match length	85
% identity	74
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	126997
Contig ID	22795_1.R1010
5'-most EST	LIB24-079-Q1-E1-G11
Method	BLASTN
NCBI GI	g4455348
BLAST score	284
E value	1.0e-158
Match length	555
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	126998
Contig ID	22813_1.R1010
5'-most EST	jC-atX24111Q1E1G04a1

Seq. No.	126999
Contig ID	22814_1.R1010
5'-most EST	jC-atXLIB327405P4c05b1
Method	BLASTN
NCBI GI	g2529657
BLAST score	171
E value	4.0e-91
Match length	374
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127000
Contig ID	22821_1.R1010
5'-most EST	LIB24-083-Q1-E1-D7
Method	BLASTN
NCBI GI	g4680765
BLAST score	233
E value	1.0e-128
Match length	264
% identity	99
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	127001
Contig ID	22825_1.R1010
5'-most EST	LIB35-014-Q1-E1-D10
Method	BLASTX
NCBI GI	g4325345
BLAST score	635
E value	2.0e-66
Match length	146
% identity	86
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	127002
Contig ID	22829_1.R1010
5'-most EST	g1216956
Method	BLASTX
NCBI GI	g4314365
BLAST score	706
E value	1.0e-74
Match length	158
% identity	91
NCBI Description	(AC006340) putative copia-like retrotransposon Hopscotch [Arabidopsis thaliana]

Seq. No.	127003
Contig ID	22831_1.R1010
5'-most EST	jC-atXLIB327405P2e11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	4.0e-14

Match length	76
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127004
Contig ID	22835_1.R1010
5'-most EST	g2048945
Method	BLASTN
NCBI GI	g4733952
BLAST score	262
E value	1.0e-145
Match length	394
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	127005
Contig ID	22836_1.R1010
5'-most EST	jC-atXLIB327408P4d01b1
Method	BLASTX
NCBI GI	g4101589
BLAST score	289
E value	1.0e-25
Match length	109
% identity	50
NCBI Description	(AF005050) aspartyl aminopeptidase [Homo sapiens]

Seq. No.	127006
Contig ID	22845_1.R1010
5'-most EST	LIB24-093-Q1-E1-H10
Method	BLASTX
NCBI GI	g1076305
BLAST score	408
E value	9.0e-40
Match length	162
% identity	49
NCBI Description	RNA-binding protein cp31 precursor - Arabidopsis thaliana >gi_681906_dbj_BAA06520_ (D31712) cp31 [Arabidopsis thaliana]

Seq. No.	127007
Contig ID	22848_1.R1010
5'-most EST	jC-alXLIB327434P1d02b1
Method	BLASTX
NCBI GI	g282964
BLAST score	350
E value	6.0e-33
Match length	93
% identity	70
NCBI Description	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia x hybrida]

Seq. No.	127008
Contig ID	22851_1.R1010
5'-most EST	jC-atXLIB327408P3g10b1

Method	BLASTX
NCBI GI	g2262105
BLAST score	563
E value	4.0e-94
Match length	259
% identity	60
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	127009
Contig ID	22854_1.R1010
5'-most EST	jC-atXLIB327405P3e12b1
Method	BLASTX
NCBI GI	g4467107
BLAST score	199
E value	3.0e-15
Match length	176
% identity	9
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	127010
Contig ID	22856_1.R1010
5'-most EST	LIB24-080-Q1-E1-G9
Method	BLASTX
NCBI GI	g4455367
BLAST score	363
E value	2.0e-34
Match length	148
% identity	35
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	127011
Contig ID	22858_1.R1010
5'-most EST	jC-atXLIB327405P2f11b2
Method	BLASTN
NCBI GI	g4309747
BLAST score	197
E value	1.0e-106
Match length	520
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127012
Contig ID	22863_1.R1010
5'-most EST	jC-atXLIB327422P2e12b2
Method	BLASTN
NCBI GI	g3702739
BLAST score	126
E value	3.0e-64
Match length	177
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	127013
Contig ID	22867_1.R1010
5'-most EST	jC-atXP85CG7H12T7b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	1.0e-28
Match length	71
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127014
Contig ID	22868_1.R1010
5'-most EST	jC-atXP91C246J11T7b1
Method	BLASTX
NCBI GI	g629858
BLAST score	566
E value	4.0e-58
Match length	128
% identity	82
NCBI Description	protein kinase C inhibitor - maize

Seq. No.	127015
Contig ID	22873_1.R1010
5'-most EST	jC-atXLIB327405P4f08b1
Method	BLASTX
NCBI GI	g2498731
BLAST score	517
E value	2.0e-52
Match length	152
% identity	63
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	127016
Contig ID	22876_1.R1010
5'-most EST	jC-atXLIB327427P2c02b1
Method	BLASTX
NCBI GI	g133938
BLAST score	580
E value	2.0e-59
Match length	123
% identity	90
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70866_pir__R3SP3 ribosomal protein S3 - spinach chloroplast >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3 [Spinacia oleracea]

Seq. No.	127017
Contig ID	22876_3.R1010
5'-most EST	LIB3175-054-P1-K1-B12
Method	BLASTX
NCBI GI	g133938
BLAST score	645
E value	1.0e-67
Match length	161
% identity	78

NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70866_pir__R3SP3 ribosomal protein S3 - spinach chloroplast >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3 [Spinacia oleracea]
Seq. No.	127018
Contig ID	22883_1.R1010
5'-most EST	LIB25-025-Q1-E1-B4
Method	BLASTX
NCBI GI	g120941
BLAST score	326
E value	7.0e-30
Match length	97
% identity	61
NCBI Description	GAR1 PROTEIN >gi_83030_pir__S19634 nucleolar protein GAR1 - yeast (Saccharomyces cerevisiae) >gi_3728_emb_CAA45162_ (X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Gar1p: Small nucleolar RNA protein required for pre-rRNA splicing [Saccharomyces cerevisiae]
Seq. No.	127019
Contig ID	22887_1.R1010
5'-most EST	jC-atXLIB327430P1b08b1
Method	BLASTX
NCBI GI	g4501865
BLAST score	231
E value	3.0e-36
Match length	138
% identity	54
NCBI Description	ATP citrate lyase >gi_1703083_sp_P53396_ACLY_HUMAN ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_105392_pir__S21173 ATP citrate (pro-S)-lyase - human >gi_28935_emb_CAA45614_ (X64330) ATP-citrate (pro-S-)-lyase [Homo sapiens]
Seq. No.	127020
Contig ID	22887_2.R1010
5'-most EST	g397254
Method	BLASTX
NCBI GI	g4107343
BLAST score	504
E value	4.0e-51
Match length	163
% identity	60
NCBI Description	(AJ224922) ATP citrate lyase [Sordaria macrospora]
Seq. No.	127021
Contig ID	22892_1.R1010
5'-most EST	LIB24-081-Q1-E1-D2
Method	BLASTX
NCBI GI	g4455185
BLAST score	180
E value	3.0e-13
Match length	89
% identity	38
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	127022
Contig ID	22894_1.R1010
5'-most EST	LIB3176-067-P1-K1-E7

Seq. No.	127023
Contig ID	22899_1.R1010
5'-most EST	jC-atXLIB327430P4f06b1

Seq. No.	127024
Contig ID	22900_1.R1010
5'-most EST	jC-atXLIB327405P2g12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	2.0e-26
Match length	70
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127025
Contig ID	22900_3.R1010
5'-most EST	jC-atXLIB327405P2g12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127026
Contig ID	22906_1.R1010
5'-most EST	jC-atXLIB327405P3g02b1
Method	BLASTN
NCBI GI	g2244829
BLAST score	394
E value	0.0e+00
Match length	485
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	127027
Contig ID	22912_1.R1010
5'-most EST	LIB24-103-Q1-E2-D9

Seq. No.	127028
Contig ID	22912_2.R1010
5'-most EST	jC-atXLIB327405P3g08b1

Seq. No.	127029
Contig ID	22915_1.R1010
5'-most EST	jC-atXLIB327431P4c11a1
Method	BLASTX
NCBI GI	g3335371
BLAST score	856

E value	1.0e-101
Match length	222
% identity	89
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	127030
Contig ID	22915_2.R1010
5'-most EST	LIB25-024-Q1-E1-D3
Method	BLASTX
NCBI GI	g3335371
BLAST score	683
E value	6.0e-72
Match length	143
% identity	98
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	127031
Contig ID	22916_1.R1010
5'-most EST	LIB24-081-Q1-E1-F8
Method	BLASTN
NCBI GI	g4159704
BLAST score	507
E value	0.0e+00
Match length	580
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	127032
Contig ID	22920_1.R1010
5'-most EST	LIB24-081-Q1-E1-G11

Seq. No.	127033
Contig ID	22925_1.R1010
5'-most EST	jC-atXLIB327405P3g10b1

Seq. No.	127034
Contig ID	22928_1.R1010
5'-most EST	jC-alX24100Q1E1A10b1
Method	BLASTX
NCBI GI	g1931642
BLAST score	736
E value	2.0e-78
Match length	142
% identity	99
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	127035
Contig ID	22930_1.R1010
5'-most EST	jC-alX24086Q1E1B09b1
Method	BLASTN
NCBI GI	g1070003
BLAST score	46
E value	2.0e-16

Match length	46
% identity	100
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	127036
Contig ID	22930_2.R1010
5'-most EST	jC-atXLIB327414P3f05a1

Seq. No.	127037
Contig ID	22942_1.R1010
5'-most EST	jC-atXLIB327405P3f01a1
Method	BLASTN
NCBI GI	g3169169
BLAST score	178
E value	3.0e-95
Match length	293
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127038
Contig ID	22946_1.R1010
5'-most EST	jC-atXP73CF3D11T7b1
Method	BLASTX
NCBI GI	g4325369
BLAST score	692
E value	7.0e-73
Match length	129
% identity	98
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	127039
Contig ID	22952_1.R1010
5'-most EST	jC-atXLIB327402P1d11a1
Method	BLASTX
NCBI GI	g2245066
BLAST score	206
E value	5.0e-16
Match length	108
% identity	34
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	127040
Contig ID	22954_1.R1010
5'-most EST	jC-atXLIB327421P3d07b1

Seq. No.	127041
Contig ID	22956_1.R1010
5'-most EST	jC-atX25002Q1E1A07b1
Method	BLASTX
NCBI GI	g1351359
BLAST score	270
E value	8.0e-24
Match length	61
% identity	72

NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein - potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	127042
Contig ID	22964_1.R1010
5'-most EST	jC-atXP82CG1G6T7b1
Method	BLASTN
NCBI GI	g2924654
BLAST score	439
E value	0.0e+00
Match length	562
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]

Seq. No.	127043
Contig ID	22965_1.R1010
5'-most EST	jC-alX24081Q1E1E09b1
Method	BLASTN
NCBI GI	g3785992
BLAST score	296
E value	1.0e-165
Match length	651
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127044
Contig ID	22969_1.R1010
5'-most EST	jC-atXLIB327405P2g09b2
Method	BLASTN
NCBI GI	g3242970
BLAST score	500
E value	0.0e+00
Match length	548
% identity	99
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	127045
Contig ID	22971_1.R1010
5'-most EST	g957736

Seq. No.	127046
Contig ID	22988_1.R1010
5'-most EST	jC-atXP118C144H8T7077d2
Method	BLASTX
NCBI GI	g3327222
BLAST score	374
E value	1.0e-35
Match length	182
% identity	42
NCBI Description	(AB014604) KIAA0704 protein [Homo sapiens]

Seq. No.	127047
Contig ID	22988_3.R1010
5'-most EST	jC-atXLIB327406P2a04b1
Method	BLASTX
NCBI GI	g2239236
BLAST score	161
E value	9.0e-11
Match length	71
% identity	46
NCBI Description	(Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]

Seq. No.	127048
Contig ID	22990_2.R1010
5'-most EST	g2393214
Method	BLASTN
NCBI GI	g2351066
BLAST score	417
E value	0.0e+00
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	127049
Contig ID	22990_3.R1010
5'-most EST	LIB24-082-Q1-E1-F3
Method	BLASTX
NCBI GI	g2829792
BLAST score	793
E value	7.0e-85
Match length	190
% identity	73
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS I) >gi_1781353_emb_CAA71442_ (Y10416) soluble starch (bacterial glycogen) synthase [Solanum tuberosum]

Seq. No.	127050
Contig ID	22990_4.R1010
5'-most EST	g2596716
Method	BLASTX
NCBI GI	g2833377
BLAST score	160
E value	8.0e-11
Match length	37
% identity	73
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SSS) >gi_542161_pir__JQ2322 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - rice >gi_450485_dbj_BAA03739_ (D16202) soluble starch synthase precursor [Oryza sativa]

Seq. No.	127051
Contig ID	22991_1.R1010
5'-most EST	jC-atXP73CF2H7T7d2
Method	BLASTX
NCBI GI	g3859591

BLAST score	221
E value	1.0e-17
Match length	99
% identity	41
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	127052
Contig ID	23002_1.R1010
5'-most EST	LIB3177-079-P1-K1-G10
Method	BLASTN
NCBI GI	g4678705
BLAST score	40
E value	5.0e-13
Match length	225
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	127053
Contig ID	23009_1.R1010
5'-most EST	jC-atXLIB327405P1h04b2
Method	BLASTX
NCBI GI	g4154352
BLAST score	293
E value	6.0e-26
Match length	215
% identity	36
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	127054
Contig ID	23015_1.R1010
5'-most EST	LIB24-082-Q1-E1-H9

Seq. No.	127055
Contig ID	23016_1.R1010
5'-most EST	jC-alX24084Q1E1C09b1
Method	BLASTN
NCBI GI	g2335089
BLAST score	102
E value	3.0e-50
Match length	298
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127056
Contig ID	23019_1.R1010
5'-most EST	g2759702
Method	BLASTN
NCBI GI	g2337888
BLAST score	283
E value	1.0e-158
Match length	339
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	127057
Contig ID	23021_1.R1010
5'-most EST	jC-atXLIB327417P4g02b1
Method	BLASTN
NCBI GI	g4220645
BLAST score	266
E value	1.0e-147
Match length	750
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	127058
Contig ID	23023_1.R1010
5'-most EST	jC-atXLIB327405P2f10b2

Seq. No.	127059
Contig ID	23025_1.R1010
5'-most EST	jC-atXLIB327405P4f03b1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	5.0e-19
Match length	50
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	127060
Contig ID	23028_1.R1010
5'-most EST	jC-atXLIB327405P3f02b1
Method	BLASTX
NCBI GI	g1001430
BLAST score	182
E value	3.0e-13
Match length	148
% identity	36
NCBI Description	(D63999) ORF1 [Synechocystis sp.]

Seq. No.	127061
Contig ID	23031_1.R1010
5'-most EST	jC-atXLIB327405P3f12b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127062
Contig ID	23035_1.R1010
5'-most EST	jC-atXLIB327405P4f09b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	463
E value	3.0e-46
Match length	115

% identity	77
NCBI Description	(AC006232) putative lipase. [Arabidopsis thaliana]

Seq. No.	127063
Contig ID	23036_1.R1010
5'-most EST	jC-atXLIB327405P4f10b1
Method	BLASTN
NCBI GI	g3510340
BLAST score	155
E value	1.0e-81
Match length	350
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	127064
Contig ID	23038_1.R1010
5'-most EST	LIB3176-056-P1-K1-H7

Seq. No.	127065
Contig ID	23046_1.R1010
5'-most EST	jC-atXLIB327405P2g05b2
Method	BLASTX
NCBI GI	g4415915
BLAST score	373
E value	3.0e-37
Match length	139
% identity	58
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	127066
Contig ID	23052_1.R1010
5'-most EST	jC-atXLIB327420P1d03b1
Method	BLASTX
NCBI GI	g4204257
BLAST score	471
E value	4.0e-47
Match length	133
% identity	64
NCBI Description	(AC005223) 5493 [Arabidopsis thaliana]

Seq. No.	127067
Contig ID	23056_1.R1010
5'-most EST	g2749363
Method	BLASTN
NCBI GI	g4775267
BLAST score	303
E value	1.0e-170
Match length	412
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for AGP6 protein

Seq. No.	127068
Contig ID	23056_2.R1010
5'-most EST	LIB24-083-Q1-E1-E7
Method	BLASTN

NCBI GI	g4775267
BLAST score	372
E value	0.0e+00
Match length	408
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for AGP6 protein

Seq. No.	127069
Contig ID	23058_1.R1010
5'-most EST	jC-atXP73CF3E1T7d2
Method	BLASTX
NCBI GI	g3367523
BLAST score	544
E value	3.0e-92
Match length	180
% identity	98
NCBI Description	(AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No.	127070
Contig ID	23058_2.R1010
5'-most EST	jC-atXLIB327405P3g04b1
Method	BLASTN
NCBI GI	g3282170
BLAST score	202
E value	1.0e-109
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127071
Contig ID	23062_1.R1010
5'-most EST	LIB24-083-Q1-E1-F5

Seq. No.	127072
Contig ID	23062_2.R1010
5'-most EST	jC-atX22083Q1E2A08a1

Seq. No.	127073
Contig ID	23063_1.R1010
5'-most EST	g406638
Method	BLASTN
NCBI GI	g3046850
BLAST score	232
E value	1.0e-128
Match length	276
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	127074
Contig ID	23065_1.R1010
5'-most EST	jC-atXLIB327405P2h03b2
Method	BLASTN
NCBI GI	g2618599
BLAST score	184

E value	6.0e-99
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	127075
Contig ID	23070_1.R1010
5'-most EST	jC-atXLIB327422P1d05b1
Method	BLASTN
NCBI GI	g4589950
BLAST score	384
E value	0.0e+00
Match length	682
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	127076
Contig ID	23072_1.R1010
5'-most EST	jC-atXLIB327417P2a01b1
Method	BLASTN
NCBI GI	g4220640
BLAST score	224
E value	1.0e-122
Match length	613
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	127077
Contig ID	23077_1.R1010
5'-most EST	jC-atXLIB327409P3e06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	4.0e-24
Match length	63
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127078
Contig ID	23077_2.R1010
5'-most EST	jC-alXLIB327436P2c05b1
Method	BLASTX
NCBI GI	g4538939
BLAST score	847
E value	7.0e-91
Match length	293
% identity	63
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	127079
Contig ID	23081_1.R1010
5'-most EST	jC-atXLIB327406P2b09b1

Seq. No.	127080
Contig ID	23082_1.R1010
5'-most EST	jC-atXLIB327405P2g11b2
Method	BLASTX
NCBI GI	g4376650
BLAST score	466
E value	1.0e-46
Match length	144
% identity	63
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	127081
Contig ID	23090_1.R1010
5'-most EST	jC-atXLIB327405P3f10b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	297
E value	1.0e-26
Match length	141
% identity	41
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	127082
Contig ID	23096_1.R1010
5'-most EST	jC-atXP78C229N15T7b1
Method	BLASTX
NCBI GI	g1086263
BLAST score	415
E value	3.0e-40
Match length	195
% identity	47
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	127083
Contig ID	23096_2.R1010
5'-most EST	jC-atXL1040Q1E1B01a1
Method	BLASTX
NCBI GI	g1086263
BLAST score	375
E value	1.0e-35
Match length	161
% identity	50
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	127084
Contig ID	23099_1.R1010
5'-most EST	jC-alX24082Q1E1G10b1

Seq. No.	127085
Contig ID	23099_2.R1010
5'-most EST	LIB3168-053-P1-K1-D4

Seq. No.	127086
Contig ID	23103_1.R1010

5'-most EST	g16963
Method	BLASTN
NCBI GI	g2828187
BLAST score	319
E value	1.0e-179
Match length	549
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No.	127087
Contig ID	23104_1.R1010
5'-most EST	LIB24-084-Q1-E1-F5
Method	BLASTN
NCBI GI	g3319365
BLAST score	172
E value	8.0e-92
Match length	384
% identity	91
NCBI Description	Arabidopsis thaliana BAC T24M8

Seq. No.	127088
Contig ID	23105_1.R1010
5'-most EST	g2062943
Method	BLASTX
NCBI GI	g2330739
BLAST score	312
E value	2.0e-28
Match length	91
% identity	59
NCBI Description	(Z98598) putative transcriptional regulator [Schizosaccharomyces pombe]

Seq. No.	127089
Contig ID	23107_1.R1010
5'-most EST	jC-atXP82CG2B10T7b1
Method	BLASTX
NCBI GI	g4587615
BLAST score	1009
E value	1.0e-110
Match length	200
% identity	98
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	127090
Contig ID	23114_4.R1010
5'-most EST	ARABL1-038-Q1-B1-F5
Method	BLASTN
NCBI GI	g11957
BLAST score	79
E value	3.0e-36
Match length	83
% identity	49
NCBI Description	Rice complete chloroplast genome

Seq. No.	127091
Contig ID	23116_1.R1010
5'-most EST	jC-atXLIB327405P2h08b2
Method	BLASTX
NCBI GI	g3540196
BLAST score	681
E value	2.0e-71
Match length	173
% identity	76
NCBI Description	(AC004260) Putative amp-binding protein [Arabidopsis thaliana]

Seq. No.	127092
Contig ID	23117_1.R1010
5'-most EST	jC-atXP25C125I3T7073a1
Method	BLASTN
NCBI GI	g3449315
BLAST score	508
E value	0.0e+00
Match length	623
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	127093
Contig ID	23128_1.R1010
5'-most EST	LIB24-085-Q1-E1-B4
Method	BLASTX
NCBI GI	g1723761
BLAST score	239
E value	5.0e-20
Match length	145
% identity	34
NCBI Description	HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION >gi_2132628_pir__S64571 probable membrane protein YGR245c - yeast (Saccharomyces cerevisiae) >gi_1323444_emb_CAA97274_ (Z73030) ORF YGR245c [Saccharomyces cerevisiae] >gi_1702955_emb_CAA68967_ (Y07703) unknown ORF [Saccharomyces cerevisiae]

Seq. No.	127094
Contig ID	23146_1.R1010
5'-most EST	jC-atXLIB327406P1a08b1
Method	BLASTN
NCBI GI	g4589436
BLAST score	290
E value	1.0e-162
Match length	313
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	127095
Contig ID	23155_1.R1010
5'-most EST	jC-atXLIB327406P1a07b1
Method	BLASTN
NCBI GI	g2980787

BLAST score	297
E value	1.0e-166
Match length	443
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	127096
Contig ID	23161_1.R1010
5'-most EST	jC-alX24085Q1E1E02b1

Seq. No.	127097
Contig ID	23165_1.R1010
5'-most EST	g3449731
Method	BLASTX
NCBI GI	g2970034
BLAST score	134
E value	1.0e-15
Match length	73
% identity	60
NCBI Description	(D88536) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	127098
Contig ID	23169_1.R1010
5'-most EST	jC-atXLIB327406P2b02b1
Method	BLASTN
NCBI GI	g2529657
BLAST score	236
E value	1.0e-130
Match length	483
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127099
Contig ID	23176_1.R1010
5'-most EST	LIB24-085-Q1-E1-H10
Method	BLASTN
NCBI GI	g2351065
BLAST score	44
E value	2.0e-15
Match length	423
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	127100
Contig ID	23178_1.R1010
5'-most EST	jC-alX24085Q1E1F08b1
Method	BLASTX
NCBI GI	g2244793
BLAST score	734
E value	4.0e-78
Match length	149
% identity	45
NCBI Description	(Z97336) TMV resistance protein homolog [Arabidopsis thaliana]

Seq. No.	127101
Contig ID	23179_1.R1010
5'-most EST	LIB25-046-Q1-E1-A3
Method	BLASTX
NCBI GI	g2760326
BLAST score	1144
E value	1.0e-125
Match length	318
% identity	70
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	127102
Contig ID	23186_1.R1010
5'-most EST	LIB24-085-Q1-E1-G5
Method	BLASTN
NCBI GI	g4006885
BLAST score	158
E value	2.0e-83
Match length	408
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	127103
Contig ID	23202_1.R1010
5'-most EST	LIB24-086-Q1-E1-A11

Seq. No.	127104
Contig ID	23203_1.R1010
5'-most EST	jC-atXLIB327405P2h09b2

Seq. No.	127105
Contig ID	23203_2.R1010
5'-most EST	jC-atX24086Q1E1A02a1
Method	BLASTX
NCBI GI	g3183405
BLAST score	201
E value	2.0e-15
Match length	72
% identity	53
NCBI Description	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi_3451305_emb_CAA20442_ (AL031324) very hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	127106
Contig ID	23205_1.R1010
5'-most EST	jC-atXLIB327417P1f04b1
Method	BLASTX
NCBI GI	g2147328
BLAST score	491
E value	5.0e-49
Match length	242
% identity	42
NCBI Description	dioscorin class B - Dioscorea cayenensis (fragment)

Seq. No. 127107

Contig ID	23209_1.R1010
5'-most EST	LIB24-086-Q1-E1-A8
Method	BLASTX
NCBI GI	g4335750
BLAST score	553
E value	2.0e-56
Match length	146
% identity	74
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	127108
Contig ID	23215_1.R1010
5'-most EST	LIB25-025-Q1-E1-B10
Method	BLASTX
NCBI GI	g2736147
BLAST score	548
E value	3.0e-56
Match length	130
% identity	70
NCBI Description	(AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No.	127109
Contig ID	23216_1.R1010
5'-most EST	jC-atXLIB327406P2a06b1
Method	BLASTX
NCBI GI	g4559398
BLAST score	692
E value	5.0e-73
Match length	150
% identity	88
NCBI Description	(AC006526) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	127110
Contig ID	23218_1.R1010
5'-most EST	jC-atXLIB327405P3h03b1
Method	BLASTX
NCBI GI	g2501021
BLAST score	361
E value	7.0e-36
Match length	154
% identity	58
NCBI Description	LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	127111
Contig ID	23234_1.R1010
5'-most EST	g498683

Seq. No.	127112
Contig ID	23239_1.R1010
5'-most EST	jC-atXLIB327406P2a07b1
Method	BLASTX

NCBI GI	g3281850
BLAST score	892
E value	2.0e-96
Match length	168
% identity	99
NCBI Description	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]

Seq. No.	127113
Contig ID	23246_1.R1010
5'-most EST	jC-atXP115C250G2T7069d1
Method	BLASTX
NCBI GI	g3355474
BLAST score	58
E value	1.0e-66
Match length	145
% identity	87
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	127114
Contig ID	23246_2.R1010
5'-most EST	g907230
Method	BLASTX
NCBI GI	g3355474
BLAST score	1035
E value	1.0e-113
Match length	218
% identity	93
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	127115
Contig ID	23248_1.R1010
5'-most EST	jC-atXLIB327414P4e12a2
Method	BLASTX
NCBI GI	g2244783
BLAST score	513
E value	7.0e-52
Match length	124
% identity	86
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127116
Contig ID	23250_1.R1010
5'-most EST	jC-atXLIB327406P3a05b2
Method	BLASTX
NCBI GI	g2982311
BLAST score	329
E value	3.0e-30
Match length	160
% identity	49
NCBI Description	(AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No.	127117
Contig ID	23252_1.R1010
5'-most EST	jC-atXLIB327406P3a06b2
Method	BLASTX

NCBI GI	g4239692
BLAST score	680
E value	1.0e-71
Match length	148
% identity	85
NCBI Description	(AJ132745) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127118
Contig ID	23253_1.R1010
5'-most EST	jC-atXLIB327404P3a07a1
Method	BLASTN
NCBI GI	g3449329
BLAST score	549
E value	0.0e+00
Match length	556
% identity	50
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	127119
Contig ID	23253_2.R1010
5'-most EST	jC-atXLIB327406P1b03b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	51
E value	1.0e-19
Match length	403
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	127120
Contig ID	23259_1.R1010
5'-most EST	jC-atXLIB327418P4c03b1

Seq. No.	127121
Contig ID	23260_1.R1010
5'-most EST	jC-atXLIB327407P1e07b2
Method	BLASTX
NCBI GI	g4455270
BLAST score	270
E value	2.0e-23
Match length	131
% identity	46
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	127122
Contig ID	23260_2.R1010
5'-most EST	LIB35-056-Q1-E2-D3
Method	BLASTX
NCBI GI	g2501337
BLAST score	246
E value	5.0e-21
Match length	100
% identity	46
NCBI Description	AMINE OXIDASE PRECURSOR [COPPER-CONTAINING] >gi_2129875_pir__C44239 amine oxidase (copper-containing)

(EC 1.4.3.6) precursor - garden pea >gi_685198 (L39931) copper amine oxidase [Pisum sativum]

Seq. No.	127123
Contig ID	23261_1.R1010
5'-most EST	jC-atXLIB327406P1b07b1

Seq. No.	127124
Contig ID	23272_1.R1010
5'-most EST	jC-atXLIB327408P2b05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	3.0e-30
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127125
Contig ID	23276_1.R1010
5'-most EST	ARABL1-02-Q1-B1-B10
Method	BLASTN
NCBI GI	g4314374
BLAST score	318
E value	1.0e-179
Match length	366
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127126
Contig ID	23280_1.R1010
5'-most EST	g1053382
Method	BLASTX
NCBI GI	g4587609
BLAST score	598
E value	4.0e-62
Match length	112
% identity	100
NCBI Description	(AC006951) unknown protein [Arabidopsis thaliana]

Seq. No.	127127
Contig ID	23291_1.R1010
5'-most EST	g502099
Method	BLASTX
NCBI GI	g2462840
BLAST score	609
E value	4.0e-63
Match length	114
% identity	100
NCBI Description	(AF000657) cytochrome C [Arabidopsis thaliana]

Seq. No.	127128
Contig ID	23292_1.R1010
5'-most EST	jC-atXLIB327405P2h11b2
Method	BLASTN

NCBI GI	g3241917
BLAST score	585
E value	0.0e+00
Match length	785
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	127129
Contig ID	23294_1.R1010
5'-most EST	LIB24-087-Q1-E1-B8
Method	BLASTX
NCBI GI	g4455313
BLAST score	477
E value	1.0e-47
Match length	191
% identity	52
NCBI Description	(AL035528) fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]

Seq. No.	127130
Contig ID	23304_1.R1010
5'-most EST	jC-atXLIB327406P1a04b1

Seq. No.	127131
Contig ID	23306_1.R1010
5'-most EST	jC-atXLIB327406P1a05b1
Method	BLASTX
NCBI GI	g3776574
BLAST score	443
E value	9.0e-44
Match length	100
% identity	88
NCBI Description	(AC005388) Similar to T11J7.13 gi_2880051 putative protein kinase from Arabidopsis thaliana BAC gb_AC002340. [Arabidopsis thaliana]

Seq. No.	127132
Contig ID	23307_1.R1010
5'-most EST	g410357
Method	BLASTX
NCBI GI	g4406819
BLAST score	333
E value	8.0e-31
Match length	197
% identity	42
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	127133
Contig ID	23307_2.R1010
5'-most EST	LIB25-020-Q1-E1-B4
Method	BLASTN
NCBI GI	g4159700
BLAST score	544
E value	0.0e+00
Match length	544
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence
Seq. No.	127134
Contig ID	23308_1.R1010
5'-most EST	g937717
Seq. No.	127135
Contig ID	23312_1.R1010
5'-most EST	jC-atXLIB327406P3a01b2
Method	BLASTN
NCBI GI	g4220637
BLAST score	418
E value	0.0e+00
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]
Seq. No.	127136
Contig ID	23314_1.R1010
5'-most EST	jC-atXLIB327406P4a01b2
Method	BLASTN
NCBI GI	g2264314
BLAST score	65
E value	9.0e-28
Match length	197
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.	127137
Contig ID	23316_1.R1010
5'-most EST	LIB24-087-Q1-E1-E7
Seq. No.	127138
Contig ID	23318_1.R1010
5'-most EST	jC-atXLIB327406P3a10b2
Method	BLASTX
NCBI GI	g4585993
BLAST score	394
E value	4.0e-38
Match length	75
% identity	100
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]
Seq. No.	127139
Contig ID	23321_1.R1010
5'-most EST	jC-atXLIB327406P4a10b2
Method	BLASTN
NCBI GI	g4519187
BLAST score	270
E value	1.0e-150
Match length	454
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K1G2, complete sequence

Seq. No.	127140
Contig ID	23325_1.R1010
5'-most EST	LIB24-087-Q1-E1-G4

Seq. No.	127141
Contig ID	23326_1.R1010
5'-most EST	jC-atXLIB327422P2f07b2
Method	BLASTX
NCBI GI	g3122936
BLAST score	221
E value	2.0e-17
Match length	81
% identity	52
NCBI Description	THIOREDOXIN (TRX) >gi_2511765 (AF023161) thioredoxin [Mycobacterium smegmatis]

Seq. No.	127142
Contig ID	23329_1.R1010
5'-most EST	jC-atXLIB327406P1b05b1
Method	BLASTX
NCBI GI	g4115381
BLAST score	618
E value	2.0e-64
Match length	127
% identity	95
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No.	127143
Contig ID	23333_1.R1010
5'-most EST	jC-atXLIB327406P2b10b1
Method	BLASTX
NCBI GI	g2160176
BLAST score	230
E value	1.0e-18
Match length	177
% identity	34
NCBI Description	(AC000132) F21M12.25 gene product [Arabidopsis thaliana]

Seq. No.	127144
Contig ID	23353_1.R1010
5'-most EST	LIB24-088-Q1-E1-C7
Method	BLASTX
NCBI GI	g541980
BLAST score	340
E value	9.0e-32
Match length	70
% identity	91
NCBI Description	guanine nucleotide regulatory protein - fava bean

Seq. No.	127145
Contig ID	23354_1.R1010
5'-most EST	LIB24-088-Q1-E1-C8
Method	BLASTX
NCBI GI	g3335375
BLAST score	575

E value	2.0e-59
Match length	106
% identity	98
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	127146
Contig ID	23358_1.R1010
5'-most EST	jC-atXLIB327406P1a02b1

Seq. No.	127147
Contig ID	23361_1.R1010
5'-most EST	LIB24-090-Q1-E1-D7
Method	BLASTN
NCBI GI	g4582444
BLAST score	138
E value	1.0e-71
Match length	355
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	127148
Contig ID	23362_1.R1010
5'-most EST	jC-alX24090Q1E1G05b1
Method	BLASTX
NCBI GI	g3184073
BLAST score	202
E value	9.0e-16
Match length	123
% identity	35
NCBI Description	(AL023779) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	127149
Contig ID	23369_1.R1010
5'-most EST	LIB24-088-Q1-E1-F2
Method	BLASTN
NCBI GI	g3193311
BLAST score	152
E value	6.0e-80
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	127150
Contig ID	23370_1.R1010
5'-most EST	LIB24-088-Q1-E1-F5
Method	BLASTX
NCBI GI	g3281853
BLAST score	193
E value	2.0e-14
Match length	65
% identity	55
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	127151
Contig ID	23374_1.R1010
5'-most EST	jC-atXmonuni10Bb04b1

Method	BLASTX
NCBI GI	g585421
BLAST score	803
E value	7.0e-86
Match length	246
% identity	60
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	127152
Contig ID	23384_1.R1010
5'-most EST	jC-atXP125C133I5T7036a1
Method	BLASTX
NCBI GI	g3511285
BLAST score	161
E value	4.0e-53
Match length	188
% identity	62
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	127153
Contig ID	23384_2.R1010
5'-most EST	jC-atXLIB327406P1a11b1
Method	BLASTX
NCBI GI	g3511285
BLAST score	458
E value	1.0e-45
Match length	129
% identity	67
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	127154
Contig ID	23385_1.R1010
5'-most EST	jC-alXLIB327435P4b11b1
Method	BLASTN
NCBI GI	g3133272
BLAST score	628
E value	0.0e+00
Match length	636
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No.	127155
Contig ID	23390_1.R1010
5'-most EST	jC-atXP37C157O19T7d2
Method	BLASTN
NCBI GI	g4757400
BLAST score	180
E value	2.0e-96
Match length	620
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20, complete sequence

Seq. No.	127156
Contig ID	23390_2.R1010
5'-most EST	jC-alX24089Q1E1A11b1
Method	BLASTN
NCBI GI	g4757400
BLAST score	303
E value	1.0e-170
Match length	399
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20, complete sequence

Seq. No.	127157
Contig ID	23411_1.R1010
5'-most EST	jC-atXLIB327411P1f03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	61
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	127158
Contig ID	23413_1.R1010
5'-most EST	LIB3234-026-Q1-K1-F8

Seq. No.	127159
Contig ID	23417_1.R1010
5'-most EST	LIB24-089-Q1-E1-D11
Method	BLASTX
NCBI GI	g3080395
BLAST score	242
E value	2.0e-20
Match length	121
% identity	55
NCBI Description	(AL022603) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127160
Contig ID	23419_1.R1010
5'-most EST	LIB25-116-Q1-E1-C8
Method	BLASTX
NCBI GI	g4049348
BLAST score	545
E value	9.0e-56
Match length	119
% identity	92
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	127161
Contig ID	23422_1.R1010
5'-most EST	LIB24-089-Q1-E1-D7
Method	BLASTX
NCBI GI	g2842757
BLAST score	329

E value	3.0e-30
Match length	204
% identity	47
NCBI Description	LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi_1806261_emb_CAA41453_ (X58577) DNA-binding protein; bZIP type [Petroselinum crispum]

Seq. No.	127162
Contig ID	23425_1.R1010
5'-most EST	jC-atXLIB327406P3c08b2
Method	BLASTN
NCBI GI	g4757678
BLAST score	305
E value	1.0e-171
Match length	417
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	127163
Contig ID	23434_1.R1010
5'-most EST	jC-atXLIB327406P2d04b1
Method	BLASTX
NCBI GI	g4732105
BLAST score	148
E value	3.0e-34
Match length	220
% identity	39
NCBI Description	(AF129081) COP9 complex homolog subunit 3 DCH3 [Drosophila melanogaster]

Seq. No.	127164
Contig ID	23435_1.R1010
5'-most EST	jC-atXLIB327406P1d06b1
Method	BLASTN
NCBI GI	g3399678
BLAST score	211
E value	1.0e-115
Match length	376
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127165
Contig ID	23439_1.R1010
5'-most EST	jC-atXLIB327401P3f04b2
Method	BLASTX
NCBI GI	g3122673
BLAST score	991
E value	1.0e-108
Match length	204
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	127166
Contig ID	23441_1.R1010

5'-most EST	jC-atXLIB327408P1a09b1
Method	BLASTX
NCBI GI	g3212866
BLAST score	1133
E value	0.0e+00
Match length	407
% identity	90
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	127167
Contig ID	23444_1.R1010
5'-most EST	LIB24-089-Q1-E1-G11
Method	BLASTX
NCBI GI	g3176725
BLAST score	643
E value	2.0e-67
Match length	167
% identity	65
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]

Seq. No.	127168
Contig ID	23450_1.R1010
5'-most EST	LIB25-023-Q1-E1-E3
Method	BLASTX
NCBI GI	g3785990
BLAST score	200
E value	2.0e-15
Match length	119
% identity	35
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127169
Contig ID	23454_1.R1010
5'-most EST	jC-atXLIB327406P4d10b2
Method	BLASTX
NCBI GI	g3337366
BLAST score	554
E value	8.0e-57
Match length	183
% identity	67
NCBI Description	(AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	127170
Contig ID	23469_1.R1010
5'-most EST	LIB3234-010-P1-K1-G2
Method	BLASTN
NCBI GI	g4199934
BLAST score	83
E value	1.0e-38
Match length	182
% identity	86
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No. 127171

Contig ID	23473_1.R1010
5'-most EST	LIB25-081-Q1-E1-D2
Method	BLASTN
NCBI GI	g2980757
BLAST score	464
E value	0.0e+00
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	127172
Contig ID	23476_1.R1010
5'-most EST	LIB24-090-Q1-E1-B6
Method	BLASTX
NCBI GI	g4559333
BLAST score	603
E value	9.0e-63
Match length	139
% identity	61
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	127173
Contig ID	23485_1.R1010
5'-most EST	LIB24-090-Q1-E1-C5

Seq. No.	127174
Contig ID	23499_1.R1010
5'-most EST	g1054319
Method	BLASTX
NCBI GI	g3859114
BLAST score	961
E value	1.0e-104
Match length	187
% identity	99
NCBI Description	(AF031608) MS5-like protein [Arabidopsis thaliana]

Seq. No.	127175
Contig ID	23502_1.R1010
5'-most EST	jC-atXLIB327406P4c09b2
Method	BLASTN
NCBI GI	g4584339
BLAST score	280
E value	1.0e-156
Match length	640
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence

Seq. No.	127176
Contig ID	23513_1.R1010
5'-most EST	jC-atXLIB327427P3d04b2
Method	BLASTX
NCBI GI	g1903364
BLAST score	765
E value	3.0e-81
Match length	153

% identity	99
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	127177
Contig ID	23514_1.R1010
5'-most EST	g2048554
Method	BLASTN
NCBI GI	g3152602
BLAST score	311
E value	1.0e-174
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127178
Contig ID	23521_1.R1010
5'-most EST	g906320
Method	BLASTX
NCBI GI	g3337091
BLAST score	127
E value	1.0e-06
Match length	182
% identity	58
NCBI Description	(AB016204) polygalacturonase inhibitor (PGIP) [Citrus unshiu]

Seq. No.	127179
Contig ID	23521_2.R1010
5'-most EST	LIB24-090-Q1-E1-F9
Method	BLASTX
NCBI GI	g3337091
BLAST score	717
E value	7.0e-76
Match length	187
% identity	44
NCBI Description	(AB016204) polygalacturonase inhibitor (PGIP) [Citrus unshiu]

Seq. No.	127180
Contig ID	23527_1.R1010
5'-most EST	jC-atXLIB327417P1d05b1

Seq. No.	127181
Contig ID	23535_1.R1010
5'-most EST	jC-atXLIB327406P4d11b1
Method	BLASTX
NCBI GI	g4455192
BLAST score	259
E value	1.0e-156
Match length	309
% identity	92
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	127182
Contig ID	23543_1.R1010

5'-most EST	LIB24-090-Q1-E1-H9
Method	BLASTX
NCBI GI	g3367576
BLAST score	165
E value	2.0e-11
Match length	84
% identity	42
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	127183
Contig ID	23544_1.R1010
5'-most EST	LIB24-091-Q1-E1-A1
Method	BLASTN
NCBI GI	g4538949
BLAST score	148
E value	1.0e-77
Match length	367
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	127184
Contig ID	23547_1.R1010
5'-most EST	jC-alX24091Q1E1A12b1

Seq. No.	127185
Contig ID	23549_2.R1010
5'-most EST	jC-atXLIB327406P3b05b2
Method	BLASTX
NCBI GI	g3928150
BLAST score	461
E value	6.0e-46
Match length	158
% identity	57
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	127186
Contig ID	23562_1.R1010
5'-most EST	jC-atXLIB327406P2c04b1
Method	BLASTX
NCBI GI	g4102582
BLAST score	637
E value	2.0e-66
Match length	204
% identity	45
NCBI Description	(AF013115) CAO [Arabidopsis thaliana]

Seq. No.	127187
Contig ID	23567_1.R1010
5'-most EST	jC-atXLIB327406P2c02b1
Method	BLASTX
NCBI GI	g932
BLAST score	167
E value	2.0e-11
Match length	115
% identity	37
NCBI Description	(X53744) 68kDA subunit of signal recognition particle

[Canis familiaris]

Seq. No.	127188
Contig ID	23571_1.R1010
5'-most EST	jC-atXLIB327406P1c11b1
Method	BLASTN
NCBI GI	g2924653
BLAST score	366
E value	0.0e+00
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	127189
Contig ID	23572_1.R1010
5'-most EST	jC-atXLIB327406P2c11b1

Seq. No.	127190
Contig ID	23596_1.R1010
5'-most EST	LIB3176-034-P1-K1-C4
Method	BLASTX
NCBI GI	g3150415
BLAST score	885
E value	1.0e-95
Match length	162
% identity	30
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	127191
Contig ID	23605_1.R1010
5'-most EST	jC-atXLIB327406P2d10b1
Method	BLASTN
NCBI GI	g3548797
BLAST score	455
E value	0.0e+00
Match length	475
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127192
Contig ID	23609_1.R1010
5'-most EST	jC-alX24091Q1E1H11b1
Method	BLASTN
NCBI GI	g4165340
BLAST score	239
E value	1.0e-132
Match length	463
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127193
Contig ID	23611_1.R1010

5'-most EST	jC-alXLIB327435P2g05a1
Method	BLASTX
NCBI GI	g4538959
BLAST score	494
E value	3.0e-72
Match length	133
% identity	97
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No.	127194
Contig ID	23613_1.R1010
5'-most EST	LIB3175-066-P1-K1-G6
Method	BLASTX
NCBI GI	g2244971
BLAST score	1141
E value	1.0e-125
Match length	248
% identity	89
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127195
Contig ID	23615_1.R1010
5'-most EST	jC-atXLIB327406P3d05b2
Method	BLASTX
NCBI GI	g2244906
BLAST score	555
E value	5.0e-57
Match length	105
% identity	100
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	127196
Contig ID	23633_1.R1010
5'-most EST	jC-atXLIB327409P2d03b1
Method	BLASTX
NCBI GI	g4206206
BLAST score	906
E value	8.0e-98
Match length	186
% identity	94
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	127197
Contig ID	23633_2.R1010
5'-most EST	LIB3175-019-P1-K1-A8
Method	BLASTX
NCBI GI	g4206206
BLAST score	334
E value	5.0e-32
Match length	108
% identity	80
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	127198
Contig ID	23636_1.R1010
5'-most EST	jC-atXLIB327406P1c05b1
Method	BLASTN
NCBI GI	g4512690
BLAST score	374
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	127199
Contig ID	23637_1.R1010
5'-most EST	g2722236

Seq. No.	127200
Contig ID	23640_1.R1010
5'-most EST	jC-atXLIB327406P2c10b1
Method	BLASTX
NCBI GI	g4581114
BLAST score	618
E value	3.0e-64
Match length	125
% identity	96
NCBI Description	(AC005825) putative HesB-like protein;required for efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	127201
Contig ID	23643_1.R1010
5'-most EST	jC-atXLIB327421P4f07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	5.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127202
Contig ID	23645_1.R1010
5'-most EST	LIB24-092-Q1-E1-D7
Method	BLASTN
NCBI GI	g2584827
BLAST score	411
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127203
Contig ID	23648_1.R1010
5'-most EST	jC-atXLIB327401P4e02b1

Method	BLASTN
NCBI GI	g3928542
BLAST score	122
E value	6.0e-62
Match length	309
% identity	85
NCBI Description	Arabidopsis thaliana mRNA for UDP-glucose glucosyltransferase, complete cds

Seq. No.	127204
Contig ID	23652_1.R1010
5'-most EST	jC-alX24092Q1E1E02b1
Method	BLASTX
NCBI GI	g2252855
BLAST score	949
E value	1.0e-103
Match length	212
% identity	85
NCBI Description	(AF013294) similar to the myc family of helix-loop-helix transcription factors [Arabidopsis thaliana]

Seq. No.	127205
Contig ID	23661_1.R1010
5'-most EST	jC-alXLIB327435P4g03b1
Method	BLASTX
NCBI GI	g3914667
BLAST score	635
E value	4.0e-66
Match length	140
% identity	89
NCBI Description	50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR >gi_2459427 (AC002332) putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana]

Seq. No.	127206
Contig ID	23666_1.R1010
5'-most EST	LIB24-092-Q1-E1-F4
Method	BLASTX
NCBI GI	g3287696
BLAST score	291
E value	3.0e-26
Match length	123
% identity	54
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	127207
Contig ID	23677_2.R1010
5'-most EST	jC-atXLIB327408P2g02a1

Seq. No.	127208
Contig ID	23678_1.R1010
5'-most EST	jC-atXLIB327406P1d10b1
Method	BLASTX
NCBI GI	g1363487

BLAST score	1125
E value	1.0e-123
Match length	243
% identity	91
NCBI Description	IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No.	127209
Contig ID	23679_1.R1010
5'-most EST	jC-atXLIB327406P1d11b1
Method	BLASTX
NCBI GI	g3885331
BLAST score	194
E value	1.0e-14
Match length	69
% identity	57
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	127210
Contig ID	23680_1.R1010
5'-most EST	LIB24-092-Q1-E1-H1
Method	BLASTX
NCBI GI	g2739010
BLAST score	289
E value	6.0e-26
Match length	97
% identity	53
NCBI Description	(AF022464) CYP77A3p [Glycine max]

Seq. No.	127211
Contig ID	23681_1.R1010
5'-most EST	jC-atXLIB327406P3d06b2
Method	BLASTX
NCBI GI	g4063748
BLAST score	390
E value	1.0e-37
Match length	69
% identity	100
NCBI Description	(AC005851) unknown protein [Arabidopsis thaliana]

Seq. No.	127212
Contig ID	23684_1.R1010
5'-most EST	g2758905
Method	BLASTX
NCBI GI	g4539343
BLAST score	466
E value	1.0e-46
Match length	151
% identity	67
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	127213
Contig ID	23689_1.R1010
5'-most EST	jC-atXLIB327406P3d04b2
Method	BLASTN
NCBI GI	g4539415

BLAST score	317
E value	1.0e-178
Match length	832
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	127214
Contig ID	23697_1.R1010
5'-most EST	jC-atXLIB327406P1e06b1

Seq. No.	127215
Contig ID	23706_1.R1010
5'-most EST	jC-atXLIB327406P1e10b1
Method	BLASTX
NCBI GI	g2194131
BLAST score	583
E value	2.0e-60
Match length	112
% identity	99
NCBI Description	(AC002062) Similar to Synechocystis antiviral protein (gb_D90917). [Arabidopsis thaliana]

Seq. No.	127216
Contig ID	23713_1.R1010
5'-most EST	jC-atXmonuni27Ba04b1
Method	BLASTX
NCBI GI	g4490333
BLAST score	423
E value	2.0e-41
Match length	85
% identity	53
NCBI Description	(AL035656) EF-Hand containing protein-like [Arabidopsis thaliana]

Seq. No.	127217
Contig ID	23715_1.R1010
5'-most EST	LIB25-063-Q1-E1-B2
Method	BLASTN
NCBI GI	g4490291
BLAST score	282
E value	1.0e-157
Match length	636
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	127218
Contig ID	23721_1.R1010
5'-most EST	jC-atXLIB327406P3e12b2
Method	BLASTX
NCBI GI	g4506387
BLAST score	150
E value	2.0e-09
Match length	73
% identity	41
NCBI Description	RAD23 (S. cerevisiae) homolog B

>gi_1709985_sp_P54727_R23B_HUMAN UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B (HHR23B) (XP-C REPAIR COMPLEMENTING COMPLEX 58 KD PROTEIN) (P58) >gi_1082758_pir__S44346 RAD23 protein homolog - human >gi_498148_dbj_BAA04652_ (D21090) XP-C repair complementing protein (p58/HHR23B) [Homo sapiens]

Seq. No.	127219
Contig ID	23726_1.R1010
5'-most EST	jC-atXLIB327406P4e11b2

Seq. No.	127220
Contig ID	23728_2.R1010
5'-most EST	jC-alX24094Q1E1E10b1
Method	BLASTX
NCBI GI	g2244884
BLAST score	575
E value	4.0e-59
Match length	159
% identity	67
NCBI Description	(Z97338) glucosyltransferase [Arabidopsis thaliana]

Seq. No.	127221
Contig ID	23736_1.R1010
5'-most EST	jC-atXLIB327409P2b02b1
Method	BLASTX
NCBI GI	g2583128
BLAST score	389
E value	1.0e-37
Match length	77
% identity	100
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127222
Contig ID	23737_1.R1010
5'-most EST	LIB3168-029-P1-K1-D1

Seq. No.	127223
Contig ID	23745_1.R1010
5'-most EST	jC-atXP17C113I4T7d3
Method	BLASTX
NCBI GI	g3643607
BLAST score	139
E value	1.0e-122
Match length	265
% identity	79
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	127224
Contig ID	23748_1.R1010
5'-most EST	jC-atXLIB327406P4f09b2
Method	BLASTX
NCBI GI	g4469014
BLAST score	429
E value	3.0e-42
Match length	105
% identity	79

NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	127225
Contig ID	23755_1.R1010
5'-most EST	LIB24-093-Q1-E1-G5
Method	BLASTX
NCBI GI	g3785980
BLAST score	381
E value	9.0e-37
Match length	133
% identity	19
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.	127226
Contig ID	23758_1.R1010
5'-most EST	jC-atXLIB327406P4f12b2
Method	BLASTX
NCBI GI	g3688193
BLAST score	411
E value	6.0e-40
Match length	97
% identity	72
NCBI Description	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
Seq. No.	127227
Contig ID	23762_1.R1010
5'-most EST	jC-atXLIB327406P1g09b1
Method	BLASTX
NCBI GI	g2462749
BLAST score	637
E value	2.0e-66
Match length	125
% identity	98
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
Seq. No.	127228
Contig ID	23768_1.R1010
5'-most EST	jC-atXL1040Q1E1H12a1
Seq. No.	127229
Contig ID	23781_1.R1010
5'-most EST	jC-atXP100CE1A12T7b1
Method	BLASTX
NCBI GI	g4454026
BLAST score	802
E value	8.0e-86
Match length	195
% identity	84
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.	127230
Contig ID	23781_2.R1010
5'-most EST	jC-atXLIB327406P4e01b2
Method	BLASTX
NCBI GI	g4454026
BLAST score	677

E value	2.0e-71
Match length	151
% identity	87
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	127231
Contig ID	23784_1.R1010
5'-most EST	LIB24-094-Q1-E1-B7

Seq. No.	127232
Contig ID	23786_1.R1010
5'-most EST	g2445975
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	8.0e-16
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127233
Contig ID	23786_2.R1010
5'-most EST	jC-atXLIB327431P2f09a1
Method	BLASTX
NCBI GI	g4589536
BLAST score	206
E value	1.0e-15
Match length	189
% identity	32
NCBI Description	(AB023163) KIAA0946 protein [Homo sapiens]

Seq. No.	127234
Contig ID	23789_1.R1010
5'-most EST	LIB24-094-Q1-E1-C12
Method	BLASTX
NCBI GI	g4163997
BLAST score	549
E value	3.0e-56
Match length	117
% identity	92
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	127235
Contig ID	23797_1.R1010
5'-most EST	LIB3177-069-P1-K1-D9
Method	BLASTX
NCBI GI	g4544387
BLAST score	637
E value	1.0e-66
Match length	134
% identity	90
NCBI Description	(AC007047) putative purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	127236
Contig ID	23809_1.R1010

5'-most EST	LIB24-094-Q1-E1-E10
Method	BLASTX
NCBI GI	g4678259
BLAST score	813
E value	3.0e-87
Match length	168
% identity	31
NCBI Description	(AL049657) putative protein [Arabidopsis thaliana]

Seq. No.	127237
Contig ID	23811_1.R1010
5'-most EST	LIB24-094-Q1-E1-E12
Method	BLASTN
NCBI GI	g4159708
BLAST score	420
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	127238
Contig ID	23815_1.R1010
5'-most EST	jC-atXLIB327406P2f05b1
Method	BLASTX
NCBI GI	g4510373
BLAST score	496
E value	4.0e-50
Match length	126
% identity	78
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	127239
Contig ID	23820_1.R1010
5'-most EST	g2758803
Method	BLASTX
NCBI GI	g1321941
BLAST score	621
E value	1.0e-64
Match length	210
% identity	60
NCBI Description	(Z48564) dihydrolipoamide dehydrogenase [Synechocystis PCC6803]

Seq. No.	127240
Contig ID	23839_1.R1010
5'-most EST	jC-atXLIB327406P4f11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	44
E value	4.0e-15
Match length	72
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127241
Contig ID	23841_1.R1010
5'-most EST	LIB24-094-Q1-E1-H1
Method	BLASTN
NCBI GI	g2244870
BLAST score	257
E value	1.0e-142
Match length	580
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	127242
Contig ID	23842_1.R1010
5'-most EST	jC-atXLIB327406P1g08b1
Method	BLASTX
NCBI GI	g1679794
BLAST score	340
E value	8.0e-32
Match length	120
% identity	55
NCBI Description	(U77627) Allele: hi2 [Danio rerio]

Seq. No.	127243
Contig ID	23843_1.R1010
5'-most EST	jC-atXP79C230N7T7b1

Seq. No.	127244
Contig ID	23847_1.R1010
5'-most EST	LIB24-110-Q1-E1-E4
Method	BLASTX
NCBI GI	g2252844
BLAST score	266
E value	3.0e-23
Match length	129
% identity	43
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	127245
Contig ID	23851_1.R1010
5'-most EST	LIB24-132-Q1-E1-E6
Method	BLASTN
NCBI GI	g3510344
BLAST score	353
E value	0.0e+00
Match length	369
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	127246
Contig ID	23855_1.R1010
5'-most EST	g2062819
Method	BLASTX
NCBI GI	g4033431
BLAST score	262

E value	2.0e-22
Match length	96
% identity	61
NCBI Description	PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like protein [Arabidopsis thaliana]

Seq. No.	127247
Contig ID	23858_1.R1010
5'-most EST	jC-atX24036Q1E1D03b1
Method	BLASTN
NCBI GI	g3702315
BLAST score	337
E value	0.0e+00
Match length	671
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127248
Contig ID	23859_1.R1010
5'-most EST	jC-alX24048Q1E2D11b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	39
E value	1.0e-12
Match length	63
% identity	90
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	127249
Contig ID	23863_1.R1010
5'-most EST	jC-atXLIB327406P2e06b1
Method	BLASTX
NCBI GI	g4544434
BLAST score	585
E value	3.0e-60
Match length	144
% identity	80
NCBI Description	(AC006955) putative DNA-directed RNA polymerase II [Arabidopsis thaliana]

Seq. No.	127250
Contig ID	23871_1.R1010
5'-most EST	jC-atXP112C128E16T7d2
Method	BLASTX
NCBI GI	g4468218
BLAST score	530
E value	1.0e-53
Match length	240
% identity	44
NCBI Description	(AJ010025) unr-interacting protein [Homo sapiens]

Seq. No.	127251
Contig ID	23871_2.R1010
5'-most EST	jC-atXLIB327408P3f04b1

Method	BLASTX
NCBI GI	g4063383
BLAST score	676
E value	2.0e-76
Match length	330
% identity	47
NCBI Description	(AF096285) serine-threonine kinase receptor-associated protein [Mus musculus]

Seq. No.	127252
Contig ID	23873_1.R1010
5'-most EST	jC-alX24095Q1E1C09b1

Seq. No.	127253
Contig ID	23874_1.R1010
5'-most EST	g2048208
Method	BLASTX
NCBI GI	g4138137
BLAST score	282
E value	5.0e-25
Match length	62
% identity	79
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	127254
Contig ID	23874_2.R1010
5'-most EST	LIB24-099-Q1-E1-C7
Method	BLASTX
NCBI GI	g4538943
BLAST score	504
E value	3.0e-51
Match length	116
% identity	77
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	127255
Contig ID	23875_1.R1010
5'-most EST	jC-atXLIB327406P3e09b2
Method	BLASTX
NCBI GI	g3643611
BLAST score	788
E value	3.0e-84
Match length	150
% identity	99
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	127256
Contig ID	23876_1.R1010
5'-most EST	jC-atXLIB327406P4e10b2

Seq. No.	127257
Contig ID	23878_1.R1010
5'-most EST	LIB24-095-Q1-E1-D3
Method	BLASTN
NCBI GI	g2459406
BLAST score	147

E value	5.0e-77
Match length	354
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127258
Contig ID	23888_1.R1010
5'-most EST	LIB3234-082-Q1-K1-C10

Seq. No.	127259
Contig ID	23890_1.R1010
5'-most EST	LIB24-095-Q1-E1-F2

Seq. No.	127260
Contig ID	23892_1.R1010
5'-most EST	jC-atXLIB327406P2f10b1
Method	BLASTX
NCBI GI	g1708971
BLAST score	219
E value	1.0e-34
Match length	169
% identity	45
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) - black cherry >gi_288116_emb_CAA51194_ (X72617) mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi_1090776_prf__2019441A mandelonitrile lyase [Prunus serotina]

Seq. No.	127261
Contig ID	23901_1.R1010
5'-most EST	g527595

Seq. No.	127262
Contig ID	23909_1.R1010
5'-most EST	LIB3175-039-P1-K1-C7
Method	BLASTN
NCBI GI	g3510341
BLAST score	405
E value	0.0e+00
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	127263
Contig ID	23915_1.R1010
5'-most EST	jC-atXLIB327401P3g02b2
Method	BLASTN
NCBI GI	g2264310
BLAST score	37
E value	4.0e-11
Match length	175
% identity	85

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.	127264
Contig ID	23920_1.R1010
5'-most EST	LIB3175-029-P1-K1-G10
Method	BLASTX
NCBI GI	g4503363
BLAST score	747
E value	4.0e-79
Match length	250
% identity	56
NCBI Description	dolichyl-phosphate mannosyltransferase polypeptide 1 >gi_3062806_dbj_BAA25646_ (D86198) dolichol-phosphate-mannose synthase [Homo sapiens]
Seq. No.	127265
Contig ID	23923_1.R1010
5'-most EST	jC-atXLIB327406P2e01b1
Method	BLASTN
NCBI GI	g2673901
BLAST score	378
E value	0.0e+00
Match length	472
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	127266
Contig ID	23940_1.R1010
5'-most EST	jC-atXP115C248K13T7044d1
Method	BLASTX
NCBI GI	g3005931
BLAST score	239
E value	2.0e-88
Match length	254
% identity	43
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]
Seq. No.	127267
Contig ID	23941_1.R1010
5'-most EST	jC-atXLIB327406P3e04b2
Method	BLASTX
NCBI GI	g1174852
BLAST score	576
E value	7.0e-68
Match length	151
% identity	81
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-19 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (TAYO29) >gi_2129757_pir__S46656 ubiquitin carrier protein E2 (clone TAY029) - Arabidopsis thaliana >gi_600389_emb_CAA51200_ (X72625) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_992708 (U33759) UBC14 [Arabidopsis thaliana]
Seq. No.	127268
Contig ID	23943_1.R1010

5'-most EST	jC-atXLIB327406P3e05b2
Method	BLASTN
NCBI GI	g2618604
BLAST score	235
E value	1.0e-129
Match length	451
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No.	127269
Contig ID	23946_1.R1010
5'-most EST	jC-atXLIB327406P3e01b2

Seq. No.	127270
Contig ID	23952_1.R1010
5'-most EST	LIB24-096-Q1-E1-D4
Method	BLASTX
NCBI GI	g4006919
BLAST score	669
E value	4.0e-70
Match length	179
% identity	82
NCBI Description	(Z99708) ribosomal protein [Arabidopsis thaliana]

Seq. No.	127271
Contig ID	23953_1.R1010
5'-most EST	jC-atXLIB327406P3e08b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	36
E value	2.0e-10
Match length	56
% identity	91
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	127272
Contig ID	23959_1.R1010
5'-most EST	jC-alX24048Q1E2F07b1
Method	BLASTX
NCBI GI	g1825645
BLAST score	305
E value	1.0e-27
Match length	72
% identity	76
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [Caenorhabditis elegans]

Seq. No.	127273
Contig ID	23960_1.R1010
5'-most EST	jC-alX24095Q1E1E03b1
Method	BLASTN
NCBI GI	g1313925
BLAST score	96
E value	1.0e-46
Match length	190

% identity	91
NCBI Description	B.oleracea mRNA for IFA binding protein (sp7)

Seq. No.	127274
Contig ID	23970_1.R1010
5'-most EST	LIB24-096-Q1-E1-F2
Method	BLASTN
NCBI GI	g4567193
BLAST score	492
E value	0.0e+00
Match length	512
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	127275
Contig ID	23974_1.R1010
5'-most EST	LIB24-096-Q1-E1-F8

Seq. No.	127276
Contig ID	23977_1.R1010
5'-most EST	jC-atXLIB327406P1g06b1

Seq. No.	127277
Contig ID	23980_1.R1010
5'-most EST	jC-atXLIB327406P4f08b2
Method	BLASTN
NCBI GI	g3985949
BLAST score	180
E value	2.0e-96
Match length	483
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	127278
Contig ID	23982_1.R1010
5'-most EST	jC-atXLIB327406P4f05b2
Method	BLASTX
NCBI GI	g2213594
BLAST score	729
E value	2.0e-77
Match length	154
% identity	93
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	127279
Contig ID	23985_1.R1010
5'-most EST	LIB24-096-Q1-E1-G9
Method	BLASTN
NCBI GI	g4589437
BLAST score	416
E value	0.0e+00
Match length	432
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	127280
Contig ID	23992_1.R1010
5'-most EST	LIB25-044-Q1-E1-C6
Method	BLASTX
NCBI GI	g4699942
BLAST score	466
E value	2.0e-82
Match length	179
% identity	91
NCBI Description	(AC007166) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	127281
Contig ID	23993_1.R1010
5'-most EST	jC-atXLIB327406P2g11b1
Method	BLASTX
NCBI GI	g4581047
BLAST score	348
E value	1.0e-32
Match length	157
% identity	47
NCBI Description	(AF134807) putative dihydroflavonol reductase [Oryza sativa]

Seq. No.	127282
Contig ID	23993_2.R1010
5'-most EST	jC-atXLIB327438P4b04a2
Method	BLASTX
NCBI GI	g4581047
BLAST score	299
E value	5.0e-27
Match length	109
% identity	53
NCBI Description	(AF134807) putative dihydroflavonol reductase [Oryza sativa]

Seq. No.	127283
Contig ID	23994_1.R1010
5'-most EST	jC-atXP37C157P9T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	59
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127284
Contig ID	23999_1.R1010
5'-most EST	jC-atXLIB327406P4g03b2
Method	BLASTX
NCBI GI	g1469394
BLAST score	66
E value	1.0e-18
Match length	204
% identity	34

NCBI Description	(U43678) homolog of the human ataxia telangiectasia gene [Mus musculus]

Seq. No.	127285
Contig ID	24002_2.R1010
5'-most EST	jC-atXLIB327406P3g05b2
Method	BLASTX
NCBI GI	g3850584
BLAST score	365
E value	1.0e-34
Match length	86
% identity	95
NCBI Description	(AC005278) ESTs gb_H37641 and gb_AA651422 come from this gene. [Arabidopsis thaliana]

Seq. No.	127286
Contig ID	24005_1.R1010
5'-most EST	jC-alX24097Q1E1G05b1
Method	BLASTX
NCBI GI	g419760
BLAST score	574
E value	4.0e-59
Match length	121
% identity	93
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	127287
Contig ID	24006_2.R1010
5'-most EST	jC-atXLIB327409P3f12a1

Seq. No.	127288
Contig ID	24006_3.R1010
5'-most EST	jC-atXLIB327421P1e11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	9.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127289
Contig ID	24006_4.R1010
5'-most EST	LIB25-006-Q1-E1-E5
Method	BLASTX
NCBI GI	g3193298
BLAST score	165
E value	4.0e-11
Match length	114
% identity	34
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	127290
Contig ID	24008_1.R1010

5'-most EST	jC-atXLIB327406P4g06b2
Method	BLASTX
NCBI GI	g2827716
BLAST score	496
E value	7.0e-50
Match length	115
% identity	84
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	127291
Contig ID	24020_1.R1010
5'-most EST	jC-atXLIB327406P3g08b2
Method	BLASTX
NCBI GI	g4262153
BLAST score	503
E value	6.0e-51
Match length	93
% identity	100
NCBI Description	(AC005275) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	127292
Contig ID	24023_1.R1010
5'-most EST	LIB25-074-Q1-E1-C6

Seq. No.	127293
Contig ID	24027_1.R1010
5'-most EST	jC-alX24097Q1E1D01b1
Method	BLASTX
NCBI GI	g3395432
BLAST score	634
E value	2.0e-66
Match length	125
% identity	99
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	127294
Contig ID	24028_1.R1010
5'-most EST	LIB24-097-Q1-E1-D6
Method	BLASTX
NCBI GI	g4006867
BLAST score	469
E value	9.0e-47
Match length	150
% identity	63
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	127295
Contig ID	24030_1.R1010
5'-most EST	jC-alXLIB327434P2f02b1
Method	BLASTX
NCBI GI	g1616787
BLAST score	1270
E value	1.0e-140
Match length	243
% identity	100
NCBI Description	(U71122) pyruvate decarboxylase [Arabidopsis thaliana]

Seq. No.	127296
Contig ID	24032_1.R1010
5'-most EST	jC-atXLIB327406P1h06b1
Method	BLASTX
NCBI GI	g3157934
BLAST score	521
E value	6.0e-53
Match length	104
% identity	100
NCBI Description	(AC002131) Similar to hypothetical protein F09E5.8 gb_U37429 from C. elegans. ESTs gb_T42019 and gb_N97000 come from this gene. [Arabidopsis thaliana]

Seq. No.	127297
Contig ID	24032_2.R1010
5'-most EST	g932910
Method	BLASTX
NCBI GI	g3157934
BLAST score	577
E value	1.0e-59
Match length	131
% identity	90
NCBI Description	(AC002131) Similar to hypothetical protein F09E5.8 gb_U37429 from C. elegans. ESTs gb_T42019 and gb_N97000 come from this gene. [Arabidopsis thaliana]

Seq. No.	127298
Contig ID	24035_1.R1010
5'-most EST	g2413188
Method	BLASTX
NCBI GI	g1352460
BLAST score	196
E value	6.0e-15
Match length	65
% identity	55
NCBI Description	IN2-1 PROTEIN >gi_100896_pir__S17743 In2-1 protein - maize >gi_22347_emb_CAA41447_ (X58573) In2-1 [Zea mays]

Seq. No.	127299
Contig ID	24035_2.R1010
5'-most EST	LIB24-097-Q1-E1-E2
Method	BLASTX
NCBI GI	g1352460
BLAST score	198
E value	5.0e-17
Match length	79
% identity	61
NCBI Description	IN2-1 PROTEIN >gi_100896_pir__S17743 In2-1 protein - maize >gi_22347_emb_CAA41447_ (X58573) In2-1 [Zea mays]

Seq. No.	127300
Contig ID	24050_1.R1010
5'-most EST	LIB3176-020-P1-K1-G2
Method	BLASTX
NCBI GI	g3367534
BLAST score	731

E value	1.0e-77
Match length	169
% identity	88
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	127301
Contig ID	24051_1.R1010
5'-most EST	jC-alX25071Q1E1F06b1
Method	BLASTN
NCBI GI	g3108025
BLAST score	499
E value	0.0e+00
Match length	515
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	127302
Contig ID	24054_1.R1010
5'-most EST	jC-atXLIB327406P3h03b2
Method	BLASTX
NCBI GI	g3334404
BLAST score	73
E value	6.0e-18
Match length	57
% identity	88
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	127303
Contig ID	24061_1.R1010
5'-most EST	jC-alX24097Q1E1G09b1
Method	BLASTN
NCBI GI	g4263762
BLAST score	152
E value	6.0e-80
Match length	307
% identity	78
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127304
Contig ID	24079_1.R1010
5'-most EST	LIB3175-028-P1-K1-A2
Method	BLASTX
NCBI GI	g3786005
BLAST score	1142
E value	1.0e-125
Match length	224
% identity	69

NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]
Seq. No.	127305
Contig ID	24090_1.R1010
5'-most EST	jC-atXLIB327406P1h07b1
Method	BLASTN
NCBI GI	g540252
BLAST score	49
E value	4.0e-18
Match length	83
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.	127306
Contig ID	24095_1.R1010
5'-most EST	jC-atXLIB327406P4g11b2
Method	BLASTX
NCBI GI	g2459433
BLAST score	454
E value	7.0e-45
Match length	175
% identity	57
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.	127307
Contig ID	24107_1.R1010
5'-most EST	LIB24-099-Q1-E1-F4
Seq. No.	127308
Contig ID	24123_1.R1010
5'-most EST	jC-atXLIB327406P1h03b1
Seq. No.	127309
Contig ID	24129_1.R1010
5'-most EST	LIB3177-065-P1-K1-D7
Method	BLASTX
NCBI GI	g1800307
BLAST score	339
E value	3.0e-31
Match length	375
% identity	17
NCBI Description	(U83883) p105 coactivator [Rattus norvegicus]
Seq. No.	127310
Contig ID	24134_1.R1010
5'-most EST	g394844
Method	BLASTN
NCBI GI	g4159712
BLAST score	120
E value	6.0e-61
Match length	299
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence
Seq. No.	127311

Contig ID	24136_1.R1010
5'-most EST	jC-atXLIB327406P2g09b1

Seq. No.	127312
Contig ID	24144_1.R1010
5'-most EST	jC-alX24100Q1E1D06b1
Method	BLASTN
NCBI GI	g4757417
BLAST score	207
E value	1.0e-113
Match length	271
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	127313
Contig ID	24148_1.R1010
5'-most EST	LIB3168-069-P1-K1-F12
Method	BLASTX
NCBI GI	g2708750
BLAST score	330
E value	9.0e-31
Match length	133
% identity	55
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	127314
Contig ID	24150_1.R1010
5'-most EST	jC-alXLIB327434P1a04b1
Method	BLASTX
NCBI GI	g4680212
BLAST score	279
E value	2.0e-24
Match length	117
% identity	52
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	127315
Contig ID	24151_1.R1010
5'-most EST	jC-atXP123C117E18T7068d1
Method	BLASTX
NCBI GI	g3269284
BLAST score	518
E value	2.0e-52
Match length	131
% identity	79
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	127316
Contig ID	24151_2.R1010
5'-most EST	jC-atXLIB327427P4b02b2
Method	BLASTX
NCBI GI	g3269284
BLAST score	480
E value	5.0e-48
Match length	121

% identity	80
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	127317
Contig ID	24155_1.R1010
5'-most EST	LIB24-100-Q1-E1-G1
Method	BLASTX
NCBI GI	g1806140
BLAST score	799
E value	2.0e-85
Match length	210
% identity	72
NCBI Description	(X97314) cdc2MsC [Medicago sativa]

Seq. No.	127318
Contig ID	24159_1.R1010
5'-most EST	jC-atXLIB327406P2h12b1

Seq. No.	127319
Contig ID	24160_1.R1010
5'-most EST	g930825
Method	BLASTX
NCBI GI	g4581146
BLAST score	971
E value	1.0e-105
Match length	209
% identity	98
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	127320
Contig ID	24160_2.R1010
5'-most EST	jC-atXLIB327406P3h04b2
Method	BLASTX
NCBI GI	g4581146
BLAST score	398
E value	3.0e-49
Match length	107
% identity	100
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	127321
Contig ID	24163_1.R1010
5'-most EST	LIB24-100-Q1-E1-H2
Method	BLASTX
NCBI GI	g4262162
BLAST score	272
E value	2.0e-23
Match length	173
% identity	35
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	127322
Contig ID	24167_1.R1010
5'-most EST	jC-atXLIB327420P3d07b1

Method	BLASTX
NCBI GI	g2282473
BLAST score	172
E value	4.0e-12
Match length	109
% identity	39
NCBI Description	(AB005911) xanthine dehydrogenase [Bombyx mori]

Seq. No.	127323
Contig ID	24173_1.R1010
5'-most EST	g2733128
Method	BLASTN
NCBI GI	g2459406
BLAST score	407
E value	0.0e+00
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127324
Contig ID	24181_1.R1010
5'-most EST	jC-atXLIB327424P4d12b1
Method	BLASTX
NCBI GI	g2829918
BLAST score	609
E value	3.0e-63
Match length	126
% identity	95
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	127325
Contig ID	24186_1.R1010
5'-most EST	jC-atXLIB327407P1b02b2
Method	BLASTX
NCBI GI	g3510259
BLAST score	1123
E value	1.0e-123
Match length	216
% identity	100
NCBI Description	(AC005310) putative inorganic pyrophosphatase [Arabidopsis thaliana] >gi_3522960 (AC004411) putative inorganic pyrophosphatase [Arabidopsis thaliana]

Seq. No.	127326
Contig ID	24192_1.R1010
5'-most EST	jC-atXLIB327407P4a12b1
Method	BLASTN
NCBI GI	g3063690
BLAST score	300
E value	1.0e-168
Match length	435
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	127327
Contig ID	24194_1.R1010
5'-most EST	jC-atXLIB327407P1b01b2

Seq. No.	127328
Contig ID	24198_1.R1010
5'-most EST	jC-alXLIB327435P2a02a1
Method	BLASTX
NCBI GI	g3482977
BLAST score	734
E value	6.0e-78
Match length	174
% identity	86
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	127329
Contig ID	24198_2.R1010
5'-most EST	LIB3234-015-P1-K1-B4
Method	BLASTN
NCBI GI	g3482964
BLAST score	251
E value	1.0e-139
Match length	343
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)

Seq. No.	127330
Contig ID	24206_1.R1010
5'-most EST	LIB24-102-Q1-E1-A7
Method	BLASTN
NCBI GI	g3821780
BLAST score	25
E value	6.0e-04
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	127331
Contig ID	24208_1.R1010
5'-most EST	jC-atXP71C221K10T7019d1
Method	BLASTN
NCBI GI	g3695372
BLAST score	342
E value	0.0e+00
Match length	591
% identity	99
NCBI Description	Arabidopsis thaliana BAC F11O4

Seq. No.	127332
Contig ID	24215_1.R1010
5'-most EST	g3449680
Method	BLASTX
NCBI GI	g968987
BLAST score	199
E value	4.0e-15
Match length	50

% identity	76
NCBI Description	(U31648) ferritin [Glycine max]

Seq. No.	127333
Contig ID	24215_2.R1010
5'-most EST	LIB24-102-Q1-E1-B7
Method	BLASTX
NCBI GI	g4586047
BLAST score	707
E value	1.0e-74
Match length	255
% identity	60
NCBI Description	(AC007020) putative ferritin protein [Arabidopsis thaliana] >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279) hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No.	127334
Contig ID	24219_1.R1010
5'-most EST	LIB24-102-Q1-E1-C2
Method	BLASTX
NCBI GI	g3879150
BLAST score	166
E value	2.0e-11
Match length	69
% identity	51
NCBI Description	(Z70686) Similarity to Yeast hypothetical protein YKE0 (SW:YKE0_YEAST); cDNA EST yk254g6.3 comes from this gene; cDNA EST yk254g6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	127335
Contig ID	24234_1.R1010
5'-most EST	jC-atXLIB327407P3a06b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	39
E value	2.0e-12
Match length	51
% identity	94
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	127336
Contig ID	24244_2.R1010
5'-most EST	LIB24-102-Q1-E1-E9
Method	BLASTX
NCBI GI	g4539460
BLAST score	210
E value	2.0e-16
Match length	202
% identity	5
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	127337
Contig ID	24245_1.R1010
5'-most EST	jC-atX24102Q1E1F01b1
Method	BLASTX

NCBI GI	g3402672
BLAST score	600
E value	2.0e-62
Match length	153
% identity	77
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]

Seq. No.	127338
Contig ID	24247_1.R1010
5'-most EST	LIB3175-016-P1-K1-F2
Method	BLASTX
NCBI GI	g3445416
BLAST score	262
E value	9.0e-23
Match length	54
% identity	98
NCBI Description	(Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]

Seq. No.	127339
Contig ID	24250_1.R1010
5'-most EST	jC-alXLIB327435P2c05b1
Method	BLASTX
NCBI GI	g1710549
BLAST score	277
E value	2.0e-24
Match length	51
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L39

Seq. No.	127340
Contig ID	24250_2.R1010
5'-most EST	g2393551
Method	BLASTX
NCBI GI	g1710549
BLAST score	277
E value	2.0e-24
Match length	51
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L39

Seq. No.	127341
Contig ID	24258_1.R1010
5'-most EST	LIB3176-011-P1-K1-C9
Method	BLASTX
NCBI GI	g3935143
BLAST score	100
E value	2.0e-81
Match length	175
% identity	90
NCBI Description	(AC005106) T25N20.7 [Arabidopsis thaliana]

Seq. No.	127342
Contig ID	24259_1.R1010
5'-most EST	jC-atXLIB327407P1b07b2
Method	BLASTX
NCBI GI	g4584527
BLAST score	455

E value	3.0e-45
Match length	183
% identity	51
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	127343
Contig ID	24266_2.R1010
5'-most EST	jC-atX24045Q1E1C01b2
Method	BLASTX
NCBI GI	g4455192
BLAST score	528
E value	7.0e-54
Match length	164
% identity	67
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	127344
Contig ID	24270_1.R1010
5'-most EST	jC-atX24102Q1E1H04b1
Method	BLASTX
NCBI GI	g4582487
BLAST score	773
E value	1.0e-82
Match length	150
% identity	52
NCBI Description	(AL021768) resistence protein-like [Arabidopsis thaliana]

Seq. No.	127345
Contig ID	24271_1.R1010
5'-most EST	LIB24-102-Q1-E1-H5
Method	BLASTX
NCBI GI	g4678349
BLAST score	349
E value	1.0e-32
Match length	158
% identity	16
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	127346
Contig ID	24274_1.R1010
5'-most EST	jC-atXLIB327407P1b11b2
Method	BLASTN
NCBI GI	g3399678
BLAST score	525
E value	0.0e+00
Match length	573
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127347
Contig ID	24283_1.R1010
5'-most EST	jC-atXP104CE10G6T7b1
Method	BLASTX
NCBI GI	g1351239
BLAST score	396
E value	4.0e-38

Match length	108
% identity	62
NCBI Description	THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi_481594_pir__S38909 thioredoxin m precursor - garden pea >gi_431957_emb_CAA53900_ (X76269) thioredoxin m [Pisum sativum]

Seq. No.	127348
Contig ID	24283_2.R1010
5'-most EST	jC-atXLIB327407P1a02b2
Method	BLASTX
NCBI GI	g2809238
BLAST score	341
E value	9.0e-32
Match length	97
% identity	61
NCBI Description	(AC002560) F21B7.7 [Arabidopsis thaliana]

Seq. No.	127349
Contig ID	24289_1.R1010
5'-most EST	jC-atXLIB327407P1a08b2
Method	BLASTX
NCBI GI	g2462749
BLAST score	502
E value	1.0e-50
Match length	129
% identity	80
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	127350
Contig ID	24291_1.R1010
5'-most EST	jC-atXLIB327407P1a07b2
Method	BLASTX
NCBI GI	g2281090
BLAST score	569
E value	2.0e-58
Match length	207
% identity	59
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127351
Contig ID	24291_2.R1010
5'-most EST	LIB3168-095-P1-K1-F12
Method	BLASTX
NCBI GI	g2281090
BLAST score	596
E value	2.0e-61
Match length	223
% identity	59
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127352
Contig ID	24300_1.R1010
5'-most EST	LIB24-103-Q1-E1-E6
Method	BLASTX
NCBI GI	g2114207

BLAST score	301
E value	2.0e-27
Match length	83
% identity	67
NCBI Description	(D86744) glutaredoxin [Oryza sativa]

Seq. No.	127353
Contig ID	24301_1.R1010
5'-most EST	jC-atXLIB327407P4a02b1
Method	BLASTX
NCBI GI	g2832698
BLAST score	677
E value	3.0e-71
Match length	177
% identity	91
NCBI Description	(AL021713) starch synthase-like protein [Arabidopsis thaliana]

Seq. No.	127354
Contig ID	24310_1.R1010
5'-most EST	jC-atXmonuni26Ab09b1
Method	BLASTN
NCBI GI	g3702733
BLAST score	149
E value	4.0e-78
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJP23, complete sequence [Arabidopsis thaliana]

Seq. No.	127355
Contig ID	24313_1.R1010
5'-most EST	LIB24-103-Q1-E1-G6
Method	BLASTN
NCBI GI	g4589428
BLAST score	231
E value	1.0e-127
Match length	540
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	127356
Contig ID	24322_1.R1010
5'-most EST	LIB3175-051-P1-K1-B7
Method	BLASTX
NCBI GI	g2194132
BLAST score	254
E value	1.0e-21
Match length	80
% identity	34
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	127357
Contig ID	24327_1.R1010
5'-most EST	jC-atXP83C241K15T7034d1
Method	BLASTX

NCBI GI	g3599491
BLAST score	964
E value	1.0e-104
Match length	226
% identity	78
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	127358
Contig ID	24327_2.R1010
5'-most EST	jC-atXP89C245C9T7071d1
Method	BLASTX
NCBI GI	g3599491
BLAST score	600
E value	3.0e-62
Match length	157
% identity	70
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	127359
Contig ID	24327_3.R1010
5'-most EST	LIB3177-093-P1-K1-F7
Method	BLASTX
NCBI GI	g3599491
BLAST score	80
E value	6.0e-01
Match length	136
% identity	58
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	127360
Contig ID	24327_4.R1010
5'-most EST	LIB3175-024-P1-K1-H11
Method	BLASTX
NCBI GI	g3599491
BLAST score	642
E value	4.0e-67
Match length	184
% identity	66
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	127361
Contig ID	24334_2.R1010
5'-most EST	LIB3168-017-P1-K1-H6
Method	BLASTX
NCBI GI	g2842424
BLAST score	934
E value	1.0e-101
Match length	237
% identity	71
NCBI Description	(AJ223948) RNA helicase [Homo sapiens]

Seq. No.	127362
Contig ID	24336_1.R1010
5'-most EST	jC-atXLIB327407P1b09b2
Method	BLASTX
NCBI GI	g3668075
BLAST score	862

E value	7.0e-93
Match length	168
% identity	98
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127363
Contig ID	24342_1.R1010
5'-most EST	LIB24-104-Q1-E2-G4
Method	BLASTX
NCBI GI	g4406761
BLAST score	531
E value	3.0e-54
Match length	131
% identity	85
NCBI Description	(AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]

Seq. No.	127364
Contig ID	24342_2.R1010
5'-most EST	jC-atXLIB327407P1b06b2
Method	BLASTN
NCBI GI	g4406752
BLAST score	548
E value	0.0e+00
Match length	548
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127365
Contig ID	24343_1.R1010
5'-most EST	jC-atXLIB327406P3h08b2

Seq. No.	127366
Contig ID	24345_1.R1010
5'-most EST	jC-atXLIB327408P1a11b1
Method	BLASTN
NCBI GI	g4490291
BLAST score	547
E value	0.0e+00
Match length	717
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	127367
Contig ID	24346_1.R1010
5'-most EST	jC-atX24104Q1E2B03b1
Method	BLASTX
NCBI GI	g2224605
BLAST score	346
E value	2.0e-32
Match length	94
% identity	63
NCBI Description	(AB002330) KIAA0332 [Homo sapiens]

Seq. No. 127368

Contig ID	24347_1.R1010
5'-most EST	g2763097
Method	BLASTN
NCBI GI	g4756963
BLAST score	251
E value	1.0e-139
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	127369
Contig ID	24355_1.R1010
5'-most EST	jC-alX25086Q1E1D03b1
Method	BLASTX
NCBI GI	g4262240
BLAST score	1100
E value	1.0e-121
Match length	204
% identity	61
NCBI Description	(AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No.	127370
Contig ID	24360_1.R1010
5'-most EST	jC-atXLIB327437P3b06b2
Method	BLASTN
NCBI GI	g4557061
BLAST score	263
E value	1.0e-146
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence

Seq. No.	127371
Contig ID	24362_1.R1010
5'-most EST	LIB25-052-Q1-E1-H2
Method	BLASTX
NCBI GI	g4204095
BLAST score	209
E value	1.0e-16
Match length	102
% identity	45
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No.	127372
Contig ID	24364_1.R1010
5'-most EST	LIB24-104-Q1-E2-H4
Method	BLASTX
NCBI GI	g2809244
BLAST score	159
E value	4.0e-11
Match length	45
% identity	60
NCBI Description	(AC002560) F21B7.13 [Arabidopsis thaliana]

Seq. No.	127373

Contig ID	24366_1.R1010
5'-most EST	jC-atXLIB327407P3a11b1
Method	BLASTN
NCBI GI	g3449315
BLAST score	357
E value	0.0e+00
Match length	423
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	127374
Contig ID	24367_1.R1010
5'-most EST	jC-atXLIB327407P1d01b2
Method	BLASTX
NCBI GI	g1174470
BLAST score	358
E value	1.0e-33
Match length	150
% identity	49
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	127375
Contig ID	24369_1.R1010
5'-most EST	LIB24-104-Q1-E2-G11
Method	BLASTN
NCBI GI	g4589430
BLAST score	119
E value	2.0e-60
Match length	316
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	127376
Contig ID	24373_1.R1010
5'-most EST	LIB24-104-Q1-E2-G8

Seq. No.	127377
Contig ID	24376_1.R1010
5'-most EST	LIB24-104-Q1-E2-H3
Method	BLASTX
NCBI GI	g2501597
BLAST score	240
E value	3.0e-20
Match length	71
% identity	62
NCBI Description	PROTEIN 22A3 >gi_1638838_emb_CAA67982_ (X99668) unknown [Mus musculus]

Seq. No.	127378
Contig ID	24379_1.R1010
5'-most EST	jC-atXP79C231H21T7b1
Method	BLASTX

NCBI GI	g4309742
BLAST score	915
E value	7.0e-99
Match length	175
% identity	100
NCBI Description	(AC006439) putative Rer1 protein [Arabidopsis thaliana]

Seq. No.	127379
Contig ID	24379_2.R1010
5'-most EST	jC-alXLIB327434P3f01b1
Method	BLASTX
NCBI GI	g4309742
BLAST score	632
E value	7.0e-66
Match length	121
% identity	100
NCBI Description	(AC006439) putative Rer1 protein [Arabidopsis thaliana]

Seq. No.	127380
Contig ID	24393_1.R1010
5'-most EST	jC-alXLIB327434P2e05b1
Method	BLASTX
NCBI GI	g3068809
BLAST score	588
E value	9.0e-61
Match length	160
% identity	71
NCBI Description	(AF059295) Skp1 homolog [Arabidopsis thaliana]

Seq. No.	127381
Contig ID	24396_1.R1010
5'-most EST	LIB3168-080-P1-K1-A1
Method	BLASTX
NCBI GI	g2914700
BLAST score	510
E value	7.0e-52
Match length	118
% identity	87
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	127382
Contig ID	24403_1.R1010
5'-most EST	jC-alXLIB327436P1g01b1

Seq. No.	127383
Contig ID	24408_1.R1010
5'-most EST	LIB24-106-Q1-E1-B5
Method	BLASTX
NCBI GI	g1168503
BLAST score	270
E value	2.0e-23
Match length	105
% identity	54
NCBI Description	3-DEHYDROQUINATE SYNTHASE >gi_1073786_pir__G64054 3-dehydroquinate synthase (aroB) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1573167 (U32705)

	3-dehydroquinate synthase (aroB) [Haemophilus influenzae Rd]
Seq. No.	127384
Contig ID	24409_1.R1010
5'-most EST	jC-atXLIB327407P4b07b1
Method	BLASTX
NCBI GI	g2275202
BLAST score	543
E value	1.0e-55
Match length	107
% identity	97
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]
Seq. No.	127385
Contig ID	24413_1.R1010
5'-most EST	jC-atX24106Q1E1C03b2
Method	BLASTX
NCBI GI	g2244898
BLAST score	488
E value	2.0e-49
Match length	132
% identity	67
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.	127386
Contig ID	24414_1.R1010
5'-most EST	LIB24-109-Q1-E1-H4
Method	BLASTX
NCBI GI	g2462744
BLAST score	156
E value	3.0e-10
Match length	156
% identity	28
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	127387
Contig ID	24415_1.R1010
5'-most EST	jC-atXLIB327407P3b10b1
Method	BLASTN
NCBI GI	g4757399
BLAST score	622
E value	0.0e+00
Match length	687
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence
Seq. No.	127388
Contig ID	24418_2.R1010
5'-most EST	jC-atXLIB327407P1c03b2
Method	BLASTN
NCBI GI	g3985952
BLAST score	164
E value	7.0e-87

Match length	545
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	127389
Contig ID	24421_1.R1010
5'-most EST	jC-atXLIB327407P1c04b2
Method	BLASTX
NCBI GI	g1871192
BLAST score	672
E value	1.0e-70
Match length	193
% identity	63
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	127390
Contig ID	24424_1.R1010
5'-most EST	jC-atXLIB327401P4f01b2
Method	BLASTN
NCBI GI	g3510343
BLAST score	532
E value	0.0e+00
Match length	553
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	127391
Contig ID	24427_2.R1010
5'-most EST	jC-atXLIB327407P1c07b2
Method	BLASTX
NCBI GI	g4567197
BLAST score	525
E value	3.0e-53
Match length	200
% identity	49
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	127392
Contig ID	24427_3.R1010
5'-most EST	jC-atXP82CG1F7T7d3
Method	BLASTX
NCBI GI	g4567197
BLAST score	520
E value	1.0e-52
Match length	289
% identity	44
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	127393
Contig ID	24443_1.R1010
5'-most EST	jC-atXLIB327417P2f09b1
Method	BLASTX
NCBI GI	g114200
BLAST score	240

E value	9.0e-20
Match length	121
% identity	44
NCBI Description	SHIKIMATE KINASE PRECURSOR >gi_100253_pir__S21584 shikimate kinase precursor - tomato >gi_19349_emb_CAA45121_ (X63560) shikimate kinase precursor [Lycopersicon esculentum]

Seq. No.	127394
Contig ID	24446_1.R1010
5'-most EST	LIB24-106-Q1-E1-F8

Seq. No.	127395
Contig ID	24448_1.R1010
5'-most EST	LIB25-038-Q1-E1-B6

Seq. No.	127396
Contig ID	24450_1.R1010
5'-most EST	LIB25-062-Q1-E1-E4
Method	BLASTN
NCBI GI	g4263694
BLAST score	218
E value	1.0e-119
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127397
Contig ID	24457_1.R1010
5'-most EST	jC-atXLIB327407P3c08b1
Method	BLASTN
NCBI GI	g2275194
BLAST score	210
E value	1.0e-114
Match length	344
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127398
Contig ID	24457_3.R1010
5'-most EST	g2764044
Method	BLASTN
NCBI GI	g2275194
BLAST score	362
E value	0.0e+00
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127399
Contig ID	24459_1.R1010
5'-most EST	LIB24-106-Q1-E1-H4
Method	BLASTN
NCBI GI	g2264303
BLAST score	221

E value	1.0e-121
Match length	409
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	127400
Contig ID	24465_1.R1010
5'-most EST	LIB24-107-Q1-E1-A12
Method	BLASTN
NCBI GI	g4589419
BLAST score	149
E value	4.0e-78
Match length	447
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	127401
Contig ID	24469_1.R1010
5'-most EST	LIB24-107-Q1-E1-A7

Seq. No.	127402
Contig ID	24475_1.R1010
5'-most EST	g757621
Method	BLASTX
NCBI GI	g4580517
BLAST score	777
E value	1.0e-92
Match length	172
% identity	100
NCBI Description	(AF036302) scarecrow-like 5 [Arabidopsis thaliana]

Seq. No.	127403
Contig ID	24476_1.R1010
5'-most EST	jC-atX24107Q1E1C06b2
Method	BLASTX
NCBI GI	g4218122
BLAST score	753
E value	3.0e-80
Match length	168
% identity	88
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	127404
Contig ID	24478_1.R1010
5'-most EST	LIB3176-002-Q1-K1-E8

Seq. No.	127405
Contig ID	24482_1.R1010
5'-most EST	LIB3175-025-P1-K1-A12

Seq. No.	127406
Contig ID	24485_1.R1010
5'-most EST	LIB3175-078-P1-K1-A3
Method	BLASTX
NCBI GI	g2842477

BLAST score	706
E value	2.0e-74
Match length	193
% identity	72
NCBI Description	(AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No.	127407
Contig ID	24492_1.R1010
5'-most EST	jC-atXLIB327407P1c12b2
Method	BLASTX
NCBI GI	g2462739
BLAST score	917
E value	2.0e-99
Match length	171
% identity	99
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	127408
Contig ID	24495_1.R1010
5'-most EST	jC-atXLIB327401P4f02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	5.0e-23
Match length	73
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127409
Contig ID	24498_1.R1010
5'-most EST	ARABLI-15-Q1-B1-E5
Method	BLASTN
NCBI GI	g3738275
BLAST score	306
E value	1.0e-172
Match length	506
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127410
Contig ID	24500_1.R1010
5'-most EST	LIB315-045-P1-K1-G3
Method	BLASTX
NCBI GI	g4510424
BLAST score	203
E value	3.0e-58
Match length	123
% identity	98
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No.	127411
Contig ID	24506_1.R1010
5'-most EST	jC-atX24107Q1E1H02b1
Method	BLASTX

NCBI GI	g4185499
BLAST score	261
E value	1.0e-22
Match length	79
% identity	54
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	127412
Contig ID	24509_1.R1010
5'-most EST	jC-atX24107Q1E1H05b1
Method	BLASTX
NCBI GI	g3738304
BLAST score	709
E value	4.0e-75
Match length	134
% identity	100
NCBI Description	(AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127413
Contig ID	24515_1.R1010
5'-most EST	jC-atXLIB327407P4b03b1
Method	BLASTN
NCBI GI	g4757392
BLAST score	614
E value	0.0e+00
Match length	758
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	127414
Contig ID	24518_1.R1010
5'-most EST	LIB24-108-Q1-E1-H11
Method	BLASTX
NCBI GI	g481812
BLAST score	127
E value	4.0e-07
Match length	55
% identity	25
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	127415
Contig ID	24529_1.R1010
5'-most EST	LIB24-108-Q1-E1-E12

Seq. No.	127416
Contig ID	24530_2.R1010
5'-most EST	jC-atX24108Q1E1E03b1
Method	BLASTX
NCBI GI	g3281849
BLAST score	765
E value	1.0e-81

Match length	151
% identity	99
NCBI Description	(AL031004) methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	127417
Contig ID	24549_1.R1010
5'-most EST	jC-atXLIB327407P4c05b1
Method	BLASTX
NCBI GI	g4506223
BLAST score	208
E value	3.0e-16
Match length	104
% identity	40
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 >gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]

Seq. No.	127418
Contig ID	24551_1.R1010
5'-most EST	jC-atXLIB327407P3c06b1
Method	BLASTN
NCBI GI	g4584387
BLAST score	149
E value	5.0e-78
Match length	208
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	127419
Contig ID	24551_2.R1010
5'-most EST	jC-atXLIB327424P4c06a1
Method	BLASTN
NCBI GI	g4584387
BLAST score	457
E value	0.0e+00
Match length	492
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	127420
Contig ID	24554_1.R1010
5'-most EST	jC-atXLIB327417P3a06b1
Method	BLASTN
NCBI GI	g4757392
BLAST score	221
E value	1.0e-121
Match length	404
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	127421
Contig ID	24555_1.R1010
5'-most EST	LIB24-108-Q1-E1-H8

Method	BLASTN
NCBI GI	g4757401
BLAST score	267
E value	1.0e-148
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	127422
Contig ID	24558_1.R1010
5'-most EST	LIB24-109-Q1-E1-A11
Method	BLASTN
NCBI GI	g3128136
BLAST score	290
E value	1.0e-162
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	127423
Contig ID	24562_1.R1010
5'-most EST	jC-atXLIB327407P2d03b1
Method	BLASTX
NCBI GI	g4589123
BLAST score	291
E value	5.0e-26
Match length	141
% identity	46
NCBI Description	(AF126374) At14a protein [Arabidopsis thaliana]

Seq. No.	127424
Contig ID	24565_1.R1010
5'-most EST	LIB24-109-Q1-E1-B12
Method	BLASTX
NCBI GI	g2618684
BLAST score	569
E value	8.0e-59
Match length	123
% identity	93
NCBI Description	(AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana] >gi_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]

Seq. No.	127425
Contig ID	24573_1.R1010
5'-most EST	jC-atXLIB327408P2e05b1
Method	BLASTX
NCBI GI	g3096931
BLAST score	360
E value	6.0e-34
Match length	112

% identity	58
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	127426
Contig ID	24575_1.R1010
5'-most EST	jC-atXP125C182B24T7090a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127427
Contig ID	24575_2.R1010
5'-most EST	LIB3175-048-P1-K1-C10
Method	BLASTX
NCBI GI	g557472
BLAST score	179
E value	1.0e-12
Match length	135
% identity	36
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	127428
Contig ID	24578_1.R1010
5'-most EST	LIB24-109-Q1-E1-C5
Method	BLASTN
NCBI GI	g2245031
BLAST score	440
E value	0.0e+00
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	127429
Contig ID	24585_1.R1010
5'-most EST	LIB24-109-Q1-E1-D12
Method	BLASTN
NCBI GI	g3337347
BLAST score	96
E value	1.0e-46
Match length	291
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127430
Contig ID	24590_1.R1010
5'-most EST	jC-atXLIB327402P1a10b1
Method	BLASTX
NCBI GI	g4309737
BLAST score	211
E value	1.0e-16

Match length	100
% identity	52
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127431
Contig ID	24591_1.R1010
5'-most EST	jC-atXLIB327407P1e04b2
Method	BLASTX
NCBI GI	g4220524
BLAST score	280
E value	2.0e-24
Match length	133
% identity	47
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	127432
Contig ID	24606_1.R1010
5'-most EST	jC-atXLIB327403P1f05a1
Method	BLASTN
NCBI GI	g4454004
BLAST score	424
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	127433
Contig ID	24613_1.R1010
5'-most EST	jC-atXP24C123I21T7066a1
Method	BLASTN
NCBI GI	g3341671
BLAST score	190
E value	1.0e-102
Match length	587
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127434
Contig ID	24613_2.R1010
5'-most EST	g2763691
Method	BLASTN
NCBI GI	g3341671
BLAST score	264
E value	1.0e-146
Match length	546
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127435
Contig ID	24618_1.R1010
5'-most EST	LIB24-109-Q1-E1-G11
Method	BLASTX
NCBI GI	g2213595
BLAST score	375

E value	3.0e-38
Match length	157
% identity	55
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	127436
Contig ID	24628_1.R1010
5'-most EST	g1158763

Seq. No.	127437
Contig ID	24635_1.R1010
5'-most EST	jC-atXLIB327418P4e07b1
Method	BLASTX
NCBI GI	g4105798
BLAST score	397
E value	3.0e-38
Match length	132
% identity	51
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	127438
Contig ID	24635_2.R1010
5'-most EST	jC-atXLIB327418P4e07a1
Method	BLASTN
NCBI GI	g4263753
BLAST score	337
E value	0.0e+00
Match length	480
% identity	96
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	127439
Contig ID	24636_1.R1010
5'-most EST	jC-atX25090Q1E1H02b1

Seq. No.	127440
Contig ID	24637_1.R1010
5'-most EST	jC-atX24110Q1E1A10b1

Seq. No.	127441
Contig ID	24646_1.R1010
5'-most EST	jC-atX24110Q1E1B01b1
Method	BLASTN
NCBI GI	g3449313
BLAST score	399
E value	0.0e+00
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	127442
Contig ID	24647_1.R1010
5'-most EST	LIB35-012-Q1-E1-D11
Method	BLASTN
NCBI GI	g4510323

BLAST score	416
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	127443
Contig ID	24647_2.R1010
5'-most EST	g1327787
Method	BLASTX
NCBI GI	g4558563
BLAST score	377
E value	7.0e-36
Match length	118
% identity	70
NCBI Description	(AC007138) putative NifU-like metallocluster assembly factor [Arabidopsis thaliana]

Seq. No.	127444
Contig ID	24651_2.R1010
5'-most EST	jC-atX24109Q1E1B06b2
Method	BLASTN
NCBI GI	g3510347
BLAST score	40
E value	4.0e-13
Match length	84
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	127445
Contig ID	24652_1.R1010
5'-most EST	jC-atXLIB327401P3f05b2
Method	BLASTX
NCBI GI	g4539423
BLAST score	143
E value	9.0e-20
Match length	77
% identity	69
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	127446
Contig ID	24653_1.R1010
5'-most EST	jC-atXLIB327407P1d10b2
Method	BLASTX
NCBI GI	g3335372
BLAST score	446
E value	4.0e-44
Match length	169
% identity	50
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	127447
Contig ID	24657_1.R1010
5'-most EST	LIB25-111-Q1-E1-F2

Method	BLASTN
NCBI GI	g4757410
BLAST score	286
E value	1.0e-160
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	127448
Contig ID	24658_1.R1010
5'-most EST	jC-atXP11C97P17T7035d1
Method	BLASTX
NCBI GI	g3183285
BLAST score	394
E value	9.0e-60
Match length	237
% identity	54
NCBI Description	HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION >gi_1742787_dbj_BAA15475_ (D90813) ORF_ID:o322#7; similar to [SwissProt Accession Number Q06373] [Escherichia coli] >gi_1787999 (AE000266) orf, hypothetical protein [Escherichia coli]

Seq. No.	127449
Contig ID	24658_2.R1010
5'-most EST	jC-alXLIB327434P1h12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127450
Contig ID	24658_3.R1010
5'-most EST	LIB25-106-Q1-E1-C11

Seq. No.	127451
Contig ID	24662_1.R1010
5'-most EST	g937860
Method	BLASTX
NCBI GI	g3402689
BLAST score	658
E value	4.0e-69
Match length	126
% identity	99
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	127452
Contig ID	24666_1.R1010
5'-most EST	jC-atXLIB327407P4d06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62

E value 4.0e-26
Match length 70
% identity 97
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 127453
Contig ID 24668_1.R1010
5'-most EST LIB3177-020-P1-K2-D4
Method BLASTN
NCBI GI g4757410
BLAST score 273
E value 1.0e-152
Match length 514
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No. 127454
Contig ID 24670_1.R1010
5'-most EST LIB3175-081-P1-K1-E8
Method BLASTX
NCBI GI g2829911
BLAST score 223
E value 5.0e-18
Match length 184
% identity 13
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 127455
Contig ID 24676_1.R1010
5'-most EST jC-atXLIB327407P1e03b2
Method BLASTN
NCBI GI g3510347
BLAST score 132
E value 1.0e-67
Match length 541
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 127456
Contig ID 24678_1.R1010
5'-most EST jC-atX24110Q1E1D07b1
Method BLASTN
NCBI GI g2264303
BLAST score 173
E value 2.0e-92
Match length 492
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No. 127457
Contig ID 24683_1.R1010
5'-most EST jC-atXLIB327426P2d11b1
Method BLASTX

NCBI GI	g2632254
BLAST score	370
E value	4.0e-35
Match length	114
% identity	68
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	127458
Contig ID	24685_1.R1010
5'-most EST	LIB24-110-Q1-E1-E3
Method	BLASTX
NCBI GI	g1168470
BLAST score	749
E value	9.0e-80
Match length	153
% identity	96
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	127459
Contig ID	24689_1.R1010
5'-most EST	g1159689
Method	BLASTN
NCBI GI	g2088638
BLAST score	152
E value	8.0e-80
Match length	475
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127460
Contig ID	24693_1.R1010
5'-most EST	jC-atXLIB327427P4h03b2
Method	BLASTN
NCBI GI	g2264313
BLAST score	75
E value	7.0e-34
Match length	243
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	127461
Contig ID	24695_1.R1010
5'-most EST	g2758477
Method	BLASTN
NCBI GI	g1931636
BLAST score	356
E value	0.0e+00
Match length	566
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	127462
Contig ID	24699_1.R1010
5'-most EST	LIB25-108-Q1-E1-A7
Method	BLASTX
NCBI GI	g1418990
BLAST score	237
E value	7.0e-20
Match length	123
% identity	43
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	127463
Contig ID	24707_1.R1010
5'-most EST	LIB24-110-Q1-E1-G2
Method	BLASTN
NCBI GI	g4220643
BLAST score	46
E value	1.0e-16
Match length	160
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	127464
Contig ID	24713_1.R1010
5'-most EST	jC-alXLIB327435P2d07a1
Method	BLASTN
NCBI GI	g2459406
BLAST score	235
E value	1.0e-129
Match length	307
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127465
Contig ID	24723_1.R1010
5'-most EST	LIB24-110-Q1-E1-H9

Seq. No.	127466
Contig ID	24728_1.R1010
5'-most EST	jC-atX24111Q1E1A03b1
Method	BLASTX
NCBI GI	g881625
BLAST score	385
E value	8.0e-49
Match length	114
% identity	84
NCBI Description	(U29432) 22.8 kDa protein [Ipomoea trifida]

Seq. No.	127467
Contig ID	24729_1.R1010
5'-most EST	jC-atXLIB327407P1d07b2
Method	BLASTN
NCBI GI	g2564049
BLAST score	328
E value	0.0e+00

Match length	563
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	127468
Contig ID	24732_1.R1010
5'-most EST	g957654
Method	BLASTX
NCBI GI	g3746809
BLAST score	640
E value	6.0e-67
Match length	134
% identity	88
NCBI Description	(AF082882) adenylate kinase [Arabidopsis thaliana]

Seq. No.	127469
Contig ID	24737_2.R1010
5'-most EST	LIB24-111-Q1-E1-B11

Seq. No.	127470
Contig ID	24738_1.R1010
5'-most EST	jC-atXLIB327407P1d08b2

Seq. No.	127471
Contig ID	24739_1.R1010
5'-most EST	LIB25-019-Q1-E1-H2

Seq. No.	127472
Contig ID	24744_1.R1010
5'-most EST	jC-atXLIB327419P1b11a2
Method	BLASTX
NCBI GI	g1161167
BLAST score	329
E value	3.0e-30
Match length	144
% identity	43
NCBI Description	(L42466) ethylene-forming enzyme [Picea glauca]

Seq. No.	127473
Contig ID	24748_1.R1010
5'-most EST	jC-atXP3C83B5T7056a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127474
Contig ID	24748_2.R1010
5'-most EST	jC-atXLIB327407P3d03b1
Method	BLASTX
NCBI GI	g3929649
BLAST score	1285
E value	1.0e-142

Match length	289
% identity	87
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	127475
Contig ID	24754_1.R1010
5'-most EST	LIB24-111-Q1-E1-C6
Method	BLASTN
NCBI GI	g3980374
BLAST score	151
E value	3.0e-79
Match length	414
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127476
Contig ID	24758_1.R1010
5'-most EST	LIB24-111-Q1-E1-D1
Method	BLASTN
NCBI GI	g4559375
BLAST score	186
E value	1.0e-100
Match length	931
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	127477
Contig ID	24760_1.R1010
5'-most EST	LIB317-062-P1-K1-A10
Method	BLASTN
NCBI GI	g2760173
BLAST score	285
E value	1.0e-159
Match length	523
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	127478
Contig ID	24762_1.R1010
5'-most EST	g2413480

Seq. No.	127479
Contig ID	24762_2.R1010
5'-most EST	g2722288

Seq. No.	127480
Contig ID	24774_1.R1010
5'-most EST	jC-atXLIB327407P2e12b1
Method	BLASTX
NCBI GI	g1707019
BLAST score	348
E value	9.0e-33
Match length	98

% identity	67
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127481
Contig ID	24776_1.R1010
5'-most EST	jC-atX24111Q1E1E05b1

Seq. No.	127482
Contig ID	24778_1.R1010
5'-most EST	jC-alXLIB327436P2e06b1
Method	BLASTN
NCBI GI	g4581084
BLAST score	305
E value	1.0e-171
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	127483
Contig ID	24778_2.R1010
5'-most EST	LIB24-111-Q1-E1-E7
Method	BLASTN
NCBI GI	g4581084
BLAST score	165
E value	2.0e-87
Match length	587
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	127484
Contig ID	24779_1.R1010
5'-most EST	LIB35-018-Q1-E1-G3
Method	BLASTX
NCBI GI	g4680643
BLAST score	177
E value	8.0e-13
Match length	109
% identity	39
NCBI Description	(AF132936) CGI-01 protein [Homo sapiens]

Seq. No.	127485
Contig ID	24780_1.R1010
5'-most EST	jC-atXLIB327407P1e10b2
Method	BLASTX
NCBI GI	g2832708
BLAST score	962
E value	1.0e-104
Match length	193
% identity	99
NCBI Description	(AL021713) beta-1, 3-glucanase-like protein [Arabidopsis thaliana]

Seq. No.	127486
Contig ID	24788_1.R1010
5'-most EST	LIB24-111-Q1-E1-F5

Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	127487
Contig ID	24791_1.R1010
5'-most EST	jC-atXLIB327417P4g10b1
Method	BLASTX
NCBI GI	g3298443
BLAST score	652
E value	4.0e-68
Match length	146
% identity	84
NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]

Seq. No.	127488
Contig ID	24800_1.R1010
5'-most EST	g957833
Method	BLASTN
NCBI GI	g3046854
BLAST score	435
E value	0.0e+00
Match length	469
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	127489
Contig ID	24810_1.R1010
5'-most EST	jC-atXLIB327426P3d06b1
Method	BLASTN
NCBI GI	g3928074
BLAST score	283
E value	1.0e-158
Match length	484
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127490
Contig ID	24816_1.R1010
5'-most EST	LIB24-112-Q1-E1-A11
Method	BLASTX
NCBI GI	g2911073
BLAST score	223
E value	6.0e-22
Match length	137
% identity	44
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	127491
Contig ID	24826_1.R1010

5'-most EST	LIB25-033-Q1-E1-A4
Method	BLASTN
NCBI GI	g4454447
BLAST score	336
E value	0.0e+00
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127492
Contig ID	24834_1.R1010
5'-most EST	jC-atX24112Q1E1B09b1
Method	BLASTX
NCBI GI	g2894379
BLAST score	164
E value	4.0e-11
Match length	63
% identity	56
NCBI Description	(Y14573) ring finger protein [Hordeum vulgare]

Seq. No.	127493
Contig ID	24837_1.R1010
5'-most EST	jC-atXLIB327407P4d04b1
Method	BLASTN
NCBI GI	g4732168
BLAST score	138
E value	2.0e-71
Match length	468
% identity	97
NCBI Description	Arabidopsis thaliana BAC T1J24

Seq. No.	127494
Contig ID	24846_2.R1010
5'-most EST	g2413552

Seq. No.	127495
Contig ID	24848_1.R1010
5'-most EST	jC-atXLIB327407P4d12b1
Method	BLASTX
NCBI GI	g4415916
BLAST score	153
E value	7.0e-10
Match length	88
% identity	41
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	127496
Contig ID	24850_1.R1010
5'-most EST	jC-atX24112Q1E1D03b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	753
E value	3.0e-80
Match length	156
% identity	92

NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	127497
Contig ID	24851_1.R1010
5'-most EST	jC-alXLIB327436P2a12b1
Method	BLASTX
NCBI GI	g4583544
BLAST score	224
E value	3.0e-18
Match length	109
% identity	38
NCBI Description	(Z95637) acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	127498
Contig ID	24851_2.R1010
5'-most EST	LIB24-112-Q1-E1-D5

Seq. No.	127499
Contig ID	24855_1.R1010
5'-most EST	jC-atXLIB327427P4b03b2

Seq. No.	127500
Contig ID	24857_1.R1010
5'-most EST	jC-atXLIB327407P2e10b1

Seq. No.	127501
Contig ID	24860_1.R1010
5'-most EST	ARABL1-042-Q1-E1-B8
Method	BLASTX
NCBI GI	g3901294
BLAST score	713
E value	3.0e-75
Match length	270
% identity	49
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	127502
Contig ID	24864_1.R1010
5'-most EST	jC-atXLIB327407P1e08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	44
E value	3.0e-15
Match length	56
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127503
Contig ID	24866_1.R1010
5'-most EST	g2047832

Seq. No.	127504
Contig ID	24866_2.R1010
5'-most EST	g1268170

Seq. No.	127505
Contig ID	24868_1.R1010
5'-most EST	jC-atXLIB327401P3f12b2
Method	BLASTX
NCBI GI	g3413710
BLAST score	205
E value	5.0e-16
Match length	137
% identity	40
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127506
Contig ID	24872_1.R1010
5'-most EST	LIB25-101-Q1-E1-B9
Method	BLASTX
NCBI GI	g3132473
BLAST score	654
E value	1.0e-68
Match length	148
% identity	88
NCBI Description	(AC003096) similar to rapb transcription factor [Arabidopsis thaliana]

Seq. No.	127507
Contig ID	24885_1.R1010
5'-most EST	LIB24-112-Q1-E1-G5

Seq. No.	127508
Contig ID	24889_1.R1010
5'-most EST	jC-atXP118C155O7T7096d2
Method	BLASTX
NCBI GI	g4204303
BLAST score	182
E value	1.0e-43
Match length	170
% identity	54
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	127509
Contig ID	24889_2.R1010
5'-most EST	jC-atXLIB327418P2b07b2
Method	BLASTX
NCBI GI	g4038043
BLAST score	497
E value	5.0e-50
Match length	101
% identity	89
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	127510
Contig ID	24889_3.R1010
5'-most EST	jC-atXLIB327431P2d12a1
Method	BLASTN
NCBI GI	g2290120

BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	127511
Contig ID	24889_4.R1010
5'-most EST	g402947
Method	BLASTN
NCBI GI	g4038029
BLAST score	213
E value	1.0e-116
Match length	293
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127512
Contig ID	24891_1.R1010
5'-most EST	jC-alXLIB327434P4a01b1
Method	BLASTX
NCBI GI	g4455325
BLAST score	742
E value	1.0e-78
Match length	174
% identity	85
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	127513
Contig ID	24892_1.R1010
5'-most EST	jC-alX25043Q1E1F04b1
Method	BLASTX
NCBI GI	g3297821
BLAST score	48
E value	7.0e-88
Match length	192
% identity	35
NCBI Description	(AL031032) extensin-like protein [Arabidopsis thaliana]

Seq. No.	127514
Contig ID	24897_1.R1010
5'-most EST	g2764357
Method	BLASTN
NCBI GI	g4757414
BLAST score	34
E value	2.0e-09
Match length	127
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	127515
Contig ID	24899_1.R1010
5'-most EST	jC-atXLIB327407P2g01b1
Method	BLASTN

NCBI GI	g2618605
BLAST score	172
E value	9.0e-92
Match length	421
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	127516
Contig ID	24901_1.R1010
5'-most EST	LIB24-113-Q1-E1-A6
Method	BLASTN
NCBI GI	g3821780
BLAST score	25
E value	4.0e-04
Match length	49
% identity	51
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	127517
Contig ID	24908_1.R1010
5'-most EST	jC-atX24113Q1E1B02b1
Method	BLASTX
NCBI GI	g558606
BLAST score	145
E value	1.0e-08
Match length	123
% identity	30
NCBI Description	(X70688) Nthsp18p [Nicotiana tabacum]

Seq. No.	127518
Contig ID	24913_1.R1010
5'-most EST	jC-atXLIB327407P1g08b2
Method	BLASTX
NCBI GI	g4337025
BLAST score	709
E value	6.0e-75
Match length	172
% identity	85
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	127519
Contig ID	24919_1.R1010
5'-most EST	jC-atXP23C120M17T7s2
Method	BLASTN
NCBI GI	g1871173
BLAST score	197
E value	1.0e-106
Match length	490
% identity	66
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	127520
Contig ID	24924_1.R1010
5'-most EST	jC-atXLIB327407P4g05b1
Method	BLASTN

NCBI GI	g2244991
BLAST score	288
E value	1.0e-161
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	127521
Contig ID	24931_1.R1010
5'-most EST	LIB25-111-Q1-E1-D3

Seq. No.	127522
Contig ID	24934_1.R1010
5'-most EST	jC-atXLIB327407P1h03b2
Method	BLASTX
NCBI GI	g3150408
BLAST score	743
E value	8.0e-79
Match length	176
% identity	88
NCBI Description	(AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127523
Contig ID	24935_1.R1010
5'-most EST	jC-atX24020Q1E1F06b1
Method	BLASTN
NCBI GI	g4584841
BLAST score	246
E value	1.0e-136
Match length	246
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	127524
Contig ID	24938_1.R1010
5'-most EST	g932123
Method	BLASTN
NCBI GI	g3004543
BLAST score	170
E value	1.0e-90
Match length	486
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127525
Contig ID	24947_1.R1010
5'-most EST	LIB3177-062-P1-K1-D8

Seq. No.	127526
Contig ID	24949_1.R1010
5'-most EST	jC-atXLIB327408P2a01b1
Method	BLASTN
NCBI GI	g4432811
BLAST score	35

E value	5.0e-10
Match length	415
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127527
Contig ID	24952_1.R1010
5'-most EST	jC-atXLIB327423P1b11b1
Method	BLASTX
NCBI GI	g3738208
BLAST score	798
E value	5.0e-85
Match length	259
% identity	61
NCBI Description	(AL031853) strong similarity to human Rev interacting protein Rip-1 [Schizosaccharomyces pombe]

Seq. No.	127528
Contig ID	24963_1.R1010
5'-most EST	jC-atXLIB327401P4g04b2
Method	BLASTX
NCBI GI	g2842487
BLAST score	285
E value	3.0e-25
Match length	57
% identity	96
NCBI Description	(AL021749) SOF1 protein-like protein [Arabidopsis thaliana]

Seq. No.	127529
Contig ID	24973_1.R1010
5'-most EST	jC-atXLIB327408P3a03b1
Method	BLASTN
NCBI GI	g4558521
BLAST score	38
E value	1.0e-11
Match length	110
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	127530
Contig ID	24977_1.R1010
5'-most EST	jC-atXP115C248G5T7083d1
Method	BLASTN
NCBI GI	g4584841
BLAST score	447
E value	0.0e+00
Match length	992
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	127531
Contig ID	24979_1.R1010
5'-most EST	jC-atXP12C103E13T7d2
Method	BLASTN

NCBI GI	g3702736
BLAST score	348
E value	0.0e+00
Match length	521
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	127532
Contig ID	24980_1.R1010
5'-most EST	LIB24-114-Q1-E1-A12
Method	BLASTX
NCBI GI	g4678297
BLAST score	609
E value	3.0e-63
Match length	192
% identity	45
NCBI Description	(AL049655) protein disulfide-isomerase-like protein [Arabidopsis thaliana]

Seq. No.	127533
Contig ID	24991_1.R1010
5'-most EST	g2749566
Method	BLASTX
NCBI GI	g3372671
BLAST score	250
E value	4.0e-21
Match length	77
% identity	66
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana] >gi_4704741_gb_AAD28247.1_AF124524_1 (AF124524) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No.	127534
Contig ID	24994_1.R1010
5'-most EST	LIB25-054-Q1-E1-B9
Method	BLASTX
NCBI GI	g4454477
BLAST score	1320
E value	1.0e-146
Match length	266
% identity	96
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127535
Contig ID	25002_1.R1010
5'-most EST	jC-atXLIB327407P4g08b1
Method	BLASTX
NCBI GI	g3193318
BLAST score	265
E value	5.0e-23
Match length	57
% identity	82
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	127536
Contig ID	25007_1.R1010

5'-most EST	jC-atXLIB327407P3g05b1
Method	BLASTN
NCBI GI	g2832689
BLAST score	150
E value	1.0e-78
Match length	451
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	127537
Contig ID	25014_1.R1010
5'-most EST	jC-atXP118C144B23T7012d2
Method	BLASTX
NCBI GI	g3115852
BLAST score	252
E value	3.0e-21
Match length	206
% identity	31
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	127538
Contig ID	25014_2.R1010
5'-most EST	jC-atXLIB327407P1h01b2
Method	BLASTX
NCBI GI	g3115852
BLAST score	162
E value	9.0e-11
Match length	53
% identity	66
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	127539
Contig ID	25016_2.R1010
5'-most EST	LIB24-114-Q1-E1-D7
Method	BLASTX
NCBI GI	g2760839
BLAST score	268
E value	4.0e-23
Match length	183
% identity	36
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	127540
Contig ID	25027_1.R1010
5'-most EST	jC-atXLIB327414P3h11b1
Method	BLASTX
NCBI GI	g484656
BLAST score	268
E value	2.0e-23
Match length	78
% identity	60
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No. 127541

Contig ID	25028_1.R1010
5'-most EST	LIB3177-068-P1-K1-F11
Method	BLASTN
NCBI GI	g4519190
BLAST score	136
E value	2.0e-70
Match length	464
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	127542
Contig ID	25029_2.R1010
5'-most EST	LIB24-114-Q1-E1-F1
Method	BLASTN
NCBI GI	g4539415
BLAST score	32
E value	3.0e-08
Match length	394
% identity	72
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	127543
Contig ID	25033_1.R1010
5'-most EST	jC-atXLIB327408P1a01b1
Method	BLASTN
NCBI GI	g4589434
BLAST score	504
E value	0.0e+00
Match length	584
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	127544
Contig ID	25036_1.R1010
5'-most EST	LIB24-114-Q1-E1-F5
Method	BLASTN
NCBI GI	g3068702
BLAST score	296
E value	1.0e-166
Match length	540
% identity	96
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No.	127545
Contig ID	25038_1.R1010
5'-most EST	LIB24-114-Q1-E1-F7
Method	BLASTX
NCBI GI	g114268
BLAST score	403
E value	2.0e-39
Match length	111

% identity	66
NCBI Description	L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE) >gi_541907_pir__S23763 gene Bp10 protein - rape >gi_17789_emb_CAA45554_ (X64257) protein homologous to ascorbate oxidase [Brassica napus]
Seq. No.	127546
Contig ID	25051_1.R1010
5'-most EST	jC-atXmonuni25Af02b1
Method	BLASTX
NCBI GI	g2500497
BLAST score	314
E value	9.0e-29
Match length	72
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225.1_ (X98656) ribosomal protein S21 [Zea mays]
Seq. No.	127547
Contig ID	25056_1.R1010
5'-most EST	LIB24-114-Q1-E1-H12
Method	BLASTX
NCBI GI	g4581109
BLAST score	974
E value	1.0e-106
Match length	211
% identity	91
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]
Seq. No.	127548
Contig ID	25059_1.R1010
5'-most EST	jC-atXLIB327408P3a08b1
Method	BLASTX
NCBI GI	g2129854
BLAST score	512
E value	1.0e-51
Match length	196
% identity	52
NCBI Description	early nodulin 8 precursor - alfalfa >gi_304037 (L18899) early nodulin [Medicago sativa]
Seq. No.	127549
Contig ID	25060_1.R1010
5'-most EST	jC-atXLIB327408P4a03b1
Seq. No.	127550
Contig ID	25063_1.R1010
5'-most EST	jC-atXP118C144H8T7077a1
Method	BLASTX
NCBI GI	g4725945
BLAST score	181
E value	6.0e-13
Match length	137
% identity	34
NCBI Description	(AL049730) putative SWH1 protein [Arabidopsis thaliana]
Seq. No.	127551

Contig ID	25086_1.R1010
5'-most EST	jC-atXLIB327408P3d03b1
Method	BLASTX
NCBI GI	g2244868
BLAST score	911
E value	1.0e-174
Match length	310
% identity	99
NCBI Description	(Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	127552
Contig ID	25088_3.R1010
5'-most EST	LIB25-047-Q1-E1-H1
Method	BLASTN
NCBI GI	g4581161
BLAST score	250
E value	1.0e-138
Match length	420
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	127553
Contig ID	25093_1.R1010
5'-most EST	jC-atXLIB327408P4f02a1
Method	BLASTX
NCBI GI	g4468980
BLAST score	661
E value	3.0e-69
Match length	146
% identity	89
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	127554
Contig ID	25093_2.R1010
5'-most EST	jC-atXLIB327407P3g02b1
Method	BLASTX
NCBI GI	g4468980
BLAST score	113
E value	4.0e-05
Match length	110
% identity	75
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	127555
Contig ID	25094_1.R1010
5'-most EST	jC-atX24115Q1E1C05b1
Method	BLASTX
NCBI GI	g1076632
BLAST score	531
E value	3.0e-54
Match length	151
% identity	66
NCBI Description	protein kinase - common tobacco >gi_506534_emb_CAA50374_ (X71057) protein kinase [Nicotiana tabacum]

Seq. No. 127556

Contig ID	25101_1.R1010
5'-most EST	jC-atXLIB327409P1d12b1
Method	BLASTN
NCBI GI	g4662609
BLAST score	149
E value	8.0e-78
Match length	697
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	127557
Contig ID	25112_1.R1010
5'-most EST	LIB25-111-Q1-E1-C10
Method	BLASTN
NCBI GI	g2252639
BLAST score	197
E value	1.0e-107
Match length	332
% identity	100
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	127558
Contig ID	25117_1.R1010
5'-most EST	LIB25-048-Q1-E1-A7
Method	BLASTX
NCBI GI	g1657619
BLAST score	155
E value	3.0e-40
Match length	203
% identity	44
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No.	127559
Contig ID	25139_1.R1010
5'-most EST	jC-atXLIB327408P2a02b1
Method	BLASTX
NCBI GI	g267146
BLAST score	996
E value	1.0e-108
Match length	252
% identity	79
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	127560
Contig ID	25139_3.R1010
5'-most EST	g315486
Method	BLASTX
NCBI GI	g267146
BLAST score	546
E value	7.0e-57

Match length	128
% identity	88
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	127561
Contig ID	25140_1.R1010
5'-most EST	jC-atXLIB327408P1a03b1
Method	BLASTX
NCBI GI	g3913425
BLAST score	779
E value	3.0e-83
Match length	154
% identity	94
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	127562
Contig ID	25140_2.R1010
5'-most EST	LIB25-034-Q1-E1-B3
Method	BLASTX
NCBI GI	g3913425
BLAST score	170
E value	4.0e-64
Match length	133
% identity	91
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	127563
Contig ID	25140_3.R1010
5'-most EST	LIB3234-053-P1-K1-H7
Method	BLASTX
NCBI GI	g3913425
BLAST score	1125
E value	1.0e-123
Match length	226
% identity	96
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	127564
Contig ID	25145_1.R1010
5'-most EST	g1053236

Seq. No.	127565
Contig ID	25149_1.R1010
5'-most EST	jC-atXLIB327408P2a10b1
Method	BLASTX
NCBI GI	g2623296
BLAST score	461

E value	5.0e-46
Match length	115
% identity	82
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127566
Contig ID	25151_1.R1010
5'-most EST	jC-atXLIB327427P1c11b1
Method	BLASTX
NCBI GI	g466044
BLAST score	281
E value	1.0e-24
Match length	92
% identity	52
NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]

Seq. No.	127567
Contig ID	25151_2.R1010
5'-most EST	jC-atXLIB327427P1c11a2

Seq. No.	127568
Contig ID	25161_1.R1010
5'-most EST	jC-atXLIB327409P2b06b1
Method	BLASTX
NCBI GI	g2622920
BLAST score	345
E value	2.0e-32
Match length	152
% identity	49
NCBI Description	(AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium thermoautotrophicum]

Seq. No.	127569
Contig ID	25161_2.R1010
5'-most EST	LIB24-116-Q1-E1-A7
Method	BLASTX
NCBI GI	g4128133
BLAST score	157
E value	5.0e-28
Match length	129
% identity	53
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	127570
Contig ID	25163_1.R1010
5'-most EST	LIB3176-022-P1-K1-F10
Method	BLASTN
NCBI GI	g3128135
BLAST score	170
E value	2.0e-90
Match length	677
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	127571
Contig ID	25170_1.R1010
5'-most EST	jC-atXLIB327407P1g07b2
Method	BLASTX
NCBI GI	g1352397
BLAST score	854
E value	6.0e-92
Match length	181
% identity	93
NCBI Description	ETR1 PROTEIN >gi_625975_pir__A48246 ethylene-response protein ETR1 - Arabidopsis thaliana >gi_902360 (L24119) ETR1 gene product [Arabidopsis thaliana]

Seq. No.	127572
Contig ID	25171_1.R1010
5'-most EST	jC-atXLIB327427P4c04b2
Method	BLASTX
NCBI GI	g2828285
BLAST score	778
E value	8.0e-83
Match length	214
% identity	75
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	127573
Contig ID	25171_2.R1010
5'-most EST	g931075
Method	BLASTN
NCBI GI	g2832611
BLAST score	377
E value	0.0e+00
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	127574
Contig ID	25183_1.R1010
5'-most EST	jC-atX24116Q1E1C07b1
Method	BLASTX
NCBI GI	g4455293
BLAST score	554
E value	7.0e-57
Match length	138
% identity	86
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	127575
Contig ID	25194_1.R1010
5'-most EST	g2047693
Method	BLASTX
NCBI GI	g2618725
BLAST score	342
E value	7.0e-32
Match length	76

% identity 88
NCBI Description (U49074) IAA18 [Arabidopsis thaliana]

Seq. No. 127576
Contig ID 25194_2.R1010
5'-most EST jC-atXLIB327407P4g11b1
Method BLASTX
NCBI GI g2618725
BLAST score 1095
E value 1.0e-120
Match length 215
% identity 100
NCBI Description (U49074) IAA18 [Arabidopsis thaliana]

Seq. No. 127577
Contig ID 25201_1.R1010
5'-most EST jC-atXP49C177K9T7082a1
Method BLASTX
NCBI GI g170131
BLAST score 573
E value 7.0e-59
Match length 185
% identity 63
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 127578
Contig ID 25204_1.R1010
5'-most EST LIB3175-034-P1-K1-G7
Method BLASTX
NCBI GI g2129774
BLAST score 1148
E value 1.0e-126
Match length 223
% identity 96
NCBI Description xyloglucan endotransglycosylase-related protein XTR4 - Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No. 127579
Contig ID 25215_1.R1010
5'-most EST jC-atXLIB327416P3g12b1
Method BLASTX
NCBI GI g4512655
BLAST score 1411
E value 1.0e-157
Match length 279
% identity 100
NCBI Description (AC007048) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 127580
Contig ID 25218_1.R1010
5'-most EST g2393663
Method BLASTX
NCBI GI g1653293
BLAST score 267

E value	4.0e-23
Match length	96
% identity	58
NCBI Description	(D90912) ornithine acetyltransferase [Synechocystis sp.]

Seq. No.	127581
Contig ID	25218_2.R1010
5'-most EST	jC-atXLIB327408P1a04b1
Method	BLASTX
NCBI GI	g4056500
BLAST score	520
E value	3.0e-70
Match length	154
% identity	89
NCBI Description	(AC005896) putative acetyltransferase [Arabidopsis thaliana]

Seq. No.	127582
Contig ID	25227_1.R1010
5'-most EST	LIB3168-090-P1-K1-G4
Method	BLASTN
NCBI GI	g3449328
BLAST score	190
E value	1.0e-102
Match length	406
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCI2, complete sequence [Arabidopsis thaliana]

Seq. No.	127583
Contig ID	25229_1.R1010
5'-most EST	jC-atX25063Q1E1H02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	127584
Contig ID	25230_1.R1010
5'-most EST	jC-atXLIB327408P4a01b1
Method	BLASTX
NCBI GI	g2281089
BLAST score	399
E value	2.0e-38
Match length	87
% identity	89
NCBI Description	(AC002333) Sm protein F isolog [Arabidopsis thaliana]

Seq. No.	127585
Contig ID	25236_1.R1010
5'-most EST	jC-atXLIB327408P1a10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63

E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127586
Contig ID	25241_2.R1010
5'-most EST	jC-atXLIB327414P3d01a1
Method	BLASTX
NCBI GI	g2879811
BLAST score	433
E value	1.0e-42
Match length	89
% identity	89
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	127587
Contig ID	25241_3.R1010
5'-most EST	g2733308
Method	BLASTX
NCBI GI	g2879811
BLAST score	522
E value	3.0e-53
Match length	112
% identity	87
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	127588
Contig ID	25244_1.R1010
5'-most EST	g957981

Seq. No.	127589
Contig ID	25244_3.R1010
5'-most EST	jC-atXLIB327408P2b04b1

Seq. No.	127590
Contig ID	25248_1.R1010
5'-most EST	jC-atXLIB327408P1b02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127591
Contig ID	25249_1.R1010
5'-most EST	jC-atXLIB327408P2b07b1
Method	BLASTX
NCBI GI	g4678225
BLAST score	793
E value	1.0e-84
Match length	164
% identity	93

NCBI Description	(AC007135) unknown protein [Arabidopsis thaliana]

Seq. No.	127592
Contig ID	25250_1.R1010
5'-most EST	jC-atXLIB327408P2b10b1
Method	BLASTX
NCBI GI	g2501565
BLAST score	221
E value	7.0e-18
Match length	103
% identity	46
NCBI Description	HYPOTHETICAL 40.2 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION >gi_1078518_pir__S55087 hypothetical protein YMR101c - yeast (Saccharomyces cerevisiae) >gi_854438_emb_CAA89902_ (Z49807) unknown [Saccharomyces cerevisiae] >gi_4126459_dbj_BAA36578_ (AB013498) cis-prenyltransferase homologue [Saccharomyces cerevisiae]

Seq. No.	127593
Contig ID	25252_1.R1010
5'-most EST	jC-atXLIB327408P2b11b1
Method	BLASTX
NCBI GI	g2827552
BLAST score	242
E value	3.0e-20
Match length	97
% identity	52
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	127594
Contig ID	25256_1.R1010
5'-most EST	jC-atXLIB327408P2b08b1
Method	BLASTX
NCBI GI	g3367521
BLAST score	234
E value	2.0e-19
Match length	129
% identity	36
NCBI Description	(AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana]

Seq. No.	127595
Contig ID	25269_1.R1010
5'-most EST	jC-atXLIB327422P1d10b1

Seq. No.	127596
Contig ID	25279_1.R1010
5'-most EST	jC-atXP122C156F16T7031a1
Method	BLASTN
NCBI GI	g3869067
BLAST score	260
E value	1.0e-144
Match length	622
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	127597
Contig ID	25279_2.R1010
5'-most EST	jC-atXLIB327408P1c01b1
Method	BLASTN
NCBI GI	g3869067
BLAST score	355
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	127598
Contig ID	25292_1.R1010
5'-most EST	jC-alX24117Q1E1E09b1
Method	BLASTX
NCBI GI	g2626753
BLAST score	666
E value	4.0e-70
Match length	156
% identity	82
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	127599
Contig ID	25296_1.R1010
5'-most EST	jC-atXLIB327408P3c01b1
Method	BLASTX
NCBI GI	g2244979
BLAST score	945
E value	1.0e-102
Match length	228
% identity	86
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	127600
Contig ID	25298_1.R1010
5'-most EST	jC-atXLIB327408P3c02b1
Method	BLASTX
NCBI GI	g2262104
BLAST score	645
E value	2.0e-75
Match length	141
% identity	100
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	127601
Contig ID	25304_1.R1010
5'-most EST	jC-atXLIB327420P4a03b1
Method	BLASTN
NCBI GI	g4063730
BLAST score	146
E value	3.0e-76
Match length	382
% identity	99

NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	127602
Contig ID	25306_1.R1010
5'-most EST	LIB24-117-Q1-E1-G10
Method	BLASTX
NCBI GI	g3513727
BLAST score	1541
E value	0.0e+00
Match length	355
% identity	61
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	127603
Contig ID	25306_2.R1010
5'-most EST	jC-atXP10C97D21T7d2
Method	BLASTX
NCBI GI	g3513727
BLAST score	554
E value	7.0e-57
Match length	108
% identity	100
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	127604
Contig ID	25318_1.R1010
5'-most EST	LIB24-117-Q1-E1-H12
Method	BLASTX
NCBI GI	g4512708
BLAST score	507
E value	2.0e-59
Match length	140
% identity	87
NCBI Description	(AC006569) putative glutaredoxin [Arabidopsis thaliana]

Seq. No.	127605
Contig ID	25333_1.R1010
5'-most EST	jC-atXLIB327408P3a12b1
Method	BLASTN
NCBI GI	g1245938
BLAST score	36
E value	2.0e-10
Match length	36
% identity	62
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	127606
Contig ID	25336_1.R1010
5'-most EST	jC-atXLIB327408P2b02b1
Method	BLASTX
NCBI GI	g2352492
BLAST score	548
E value	9.0e-56
Match length	210
% identity	52
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	127607
Contig ID	25337_1.R1010
5'-most EST	jC-atXLIB327408P1b03b1
Method	BLASTX
NCBI GI	g4467096
BLAST score	503
E value	5.0e-51
Match length	122
% identity	84
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	127608
Contig ID	25339_1.R1010
5'-most EST	g1216645
Method	BLASTN
NCBI GI	g4544435
BLAST score	303
E value	1.0e-170
Match length	525
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	127609
Contig ID	25340_1.R1010
5'-most EST	jC-atXLIB327408P1b11b1
Method	BLASTN
NCBI GI	g4468103
BLAST score	290
E value	1.0e-162
Match length	622
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	127610
Contig ID	25340_2.R1010
5'-most EST	LIB35-027-Q1-E1-D7
Method	BLASTN
NCBI GI	g4468103
BLAST score	265
E value	1.0e-147
Match length	442
% identity	99

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)
Seq. No.	127611
Contig ID	25340_3.R1010
5'-most EST	g2763215
Method	BLASTN
NCBI GI	g4468103
BLAST score	268
E value	1.0e-149
Match length	564
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)
Seq. No.	127612
Contig ID	25341_1.R1010
5'-most EST	jC-atXLIB327408P1b12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	127613
Contig ID	25344_1.R1010
5'-most EST	LIB25-117-Q1-E1-E8
Method	BLASTX
NCBI GI	g4454035
BLAST score	847
E value	4.0e-91
Match length	209
% identity	77
NCBI Description	(AL035394) polyprenyltransferase like protein [Arabidopsis thaliana]
Seq. No.	127614
Contig ID	25345_1.R1010
5'-most EST	jC-atXLIB327408P1b08b1
Method	BLASTX
NCBI GI	g2980764
BLAST score	245
E value	2.0e-20
Match length	59
% identity	73
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]
Seq. No.	127615
Contig ID	25348_1.R1010
5'-most EST	jC-alXLIB327436P1b06b1
Seq. No.	127616
Contig ID	25350_1.R1010
5'-most EST	jC-atXLIB327408P4b09b1

Method	BLASTN
NCBI GI	g4056429
BLAST score	404
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127617
Contig ID	25350_2.R1010
5'-most EST	LIB3176-106-P1-K1-A12
Method	BLASTX
NCBI GI	g4056457
BLAST score	391
E value	7.0e-62
Match length	125
% identity	92
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	127618
Contig ID	25358_1.R1010
5'-most EST	jC-atXLIB327408P3b07b1
Method	BLASTN
NCBI GI	g3172156
BLAST score	187
E value	1.0e-100
Match length	595
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127619
Contig ID	25369_1.R1010
5'-most EST	LIB24-118-Q1-E1-D7
Method	BLASTX
NCBI GI	g4512707
BLAST score	642
E value	4.0e-67
Match length	137
% identity	91
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127620
Contig ID	25378_1.R1010
5'-most EST	jC-atXLIB327408P1c05b1
Method	BLASTX
NCBI GI	g124871
BLAST score	215
E value	5.0e-17
Match length	86
% identity	50
NCBI Description	INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_67792_pir__PWVKL inorganic pyrophosphatase (EC 3.6.1.1) - yeast (Kluyveromyces marxianus var. lactis) >gi_2903_emb_CAA32446_ (X14230) inorganic pyrophosphatase

(AA 1-287) [Kluyveromyces lactis]

Seq. No.	127621
Contig ID	25381_1.R1010
5'-most EST	LIB35-033-Q1-E1-H6

Seq. No.	127622
Contig ID	25386_1.R1010
5'-most EST	jC-atXLIB327408P4c02b1
Method	BLASTN
NCBI GI	g4757414
BLAST score	303
E value	1.0e-170
Match length	470
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	127623
Contig ID	25397_1.R1010
5'-most EST	jC-atXLIB327408P3c08b1
Method	BLASTX
NCBI GI	g452593
BLAST score	586
E value	2.0e-60
Match length	210
% identity	56
NCBI Description	(D21814) ORF [Lilium longiflorum]

Seq. No.	127624
Contig ID	25420_1.R1010
5'-most EST	jC-atXLIB327408P3a09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	4.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127625
Contig ID	25432_1.R1010
5'-most EST	jC-atXLIB327408P3b04b1
Method	BLASTX
NCBI GI	g3063467
BLAST score	575
E value	3.0e-59
Match length	129
% identity	89
NCBI Description	(AC003981) F22O13.29 [Arabidopsis thaliana]

Seq. No.	127626
Contig ID	25435_1.R1010
5'-most EST	jC-atXLIB327408P4b05b1
Method	BLASTX
NCBI GI	g3582339

BLAST score	779
E value	5.0e-83
Match length	145
% identity	100
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	127627
Contig ID	25437_1.R1010
5'-most EST	jC-atXLIB327408P4b07b1
Method	BLASTX
NCBI GI	g4218120
BLAST score	756
E value	1.0e-80
Match length	149
% identity	100
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	127628
Contig ID	25439_1.R1010
5'-most EST	jC-atXLIB327408P4b03b1
Method	BLASTN
NCBI GI	g2832639
BLAST score	139
E value	5.0e-72
Match length	432
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	127629
Contig ID	25441_1.R1010
5'-most EST	jC-atXLIB327408P4b04b1
Method	BLASTX
NCBI GI	g2924510
BLAST score	1245
E value	1.0e-137
Match length	263
% identity	88
NCBI Description	(AL022023) MYB-like protein [Arabidopsis thaliana]

Seq. No.	127630
Contig ID	25444_1.R1010
5'-most EST	LIB24-119-Q1-E1-D11
Method	BLASTX
NCBI GI	g3281867
BLAST score	553
E value	1.0e-56
Match length	120
% identity	93
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	127631
Contig ID	25445_1.R1010
5'-most EST	jC-atXLIB327408P3b11b1
Method	BLASTX
NCBI GI	g4522009

BLAST score	549
E value	4.0e-56
Match length	195
% identity	50
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	127632
Contig ID	25447_1.R1010
5'-most EST	jC-atXLIB327423P1h08b1
Method	BLASTX
NCBI GI	g4538926
BLAST score	1198
E value	1.0e-132
Match length	238
% identity	100
NCBI Description	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]

Seq. No.	127633
Contig ID	25447_3.R1010
5'-most EST	jC-atXLIB327408P3b10b1
Method	BLASTX
NCBI GI	g4538926
BLAST score	938
E value	1.0e-114
Match length	240
% identity	91
NCBI Description	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]

Seq. No.	127634
Contig ID	25457_1.R1010
5'-most EST	jC-atXLIB327408P1c11b1
Method	BLASTN
NCBI GI	g2351065
BLAST score	134
E value	4.0e-69
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	127635
Contig ID	25465_1.R1010
5'-most EST	jC-atXLIB327408P1c10b1
Method	BLASTN
NCBI GI	g3150395
BLAST score	432
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9D9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127636
Contig ID	25468_1.R1010
5'-most EST	jC-atXLIB327408P4c04b1

Method	BLASTX
NCBI GI	g3063460
BLAST score	950
E value	1.0e-103
Match length	251
% identity	78
NCBI Description	(AC003981) F22O13.22 [Arabidopsis thaliana]

Seq. No.	127637
Contig ID	25477_1.R1010
5'-most EST	LIB24-119-Q1-E1-H3
Method	BLASTX
NCBI GI	g1064887
BLAST score	216
E value	3.0e-17
Match length	67
% identity	69
NCBI Description	(X92955) pollen coat protein [Brassica oleracea]

Seq. No.	127638
Contig ID	25490_1.R1010
5'-most EST	LIB24-120-Q1-E1-B1
Method	BLASTX
NCBI GI	g3650028
BLAST score	582
E value	3.0e-60
Match length	134
% identity	89
NCBI Description	(AC005396) putative 22 kDa peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No.	127639
Contig ID	25495_1.R1010
5'-most EST	jC-atXP68C216B14T7d1
Method	BLASTX
NCBI GI	g2501433
BLAST score	207
E value	5.0e-16
Match length	93
% identity	51
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-EPF5) >gi_181916 (M91670) ubiquitin carrier protein [Homo sapiens]

Seq. No.	127640
Contig ID	25496_1.R1010
5'-most EST	jC-atXLIB327408P1b05b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	919
E value	2.0e-99
Match length	204
% identity	85
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	127641
Contig ID	25496_2.R1010

5'-most EST	jC-atXLIB327408P1b05a1
Method	BLASTX
NCBI GI	g4049348
BLAST score	274
E value	5.0e-24
Match length	60
% identity	83
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	127642
Contig ID	25496_4.R1010
5'-most EST	jC-atXLIB327402P1f09b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	194
E value	1.0e-14
Match length	47
% identity	79
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	127643
Contig ID	25496_5.R1010
5'-most EST	g757564
Method	BLASTX
NCBI GI	g4049348
BLAST score	464
E value	5.0e-59
Match length	136
% identity	82
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	127644
Contig ID	25499_1.R1010
5'-most EST	LIB24-120-Q1-E1-C3
Method	BLASTN
NCBI GI	g4539331
BLAST score	278
E value	1.0e-155
Match length	396
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	127645
Contig ID	25503_1.R1010
5'-most EST	jC-atXLIB327408P3b03b1
Method	BLASTX
NCBI GI	g4493908
BLAST score	148
E value	1.0e-21
Match length	127
% identity	46
NCBI Description	(AL034558) predicted using hexExon; MAL3P2.30 (PFC0305w), Putative homologue of Human EB1, len: 511 aa; Similarity to Human EB1 protein. H.sapiens EB1 protein (TR:Q156910) BLAST Score: 325, sum P(2) = 6.2e-35; 46% identity in

Seq. No.	127646
Contig ID	25507_1.R1010
5'-most EST	jC-atXLIB327408P4b12b1
Method	BLASTX
NCBI GI	g3193292
BLAST score	1050
E value	1.0e-114
Match length	220
% identity	94
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	127647
Contig ID	25507_3.R1010
5'-most EST	LIB3177-066-P1-K1-G11
Method	BLASTX
NCBI GI	g3193292
BLAST score	1061
E value	1.0e-116
Match length	212
% identity	99
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	127648
Contig ID	25508_1.R1010
5'-most EST	jC-atXLIB327408P4e04b1
Method	BLASTX
NCBI GI	g3894172
BLAST score	479
E value	5.0e-48
Match length	172
% identity	53
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	127649
Contig ID	25515_1.R1010
5'-most EST	jC-atXLIB327408P2c03b1
Method	BLASTN
NCBI GI	g4512690
BLAST score	168
E value	2.0e-89
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	127650
Contig ID	25516_1.R1010
5'-most EST	g935410
Method	BLASTX
NCBI GI	g3319357
BLAST score	896
E value	1.0e-104

Match length	202
% identity	100
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No.	127651
Contig ID	25517_1.R1010
5'-most EST	jC-atXLIB327408P1c04b1
Method	BLASTX
NCBI GI	g1785851
BLAST score	177
E value	2.0e-12
Match length	88
% identity	41
NCBI Description	(D50692) c-myc binding protein [Homo sapiens] >gi_2443310_dbj_BAA22408_ (AB007191) AMY-1 [Homo sapiens]

Seq. No.	127652
Contig ID	25518_1.R1010
5'-most EST	jC-atXLIB327408P2c04b1
Method	BLASTX
NCBI GI	g4204309
BLAST score	673
E value	1.0e-70
Match length	212
% identity	70
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	127653
Contig ID	25522_1.R1010
5'-most EST	jC-atXLIB327420P4a10b1
Method	BLASTX
NCBI GI	g3482908
BLAST score	219
E value	3.0e-17
Match length	152
% identity	34
NCBI Description	(AC005551) R26529_2, partial CDS [Homo sapiens]

Seq. No.	127654
Contig ID	25529_1.R1010
5'-most EST	LIB24-120-Q1-E1-F6
Method	BLASTX
NCBI GI	g1946369
BLAST score	453
E value	6.0e-77
Match length	229
% identity	69
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	127655
Contig ID	25540_1.R1010
5'-most EST	jC-atXLIB327408P3c10b1
Method	BLASTN
NCBI GI	g3133272
BLAST score	696

E value	0.0e+00
Match length	778
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No.	127656
Contig ID	25542_1.R1010
5'-most EST	jC-atXLIB327408P3c09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	70
E value	1.0e-30
Match length	78
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127657
Contig ID	25547_1.R1010
5'-most EST	ARABL1-034-Q1-B1-A1
Method	BLASTX
NCBI GI	g3269289
BLAST score	351
E value	2.0e-33
Match length	100
% identity	73
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	127658
Contig ID	25551_1.R1010
5'-most EST	jC-atXLIB327408P2d03b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	349
E value	0.0e+00
Match length	436
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	127659
Contig ID	25551_2.R1010
5'-most EST	LIB3176-003-P1-K1-F4
Method	BLASTN
NCBI GI	g4589412
BLAST score	270
E value	1.0e-150
Match length	465
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	127660
Contig ID	25555_1.R1010
5'-most EST	jC-atXLIB327408P2d11b1
Method	BLASTX

NCBI GI	g2829889
BLAST score	394
E value	2.0e-72
Match length	148
% identity	100
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	127661
Contig ID	25567_1.R1010
5'-most EST	jC-atXLIB327408P3d07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	2.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127662
Contig ID	25567_2.R1010
5'-most EST	g1268161
Method	BLASTN
NCBI GI	g3097257
BLAST score	36
E value	2.0e-10
Match length	80
% identity	86
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	127663
Contig ID	25573_1.R1010
5'-most EST	jC-atXLIB327409P2d06b1
Method	BLASTX
NCBI GI	g4432846
BLAST score	547
E value	5.0e-56
Match length	103
% identity	100
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	127664
Contig ID	25579_1.R1010
5'-most EST	jC-atXLIB327427P3b06b2
Method	BLASTX
NCBI GI	g2245108
BLAST score	533
E value	3.0e-54
Match length	164
% identity	71
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	127665
Contig ID	25588_1.R1010
5'-most EST	jC-atXLIB327408P2e08b1
Method	BLASTX
NCBI GI	g4505235

BLAST score	276
E value	3.0e-24
Match length	128
% identity	44
NCBI Description	mannose phosphate isomerase >gi_462567_sp_P34949_MANA_HUMAN MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) >gi_631328_pir__S41122 mannose-6-phosphate isomerase (EC 5.3.1.8) - human >gi_416017_emb_CAA53657_ (X76057) phosphomannose isomerase [Homo sapiens] >gi_740967_prf__2006245A phosphomannose isomerase [Homo sapiens]

Seq. No.	127666
Contig ID	25593_1.R1010
5'-most EST	jC-alXLIB327435P3f07b1
Method	BLASTX
NCBI GI	g4586035
BLAST score	766
E value	1.0e-81
Match length	175
% identity	88
NCBI Description	(AC007109) putative prohibitin protein [Arabidopsis thaliana]

Seq. No.	127667
Contig ID	25604_1.R1010
5'-most EST	LIB25-080-Q1-E1-E9
Method	BLASTN
NCBI GI	g3894156
BLAST score	195
E value	1.0e-105
Match length	331
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127668
Contig ID	25605_1.R1010
5'-most EST	jC-atXLIB327408P4e02b1
Method	BLASTX
NCBI GI	g2181180
BLAST score	274
E value	5.0e-24
Match length	160
% identity	36
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	127669
Contig ID	25610_1.R1010
5'-most EST	jC-atXmonuni26Ch03b1
Method	BLASTN
NCBI GI	g2245073
BLAST score	240
E value	1.0e-132
Match length	398
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No.	127670
Contig ID	25615_1.R1010
5'-most EST	jC-atXLIB327408P1f06b1
Method	BLASTX
NCBI GI	g2190548
BLAST score	253
E value	1.0e-27
Match length	69
% identity	89
NCBI Description	(AC001229) EST gb_ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	127671
Contig ID	25627_1.R1010
5'-most EST	jC-atXLIB327408P2d04b1
Method	BLASTN
NCBI GI	g1429227
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	A.thaliana mRNA for small subunit of TFIIA

Seq. No.	127672
Contig ID	25628_1.R1010
5'-most EST	jC-atXLIB327408P1d05b1
Method	BLASTX
NCBI GI	g1708464
BLAST score	497
E value	3.0e-50
Match length	154
% identity	63
NCBI Description	PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD) (2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_ (Z69795) unknown [Schizosaccharomyces pombe]

Seq. No.	127673
Contig ID	25632_1.R1010
5'-most EST	jC-atXLIB327408P2d05b1
Method	BLASTX
NCBI GI	g4585988
BLAST score	218
E value	2.0e-17
Match length	88
% identity	58
NCBI Description	(AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]

Seq. No.	127674
Contig ID	25634_1.R1010
5'-most EST	jC-atXLIB327425P1h06b1
Method	BLASTX
NCBI GI	g3776084
BLAST score	158
E value	2.0e-10

Match length	57
% identity	51
NCBI Description	(Y18251) NtN2 [Medicago truncatula]

Seq. No.	127675
Contig ID	25635_1.R1010
5'-most EST	LIB25-085-Q1-E1-B5
Method	BLASTX
NCBI GI	g2651307
BLAST score	426
E value	2.0e-60
Match length	121
% identity	98
NCBI Description	(AC002336) putative uroporphyinogen decarboxylase [Arabidopsis thaliana]

Seq. No.	127676
Contig ID	25637_1.R1010
5'-most EST	jC-atXP123C119O23T7082d1
Method	BLASTX
NCBI GI	g3935180
BLAST score	265
E value	6.0e-52
Match length	133
% identity	87
NCBI Description	(AC004557) F17L21.23 [Arabidopsis thaliana]

Seq. No.	127677
Contig ID	25650_1.R1010
5'-most EST	jC-atXLIB327408P4d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127678
Contig ID	25652_1.R1010
5'-most EST	jC-atXLIB327408P4d09b1
Method	BLASTX
NCBI GI	g2961389
BLAST score	550
E value	2.0e-56
Match length	135
% identity	76
NCBI Description	(AL022141) purple acid phosphatase like protein [Arabidopsis thaliana] >gi_4006925_emb_CAB16853.1_ (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No.	127679
Contig ID	25654_1.R1010
5'-most EST	LIB24-122-Q1-E1-C5

Seq. No.	127680

Contig ID	25659_1.R1010
5'-most EST	jC-atXLIB327408P2e02b1
Method	BLASTX
NCBI GI	g3252827
BLAST score	242
E value	5.0e-20
Match length	122
% identity	39
NCBI Description	(AC004382) Unknown gene product [Homo sapiens]

Seq. No.	127681
Contig ID	25661_1.R1010
5'-most EST	jC-atXLIB327408P2e03b1
Method	BLASTN
NCBI GI	g3449321
BLAST score	199
E value	1.0e-108
Match length	405
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	127682
Contig ID	25677_1.R1010
5'-most EST	jC-atXLIB327408P1e08b1
Method	BLASTN
NCBI GI	g4467094
BLAST score	302
E value	1.0e-169
Match length	465
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	127683
Contig ID	25678_1.R1010
5'-most EST	jC-atXLIB327408P3e02b1
Method	BLASTX
NCBI GI	g1399265
BLAST score	909
E value	3.0e-98
Match length	189
% identity	95
NCBI Description	(U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No.	127684
Contig ID	25681_1.R1010
5'-most EST	jC-atXLIB327408P3e04b1

Seq. No.	127685
Contig ID	25691_1.R1010
5'-most EST	jC-atXLIB327418P2g01b2
Method	BLASTN
NCBI GI	g2760168
BLAST score	189
E value	1.0e-102

Match length	466
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	127686
Contig ID	25692_1.R1010
5'-most EST	jC-atXLIB327408P1f01b1
Method	BLASTN
NCBI GI	g3702739
BLAST score	165
E value	2.0e-87
Match length	522
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	127687
Contig ID	25698_1.R1010
5'-most EST	jC-atXLIB327408P4e11b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	384
E value	0.0e+00
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	127688
Contig ID	25699_1.R1010
5'-most EST	LIB35-028-Q1-E1-G12
Method	BLASTX
NCBI GI	g4056457
BLAST score	508
E value	3.0e-51
Match length	135
% identity	73
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	127689
Contig ID	25699_2.R1010
5'-most EST	LIB24-122-Q1-E1-H1
Method	BLASTX
NCBI GI	g4056457
BLAST score	479
E value	7.0e-48
Match length	127
% identity	72
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	127690
Contig ID	25701_1.R1010
5'-most EST	jC-atXLIB327408P2f08b1
Method	BLASTN

NCBI GI	g3688169
BLAST score	278
E value	1.0e-155
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	127691
Contig ID	25704_1.R1010
5'-most EST	jC-atXLIB327408P1f07b1
Method	BLASTX
NCBI GI	g1352075
BLAST score	590
E value	4.0e-61
Match length	126
% identity	88
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi_669059_emb_CAA59162_ (X84684) beta-galactosidase [Brassica oleracea]

Seq. No.	127692
Contig ID	25709_1.R1010
5'-most EST	jC-atXLIB327408P1d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127693
Contig ID	25712_1.R1010
5'-most EST	jC-atXLIB327421P2c10b1
Method	BLASTN
NCBI GI	g4589435
BLAST score	145
E value	1.0e-75
Match length	440
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	127694
Contig ID	25717_1.R1010
5'-most EST	jC-atXLIB327408P1d07b1
Method	BLASTX
NCBI GI	g2618686
BLAST score	576
E value	2.0e-59
Match length	151
% identity	72
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127695
Contig ID	25720_1.R1010
5'-most EST	jC-atXLIB327408P4d04b1
Method	BLASTX
NCBI GI	g4115938
BLAST score	792
E value	9.0e-85
Match length	164
% identity	97
NCBI Description	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]

Seq. No.	127696
Contig ID	25722_1.R1010
5'-most EST	jC-atXLIB327408P3d05b1
Method	BLASTX
NCBI GI	g3367531
BLAST score	682
E value	1.0e-71
Match length	173
% identity	83
NCBI Description	(AC004392) Strong similarity to gi_2160138 F19K23.6 gene product from A. thaliana BAC gb_AC000375. [Arabidopsis thaliana]

Seq. No.	127697
Contig ID	25725_1.R1010
5'-most EST	jC-atXLIB327408P4d03b1

Seq. No.	127698
Contig ID	25729_1.R1010
5'-most EST	jC-atXLIB327408P3d12b1
Method	BLASTN
NCBI GI	g3600029
BLAST score	463
E value	0.0e+00
Match length	617
% identity	99
NCBI Description	Arabidopsis thaliana BAC T12H20

Seq. No.	127699
Contig ID	25730_1.R1010
5'-most EST	jC-atXLIB327408P3d09b1
Method	BLASTX
NCBI GI	g1552379
BLAST score	832
E value	2.0e-97
Match length	234
% identity	68
NCBI Description	(Y08155) pectin methylesterase [Silene latifolia ssp. alba]

Seq. No.	127700
Contig ID	25743_1.R1010
5'-most EST	jC-atXLIB327408P2e11b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	55
E value	5.0e-22
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127701
Contig ID	25743_2.R1010
5'-most EST	jC-atX25007Q1E1G03b1

Seq. No.	127702
Contig ID	25746_1.R1010
5'-most EST	jC-atXLIB327408P1e09b1
Method	BLASTX
NCBI GI	g1750376
BLAST score	798
E value	2.0e-85
Match length	152
% identity	100
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	127703
Contig ID	25749_1.R1010
5'-most EST	jC-atXLIB327408P1e10b1
Method	BLASTN
NCBI GI	g2852453
BLAST score	259
E value	1.0e-143
Match length	280
% identity	97
NCBI Description	Arabidopsis thaliana gene for cystathionine gamma-synthase, complete cds

Seq. No.	127704
Contig ID	25753_1.R1010
5'-most EST	jC-atXLIB327408P3e08b1
Method	BLASTX
NCBI GI	g3287857
BLAST score	312
E value	1.0e-34
Match length	185
% identity	44
NCBI Description	3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA DEHYDROGENASE) (BHBD) >gi_1209052 (U32229) HbdA [Bradyrhizobium japonicum]

Seq. No.	127705
Contig ID	25755_1.R1010
5'-most EST	LIB24-123-Q1-E1-G6
Method	BLASTX
NCBI GI	g3805760
BLAST score	256
E value	4.0e-22
Match length	88

% identity	69
NCBI Description	(AC005693) unknown protein [Arabidopsis thaliana]

Seq. No.	127706
Contig ID	25761_1.R1010
5'-most EST	LIB24-123-Q1-E2-H5

Seq. No.	127707
Contig ID	25762_1.R1010
5'-most EST	LIB24-123-Q1-E2-H6
Method	BLASTX
NCBI GI	g4582783
BLAST score	164
E value	3.0e-45
Match length	108
% identity	77
NCBI Description	(AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No.	127708
Contig ID	25770_1.R1010
5'-most EST	jC-atXLIB327408P2d09b1
Method	BLASTX
NCBI GI	g2213617
BLAST score	231
E value	5.0e-19
Match length	87
% identity	59
NCBI Description	(AC000103) F21J9.11 [Arabidopsis thaliana]

Seq. No.	127709
Contig ID	25774_1.R1010
5'-most EST	LIB24-123-Q1-E2-B9
Method	BLASTX
NCBI GI	g1922246
BLAST score	386
E value	3.0e-37
Match length	75
% identity	99
NCBI Description	(Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No.	127710
Contig ID	25802_1.R1010
5'-most EST	jC-atXLIB327420P1f07a1
Method	BLASTX
NCBI GI	g4522012
BLAST score	200
E value	1.0e-15
Match length	91
% identity	48
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127711
Contig ID	25802_2.R1010
5'-most EST	jC-atXLIB327408P2e10b1
Method	BLASTX
NCBI GI	g4522007
BLAST score	158

E value	5.0e-12
Match length	71
% identity	58
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	127712
Contig ID	25816_1.R1010
5'-most EST	jC-atXLIB327408P1d02b1
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	9.0e-15
Match length	54
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	127713
Contig ID	25817_2.R1010
5'-most EST	jC-atXLIB327408P2d02b1
Method	BLASTX
NCBI GI	g2982463
BLAST score	580
E value	1.0e-59
Match length	180
% identity	66
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	127714
Contig ID	25817_3.R1010
5'-most EST	g2393655
Method	BLASTN
NCBI GI	g4757412
BLAST score	411
E value	0.0e+00
Match length	521
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK23, complete sequence

Seq. No.	127715
Contig ID	25819_1.R1010
5'-most EST	jC-atXLIB327408P1d01b1
Method	BLASTX
NCBI GI	g2651310
BLAST score	683
E value	5.0e-72
Match length	154
% identity	88
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	127716
Contig ID	25822_1.R1010
5'-most EST	jC-atXLIB327408P2d06b1
Method	BLASTX
NCBI GI	g3924611
BLAST score	179

E value	6.0e-13
Match length	110
% identity	34
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127717
Contig ID	25826_1.R1010
5'-most EST	jC-atXLIB327408P2d07b1

Seq. No.	127718
Contig ID	25829_1.R1010
5'-most EST	jC-atXLIB327408P4d05b1
Method	BLASTX
NCBI GI	g1491710
BLAST score	292
E value	4.0e-26
Match length	114
% identity	54
NCBI Description	(X96506) alpha subunit; forms heterodimer with NC2 alpha/Dr1 [Homo sapiens]

Seq. No.	127719
Contig ID	25833_1.R1010
5'-most EST	LIB25-067-Q1-E1-D6

Seq. No.	127720
Contig ID	25849_1.R1010
5'-most EST	jC-atXLIB327408P4e09b1
Method	BLASTX
NCBI GI	g4220489
BLAST score	489
E value	3.0e-49
Match length	143
% identity	65
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127721
Contig ID	25852_1.R1010
5'-most EST	LIB35-053-Q1-E1-D10
Method	BLASTN
NCBI GI	g4662609
BLAST score	281
E value	1.0e-156
Match length	521
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	127722
Contig ID	25856_1.R1010
5'-most EST	jC-atXP37C156G16T7d2

Seq. No.	127723
Contig ID	25856_2.R1010
5'-most EST	g2047879

Seq. No. 127724

Contig ID	25856_3.R1010
5'-most EST	jC-atXLIB327408P1f03b1
Method	BLASTX
NCBI GI	g4586036
BLAST score	264
E value	9.0e-23
Match length	113
% identity	46
NCBI Description	(AC007109) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127725
Contig ID	25876_1.R1010
5'-most EST	LIB25-007-Q1-E1-E6

Seq. No.	127726
Contig ID	25880_1.R1010
5'-most EST	jC-atXLIB327408P3d10b1
Method	BLASTX
NCBI GI	g4115364
BLAST score	1428
E value	1.0e-159
Match length	276
% identity	100
NCBI Description	(AC005957) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	127727
Contig ID	25910_1.R1010
5'-most EST	jC-atXLIB327408P3f09b1
Method	BLASTX
NCBI GI	g3152587
BLAST score	547
E value	5.0e-60
Match length	243
% identity	55
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	127728
Contig ID	25911_1.R1010
5'-most EST	LIB25-078-Q1-E1-A10

Seq. No.	127729
Contig ID	25921_1.R1010
5'-most EST	jC-atXLIB327408P3g12b1
Method	BLASTN
NCBI GI	g4115912
BLAST score	276
E value	1.0e-153
Match length	492
% identity	89
NCBI Description	Arabidopsis thaliana BAC F3H7

Seq. No.	127730
Contig ID	25926_1.R1010

5'-most EST	g933673
Method	BLASTX
NCBI GI	g2959370
BLAST score	275
E value	8.0e-24
Match length	140
% identity	36
NCBI Description	(AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	127731
Contig ID	25926_2.R1010
5'-most EST	g3449817
Method	BLASTN
NCBI GI	g3510343
BLAST score	242
E value	1.0e-133
Match length	316
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	127732
Contig ID	25927_1.R1010
5'-most EST	g2747627
Method	BLASTN
NCBI GI	g2760165
BLAST score	53
E value	1.0e-20
Match length	247
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	127733
Contig ID	25929_1.R1010
5'-most EST	jC-atXLIB327408P1h07b1
Method	BLASTX
NCBI GI	g3256035
BLAST score	204
E value	1.0e-15
Match length	60
% identity	62
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	127734
Contig ID	25949_1.R1010
5'-most EST	jC-atXLIB327408P4f10b1
Method	BLASTN
NCBI GI	g4519193
BLAST score	208
E value	1.0e-113
Match length	443
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	127735
Contig ID	25951_1.R1010
5'-most EST	jC-atXLIB327408P3f08b1
Method	BLASTX
NCBI GI	g1938424
BLAST score	170
E value	2.0e-21
Match length	129
% identity	43
NCBI Description	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No.	127736
Contig ID	25955_1.R1010
5'-most EST	jC-atXLIB327408P1g06b1
Method	BLASTX
NCBI GI	g4262186
BLAST score	471
E value	4.0e-47
Match length	91
% identity	100
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	127737
Contig ID	25956_1.R1010
5'-most EST	LIB3177-098-P1-K1-C7
Method	BLASTX
NCBI GI	g2832641
BLAST score	346
E value	1.0e-32
Match length	124
% identity	52
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	127738
Contig ID	25956_2.R1010
5'-most EST	jC-atXmonuni26Ad10b1
Method	BLASTX
NCBI GI	g2832641
BLAST score	336
E value	2.0e-31
Match length	112
% identity	55
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	127739
Contig ID	25963_1.R1010
5'-most EST	LIB24-126-Q1-E1-D1
Method	BLASTX
NCBI GI	g4510395
BLAST score	881
E value	4.0e-95
Match length	203
% identity	88

NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	127740
Contig ID	25965_1.R1010
5'-most EST	jC-atXLIB327408P3g11b1
Method	BLASTX
NCBI GI	g1076660
BLAST score	86
E value	2.0e-41
Match length	264
% identity	46
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	127741
Contig ID	25974_1.R1010
5'-most EST	g958237
Method	BLASTX
NCBI GI	g4415930
BLAST score	560
E value	2.0e-57
Match length	132
% identity	80
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	127742
Contig ID	25982_1.R1010
5'-most EST	jC-atXLIB327408P4g11b1
Method	BLASTN
NCBI GI	g3319339
BLAST score	184
E value	7.0e-99
Match length	484
% identity	100
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	127743
Contig ID	25989_1.R1010
5'-most EST	LIB25-013-Q1-E1-G1
Method	BLASTX
NCBI GI	g2274862
BLAST score	680
E value	8.0e-72
Match length	128
% identity	99
NCBI Description	(AJ000497) Starch branching enzyme II [Arabidopsis thaliana] >gi_4581160_gb_AAD24644.1_AC006919_22 (AC006919) starch branching enzyme II [Arabidopsis thaliana]

Seq. No.	127744
Contig ID	26002_1.R1010
5'-most EST	jC-atXLIB327408P4h02b1

Method	BLASTX
NCBI GI	g2911066
BLAST score	583
E value	5.0e-60
Match length	122
% identity	89
NCBI Description	(AL021960) adrenodoxin-like protein [Arabidopsis thaliana]

Seq. No.	127745
Contig ID	26011_1.R1010
5'-most EST	LIB3176-019-P1-K1-G7
Method	BLASTN
NCBI GI	g2264309
BLAST score	384
E value	0.0e+00
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	127746
Contig ID	26013_1.R1010
5'-most EST	jC-atXLIB327420P1b07b1

Seq. No.	127747
Contig ID	26013_2.R1010
5'-most EST	jC-atXLIB327420P1b07a1

Seq. No.	127748
Contig ID	26015_1.R1010
5'-most EST	jC-atXLIB327408P2f12b1
Method	BLASTN
NCBI GI	g4757414
BLAST score	352
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	127749
Contig ID	26021_1.R1010
5'-most EST	jC-atXLIB327408P4f05b1
Method	BLASTX
NCBI GI	g2435519
BLAST score	309
E value	6.0e-28
Match length	205
% identity	60
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	127750
Contig ID	26022_1.R1010
5'-most EST	jC-atXLIB327408P3f05b1
Method	BLASTX

NCBI GI	g1304599
BLAST score	204
E value	1.0e-15
Match length	186
% identity	31
NCBI Description	(U41315) ZNF127-Xp [Homo sapiens]

Seq. No.	127751
Contig ID	26025_1.R1010
5'-most EST	jC-alXLIB327435P2e02a1
Method	BLASTX
NCBI GI	g4586265
BLAST score	295
E value	2.0e-26
Match length	136
% identity	45
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	127752
Contig ID	26030_1.R1010
5'-most EST	jC-atXLIB327408P2g01b1
Method	BLASTN
NCBI GI	g2618599
BLAST score	37
E value	6.0e-11
Match length	223
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	127753
Contig ID	26032_1.R1010
5'-most EST	jC-atXLIB327408P2g02b1
Method	BLASTN
NCBI GI	g2564048
BLAST score	62
E value	4.0e-26
Match length	82
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	127754
Contig ID	26048_1.R1010
5'-most EST	jC-atX25034Q1E1B02b1
Method	BLASTN
NCBI GI	g1707006
BLAST score	348
E value	0.0e+00
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127755
Contig ID	26051_1.R1010
5'-most EST	LIB3176-009-P1-K2-H3

Method	BLASTX
NCBI GI	g3250680
BLAST score	886
E value	8.0e-96
Match length	177
% identity	72
NCBI Description	(AL024486) aspartate kinase-homoserine dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	127756
Contig ID	26058_1.R1010
5'-most EST	jC-atXLIB327408P4g06b1
Method	BLASTX
NCBI GI	g4753653
BLAST score	339
E value	2.0e-31
Match length	131
% identity	49
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	127757
Contig ID	26066_1.R1010
5'-most EST	jC-atXP40C161K8T7089a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	368
E value	0.0e+00
Match length	595
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	127758
Contig ID	26068_1.R1010
5'-most EST	jC-atXLIB327408P2h04b1
Method	BLASTX
NCBI GI	g3738329
BLAST score	660
E value	5.0e-69
Match length	176
% identity	80
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	127759
Contig ID	26069_1.R1010
5'-most EST	jC-atXLIB327408P1h11b1
Method	BLASTX
NCBI GI	g4099090
BLAST score	837
E value	6.0e-90
Match length	186
% identity	87
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	127760
Contig ID	26080_1.R1010
5'-most EST	LIB3175-040-P1-K1-D9

Method	BLASTX
NCBI GI	g3914740
BLAST score	509
E value	2.0e-51
Match length	145
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	127761
Contig ID	26087_1.R1010
5'-most EST	jC-atXLIB327408P3h03b1
Method	BLASTX
NCBI GI	g3913218
BLAST score	463
E value	4.0e-46
Match length	152
% identity	67
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2318117 (AF014399) Mg-chelatase subunit D [Pisum sativum]

Seq. No.	127762
Contig ID	26089_1.R1010
5'-most EST	LIB24-128-Q1-E1-A10
Method	BLASTX
NCBI GI	g3123295
BLAST score	599
E value	4.0e-62
Match length	156
% identity	77
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	127763
Contig ID	26094_1.R1010
5'-most EST	jC-atXLIB327408P4f01b1
Method	BLASTN
NCBI GI	g3128136
BLAST score	280
E value	1.0e-156
Match length	720
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	127764
Contig ID	26106_1.R1010
5'-most EST	jC-atXLIB327423P2h06b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	38
E value	9.0e-12
Match length	42
% identity	98

NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	127765
Contig ID	26107_1.R1010
5'-most EST	jC-atXLIB327408P4f04b1
Method	BLASTN
NCBI GI	g2842474
BLAST score	453
E value	0.0e+00
Match length	477
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)

Seq. No.	127766
Contig ID	26115_1.R1010
5'-most EST	jC-atXLIB327408P1g03b1
Method	BLASTN
NCBI GI	g3426033
BLAST score	468
E value	0.0e+00
Match length	471
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127767
Contig ID	26119_1.R1010
5'-most EST	jC-atXLIB327408P4f12b1
Method	BLASTN
NCBI GI	g3510337
BLAST score	235
E value	1.0e-129
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	127768
Contig ID	26121_1.R1010
5'-most EST	jC-atXLIB327408P2g08b1

Seq. No.	127769
Contig ID	26122_1.R1010
5'-most EST	jC-atXLIB327408P1g10b1
Method	BLASTX
NCBI GI	g1723929
BLAST score	334
E value	6.0e-39
Match length	168
% identity	54
NCBI Description	HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION >gi_2131231_pir__S60416 DNA helicase YGL150c - yeast (Saccharomyces cerevisiae) >gi_1322734_emb_CAA96861_ (Z72672) ORF YGL150c [Saccharomyces cerevisiae]

Seq. No.	127770
Contig ID	26125_1.R1010
5'-most EST	jC-atXLIB327408P1g11b1
Method	BLASTN
NCBI GI	g2275194
BLAST score	457
E value	0.0e+00
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127771
Contig ID	26130_1.R1010
5'-most EST	jC-atXLIB327408P4e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127772
Contig ID	26138_1.R1010
5'-most EST	jC-atXLIB327408P4g05b1
Method	BLASTX
NCBI GI	g2894575
BLAST score	281
E value	1.0e-29
Match length	98
% identity	74
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	127773
Contig ID	26141_1.R1010
5'-most EST	jC-atXLIB327408P1h05b1
Method	BLASTX
NCBI GI	g1171161
BLAST score	675
E value	6.0e-71
Match length	202
% identity	62
NCBI Description	(U41472) pectate lyase homolog [Medicago sativa]

Seq. No.	127774
Contig ID	26143_1.R1010
5'-most EST	jC-atXLIB327408P2h06b1

Seq. No.	127775
Contig ID	26145_1.R1010
5'-most EST	jC-atXLIB327420P4h12b1
Method	BLASTX
NCBI GI	g3687243
BLAST score	260
E value	3.0e-22

Match length	66
% identity	80
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	127776
Contig ID	26146_1.R1010
5'-most EST	jC-atXLIB327408P2h02b1

Seq. No.	127777
Contig ID	26148_1.R1010
5'-most EST	jC-atXLIB327408P1h04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127778
Contig ID	26149_1.R1010
5'-most EST	jC-atXLIB327408P2h08b1
Method	BLASTN
NCBI GI	g4587641
BLAST score	350
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	127779
Contig ID	26155_1.R1010
5'-most EST	jC-atXLIB327408P1h09b1
Method	BLASTX
NCBI GI	g2970034
BLAST score	455
E value	3.0e-45
Match length	127
% identity	61
NCBI Description	(D88536) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	127780
Contig ID	26159_1.R1010
5'-most EST	jC-atXLIB327408P4h05b1
Method	BLASTX
NCBI GI	g4538903
BLAST score	566
E value	3.0e-58
Match length	155
% identity	80
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	127781
Contig ID	26161_1.R1010

5'-most EST	jC-atXLIB327408P3h05b1
Method	BLASTX
NCBI GI	g4585993
BLAST score	272
E value	8.0e-69
Match length	160
% identity	85
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	127782
Contig ID	26165_1.R1010
5'-most EST	jC-atXLIB327408P4h12b1
Method	BLASTX
NCBI GI	g3152566
BLAST score	662
E value	1.0e-69
Match length	141
% identity	94
NCBI Description	(AC002986) Similar to hypothetical protein YLR002c, gb_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No.	127783
Contig ID	26167_1.R1010
5'-most EST	jC-atXLIB327409P2a06b1
Method	BLASTN
NCBI GI	g2351066
BLAST score	388
E value	0.0e+00
Match length	566
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	127784
Contig ID	26178_1.R1010
5'-most EST	jC-atX24130Q1E1D04b1
Method	BLASTX
NCBI GI	g3912919
BLAST score	705
E value	1.0e-74
Match length	150
% identity	95
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127785
Contig ID	26187_1.R1010
5'-most EST	jC-atXLIB327409P4a08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127786
Contig ID	26193_1.R1010
5'-most EST	LIB24-129-Q1-E1-F8
Method	BLASTN
NCBI GI	g2564047
BLAST score	117
E value	4.0e-59
Match length	352
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	127787
Contig ID	26199_1.R1010
5'-most EST	jC-atXLIB327409P2b09b1
Method	BLASTX
NCBI GI	g2497540
BLAST score	732
E value	2.0e-77
Match length	182
% identity	76
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No.	127788
Contig ID	26203_1.R1010
5'-most EST	jC-atXLIB327409P4b01b1
Method	BLASTN
NCBI GI	g2815404
BLAST score	336
E value	0.0e+00
Match length	371
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	127789
Contig ID	26204_1.R1010
5'-most EST	jC-atXLIB327420P4b10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127790
Contig ID	26205_1.R1010
5'-most EST	jC-atXLIB327409P2b12b1
Method	BLASTN
NCBI GI	g3212846
BLAST score	195
E value	1.0e-105
Match length	435
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127791
Contig ID	26217_1.R1010
5'-most EST	jC-atXLIB327422P3h05b2
Method	BLASTX
NCBI GI	g3983663
BLAST score	419
E value	6.0e-41
Match length	139
% identity	60
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]

Seq. No.	127792
Contig ID	26232_1.R1010
5'-most EST	LIB3168-044-P1-K1-E5
Method	BLASTX
NCBI GI	g3096928
BLAST score	361
E value	9.0e-34
Match length	140
% identity	55
NCBI Description	(AL023094) bZIP transcription factor ATB2 [Arabidopsis thaliana]

Seq. No.	127793
Contig ID	26232_2.R1010
5'-most EST	jC-atXLIB327409P2a11b1

Seq. No.	127794
Contig ID	26233_1.R1010
5'-most EST	g1053959
Method	BLASTX
NCBI GI	g1890319
BLAST score	977
E value	1.0e-106
Match length	203
% identity	93
NCBI Description	(Y11792) peroxidase ATP27a [Arabidopsis thaliana]

Seq. No.	127795
Contig ID	26242_1.R1010
5'-most EST	jC-atXP98CH7B6T7b1
Method	BLASTX
NCBI GI	g728905
BLAST score	197
E value	4.0e-16
Match length	142
% identity	35
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi_171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi_595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]

Seq. No.	127796
Contig ID	26257_1.R1010
5'-most EST	LIB24-130-Q1-E1-F6
Method	BLASTX
NCBI GI	g2262107
BLAST score	787
E value	2.0e-84
Match length	149
% identity	97
NCBI Description	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	127797
Contig ID	26261_1.R1010
5'-most EST	jC-atXLIB327409P1b08b1
Method	BLASTX
NCBI GI	g1947137
BLAST score	313
E value	2.0e-28
Match length	204
% identity	34
NCBI Description	(AF000264) similar to the ATP-binding transport protein family (ABC transporters). [Caenorhabditis elegans]

Seq. No.	127798
Contig ID	26263_1.R1010
5'-most EST	LIB3176-027-P1-K1-B10
Method	BLASTN
NCBI GI	g4589408
BLAST score	166
E value	7.0e-88
Match length	662
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F14A1, complete sequence

Seq. No.	127799
Contig ID	26273_1.R1010
5'-most EST	jC-atXLIB327408P4h10b1
Method	BLASTN
NCBI GI	g3643588
BLAST score	123
E value	2.0e-62
Match length	475
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127800
Contig ID	26273_2.R1010
5'-most EST	jC-atXLIB327438P3e11a2
Method	BLASTX
NCBI GI	g131237
BLAST score	705
E value	1.0e-104
Match length	208
% identity	86

NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_72656_pir__FMMH32 photosystem II protein D1 precursor - green amaranth chloroplast

Seq. No.	127801
Contig ID	26279_1.R1010
5'-most EST	jC-atXLIB327408P4h09b1
Method	BLASTX
NCBI GI	g2982583
BLAST score	682
E value	7.0e-72
Match length	140
% identity	89
NCBI Description	(AJ003135) polygalacturonase [Arabidopsis thaliana] >gi_3152948_emb_CAA06610_ (AJ005584) polygalacturonase [Arabidopsis thaliana]

Seq. No.	127802
Contig ID	26286_1.R1010
5'-most EST	jC-atXLIB327409P1a06b1
Method	BLASTX
NCBI GI	g2827709
BLAST score	282
E value	5.0e-47
Match length	126
% identity	89
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	127803
Contig ID	26299_1.R1010
5'-most EST	jC-atXLIB327409P4a02b1
Method	BLASTX
NCBI GI	g4467144
BLAST score	665
E value	1.0e-69
Match length	150
% identity	87
NCBI Description	(AL035540) putative phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	127804
Contig ID	26316_1.R1010
5'-most EST	jC-atXLIB327409P4a12b1
Method	BLASTX
NCBI GI	g1495804
BLAST score	383
E value	7.0e-37
Match length	142
% identity	54
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	127805
Contig ID	26317_1.R1010
5'-most EST	jC-atXLIB327409P3a12b1

Seq. No.	127806

Contig ID	26322_1.R1010
5'-most EST	jC-atXLIB327409P1b02b1
Method	BLASTN
NCBI GI	g3128138
BLAST score	318
E value	1.0e-178
Match length	720
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	127807
Contig ID	26322_2.R1010
5'-most EST	jC-atXLIB327423P3b07a1
Method	BLASTN
NCBI GI	g3128138
BLAST score	368
E value	0.0e+00
Match length	442
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	127808
Contig ID	26335_1.R1010
5'-most EST	jC-atXLIB327409P2b05b1
Method	BLASTN
NCBI GI	g4468976
BLAST score	399
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	127809
Contig ID	26335_2.R1010
5'-most EST	jC-atXLIB327430P1e08b1
Method	BLASTN
NCBI GI	g4468976
BLAST score	407
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	127810
Contig ID	26339_1.R1010
5'-most EST	jC-atXLIB327409P2b11b1
Method	BLASTX
NCBI GI	g3646450
BLAST score	438
E value	5.0e-43
Match length	237
% identity	38
NCBI Description	(AL031603) conserved hypothetical protein.

[Schizosaccharomyces pombe]

Seq. No.	127811
Contig ID	26342_1.R1010
5'-most EST	jC-atXLIB327409P1b10b1
Method	BLASTX
NCBI GI	g4210449
BLAST score	183
E value	4.0e-13
Match length	68
% identity	54
NCBI Description	(AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No.	127812
Contig ID	26344_1.R1010
5'-most EST	LIB3175-037-P1-K1-F1
Method	BLASTN
NCBI GI	g3420042
BLAST score	139
E value	7.0e-72
Match length	665
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127813
Contig ID	26345_1.R1010
5'-most EST	jC-atXLIB327408P3h10b1
Method	BLASTX
NCBI GI	g2463509
BLAST score	611
E value	3.0e-63
Match length	160
% identity	68
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	127814
Contig ID	26348_1.R1010
5'-most EST	jC-atXLIB327408P4h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127815
Contig ID	26351_1.R1010
5'-most EST	jC-atXLIB327408P3h08b1
Method	BLASTX
NCBI GI	g2129805
BLAST score	284
E value	3.0e-25
Match length	59
% identity	95

NCBI Description	pollen allergen group II (clone 4) - turnip (fragment)
Seq. No.	127816
Contig ID	26352_1.R1010
5'-most EST	jC-atXLIB327409P2a01b1
Method	BLASTX
NCBI GI	g473949
BLAST score	203
E value	1.0e-15
Match length	88
% identity	45
NCBI Description	(D29958) KIAA0116 [Homo sapiens]
Seq. No.	127817
Contig ID	26353_1.R1010
5'-most EST	jC-atXLIB327409P2a03b1
Method	BLASTX
NCBI GI	g2245011
BLAST score	256
E value	5.0e-22
Match length	109
% identity	12
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	127818
Contig ID	26354_1.R1010
5'-most EST	jC-atXLIB327409P1a04b1
Method	BLASTX
NCBI GI	g11837
BLAST score	732
E value	2.0e-99
Match length	228
% identity	81
NCBI Description	(Z00044) NADH dehydrogenase 27kD subunit [Nicotiana tabacum] >gi_225205_prf__1211235AK bhpB gene [Nicotiana tabacum]
Seq. No.	127819
Contig ID	26368_1.R1010
5'-most EST	jC-atXLIB327409P1a10b1
Method	BLASTX
NCBI GI	g818849
BLAST score	275
E value	2.0e-24
Match length	106
% identity	59
NCBI Description	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]
Seq. No.	127820
Contig ID	26374_1.R1010
5'-most EST	jC-atXLIB327409P3a02b1
Seq. No.	127821
Contig ID	26374_2.R1010
5'-most EST	g3450084
Method	BLASTN

NCBI GI	g531828
BLAST score	50
E value	7.0e-19
Match length	50
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	127822
Contig ID	26377_1.R1010
5'-most EST	jC-atX24132Q1E1D08b1
Method	BLASTX
NCBI GI	g3183217
BLAST score	275
E value	6.0e-24
Match length	159
% identity	43
NCBI Description	HYPOTHETICAL PROTEIN KIAA0103 >gi_285943_dbj_BAA03493_ (D14659) KIAA0103 [Homo sapiens]

Seq. No.	127823
Contig ID	26383_1.R1010
5'-most EST	jC-atXLIB327409P3a06b1
Method	BLASTN
NCBI GI	g2656031
BLAST score	211
E value	1.0e-115
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	127824
Contig ID	26384_1.R1010
5'-most EST	jC-atXLIB327409P3a07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127825
Contig ID	26391_1.R1010
5'-most EST	jC-atXLIB327409P1b01b1
Method	BLASTX
NCBI GI	g1885356
BLAST score	805
E value	5.0e-86
Match length	224
% identity	69
NCBI Description	(U59323) type 1 RNA helicase pNORF1 [Homo sapiens]

Seq. No.	127826
Contig ID	26392_2.R1010
5'-most EST	LIB3175-044-P1-K1-B7

Method	BLASTX
NCBI GI	g3892712
BLAST score	344
E value	3.0e-32
Match length	67
% identity	100
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	127827
Contig ID	26392_3.R1010
5'-most EST	LIB25-003-Q1-E1-B4
Method	BLASTX
NCBI GI	g3892712
BLAST score	936
E value	1.0e-101
Match length	182
% identity	100
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	127828
Contig ID	26404_1.R1010
5'-most EST	jC-atXLIB327409P2b10b1
Method	BLASTX
NCBI GI	g4506233
BLAST score	317
E value	9.0e-29
Match length	207
% identity	36
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 >gi_1346766_sp_P48556_PSD8_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi_1362741_pir__S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi_3702282 (AC005789) PP31_HUMAN [Homo sapiens]

Seq. No.	127829
Contig ID	26404_2.R1010
5'-most EST	g2445856
Method	BLASTN
NCBI GI	g3510343
BLAST score	83
E value	1.0e-38
Match length	295
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	127830
Contig ID	26407_1.R1010
5'-most EST	jC-atXLIB327430P1f10b1
Method	BLASTX
NCBI GI	g3142300
BLAST score	378
E value	5.0e-36

Match length	153
% identity	50
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	127831
Contig ID	26412_1.R1010
5'-most EST	jC-atXLIB327409P3b09b1
Method	BLASTN
NCBI GI	g4587986
BLAST score	424
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	127832
Contig ID	26413_1.R1010
5'-most EST	jC-atXLIB327420P4a09a1
Method	BLASTN
NCBI GI	g4757407
BLAST score	69
E value	3.0e-30
Match length	350
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	127833
Contig ID	26416_1.R1010
5'-most EST	jC-atXP43C168F4T7066d1

Seq. No.	127834
Contig ID	26416_2.R1010
5'-most EST	jC-atXmonuni27Ab08b1

Seq. No.	127835
Contig ID	26422_1.R1010
5'-most EST	jC-atXLIB327409P1c05b1
Method	BLASTN
NCBI GI	g4587582
BLAST score	143
E value	2.0e-74
Match length	448
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	127836
Contig ID	26424_1.R1010
5'-most EST	jC-atXLIB327409P1c03b1
Method	BLASTX
NCBI GI	g4432860
BLAST score	439

E value	3.0e-44
Match length	244
% identity	19
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	127837
Contig ID	26424_3.R1010
5'-most EST	jC-atXmonuni27Bd01b1
Method	BLASTN
NCBI GI	g4063735
BLAST score	425
E value	0.0e+00
Match length	527
% identity	98
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	127838
Contig ID	26424_4.R1010
5'-most EST	g937831
Method	BLASTX
NCBI GI	g4432860
BLAST score	326
E value	2.0e-35
Match length	169
% identity	22
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	127839
Contig ID	26426_1.R1010
5'-most EST	jC-atXLIB327409P2c03b1

Seq. No.	127840
Contig ID	26430_1.R1010
5'-most EST	jC-atXLIB327409P2c12b1
Method	BLASTN
NCBI GI	g4757662
BLAST score	82
E value	5.0e-38
Match length	86
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	127841
Contig ID	26438_1.R1010
5'-most EST	jC-atXLIB327437P4a07b2
Method	BLASTX
NCBI GI	g2494275
BLAST score	257
E value	4.0e-22
Match length	75
% identity	63
NCBI Description	ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation factor P [Synechococcus PCC7942]

Seq. No.	127842
Contig ID	26439_1.R1010
5'-most EST	jC-atXP83CG3F4T7015a1
Method	BLASTN
NCBI GI	g2505873
BLAST score	177
E value	1.0e-94
Match length	476
% identity	97
NCBI Description	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No.	127843
Contig ID	26442_1.R1010
5'-most EST	jC-atXLIB327409P4c08b1
Method	BLASTX
NCBI GI	g99713
BLAST score	659
E value	3.0e-69
Match length	141
% identity	94
NCBI Description	homeotic protein agamous - Arabidopsis thaliana >gi_1345505_emb_CAA37642_ (X53579) agamous gene product (AA 1-285) [Arabidopsis thaliana] >gi_226968_prf__1612343A agamous gene [Arabidopsis sp.]

Seq. No.	127844
Contig ID	26446_1.R1010
5'-most EST	jC-atXLIB327409P3c02b1
Method	BLASTX
NCBI GI	g3046703
BLAST score	675
E value	5.0e-71
Match length	135
% identity	97
NCBI Description	(AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

Seq. No.	127845
Contig ID	26461_1.R1010
5'-most EST	jC-atXLIB327409P2d02b1
Method	BLASTX
NCBI GI	g4490706
BLAST score	413
E value	3.0e-40
Match length	103
% identity	74
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	127846
Contig ID	26473_1.R1010
5'-most EST	jC-atXLIB327409P4d11b1
Method	BLASTX
NCBI GI	g4220476
BLAST score	707
E value	1.0e-74
Match length	138

% identity	100
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	127847
Contig ID	26474_1.R1010
5'-most EST	jC-atXLIB327409P4d12b1
Method	BLASTX
NCBI GI	g228456
BLAST score	521
E value	5.0e-53
Match length	117
% identity	87
NCBI Description	Gln synthetase [Arabidopsis thaliana]

Seq. No.	127848
Contig ID	26476_1.R1010
5'-most EST	jC-atXLIB327409P2e01b1
Method	BLASTN
NCBI GI	g2924651
BLAST score	988
E value	0.0e+00
Match length	988
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	127849
Contig ID	26476_3.R1010
5'-most EST	g1217332
Method	BLASTN
NCBI GI	g2924651
BLAST score	255
E value	1.0e-141
Match length	283
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	127850
Contig ID	26480_1.R1010
5'-most EST	jC-atXP112C130C24T7d2
Method	BLASTX
NCBI GI	g3913410
BLAST score	279
E value	1.0e-169
Match length	338
% identity	89
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2) (SAMDC 2) >gi_2662406 (U80916) S-adenosyl-L-methionine decarboxylase [Brassica juncea]

Seq. No.	127851
Contig ID	26488_1.R1010
5'-most EST	jC-atXLIB327409P1e10b1
Method	BLASTN
NCBI GI	g3980374
BLAST score	114

E value	7.0e-57
Match length	436
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127852
Contig ID	26488_4.R1010
5'-most EST	g2759807
Method	BLASTX
NCBI GI	g3980378
BLAST score	429
E value	1.0e-44
Match length	130
% identity	76
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	127853
Contig ID	26490_1.R1010
5'-most EST	jC-atXLIB327409P2e11b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	5.0e-10
Match length	35
% identity	60
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	127854
Contig ID	26493_1.R1010
5'-most EST	jC-atXLIB327409P2e07b1
Method	BLASTX
NCBI GI	g4115939
BLAST score	746
E value	4.0e-79
Match length	135
% identity	51
NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	127855
Contig ID	26494_1.R1010
5'-most EST	jC-atXP85C241D8T7b1
Method	BLASTN
NCBI GI	g4220643
BLAST score	306
E value	1.0e-171
Match length	649
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	127856
Contig ID	26495_1.R1010
5'-most EST	jC-atXLIB327409P4b08b1

Method	BLASTX
NCBI GI	g3377843
BLAST score	550
E value	2.0e-56
Match length	135
% identity	81
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	127857
Contig ID	26498_1.R1010
5'-most EST	jC-atXLIB327409P4b09b1
Method	BLASTN
NCBI GI	g3702736
BLAST score	127
E value	6.0e-65
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	127858
Contig ID	26502_1.R1010
5'-most EST	LIB24-134-Q1-E1-A6
Method	BLASTX
NCBI GI	g1935914
BLAST score	46
E value	7.0e-10
Match length	70
% identity	51
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	127859
Contig ID	26505_1.R1010
5'-most EST	jC-atX24134Q1E1A09b1
Method	BLASTN
NCBI GI	g4586241
BLAST score	345
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	127860
Contig ID	26515_1.R1010
5'-most EST	jC-atXLIB327409P1c12b1
Method	BLASTX
NCBI GI	g2809238
BLAST score	456
E value	4.0e-83
Match length	180
% identity	89
NCBI Description	(AC002560) F21B7.7 [Arabidopsis thaliana]

Seq. No.	127861
Contig ID	26526_1.R1010

5'-most EST	LIB24-134-Q1-E1-D11
Seq. No.	127862
Contig ID	26532_1.R1010
5'-most EST	jC-atXLIB327409P4c03b1
Method	BLASTX
NCBI GI	g2911073
BLAST score	442
E value	8.0e-44
Match length	144
% identity	58
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]
Seq. No.	127863
Contig ID	26534_1.R1010
5'-most EST	jC-atXLIB327409P3c04b1
Method	BLASTN
NCBI GI	g2191157
BLAST score	258
E value	1.0e-143
Match length	434
% identity	95
NCBI Description	Arabidopsis thaliana BAC IG002P16
Seq. No.	127864
Contig ID	26540_1.R1010
5'-most EST	jC-atXLIB327409P2d05b1
Method	BLASTX
NCBI GI	g2262111
BLAST score	432
E value	2.0e-42
Match length	107
% identity	85
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]
Seq. No.	127865
Contig ID	26541_1.R1010
5'-most EST	jC-atXLIB327409P1d06b1
Method	BLASTN
NCBI GI	g2618599
BLAST score	394
E value	0.0e+00
Match length	650
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.	127866
Contig ID	26543_1.R1010
5'-most EST	jC-atXLIB327409P2d01b1
Method	BLASTN
NCBI GI	g4589436
BLAST score	236
E value	1.0e-130
Match length	484
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence
Seq. No.	127867
Contig ID	26548_1.R1010
5'-most EST	jC-atXLIB327409P3d02b1
Seq. No.	127868
Contig ID	26552_1.R1010
5'-most EST	jC-atXLIB327409P3d04b1
Method	BLASTN
NCBI GI	g4680765
BLAST score	451
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence
Seq. No.	127869
Contig ID	26552_2.R1010
5'-most EST	jC-atXLIB327402P4e06b1
Method	BLASTN
NCBI GI	g4680765
BLAST score	131
E value	2.0e-67
Match length	312
% identity	95
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence
Seq. No.	127870
Contig ID	26554_1.R1010
5'-most EST	jC-atXLIB327409P3d01b1
Method	BLASTN
NCBI GI	g2351071
BLAST score	310
E value	1.0e-174
Match length	334
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]
Seq. No.	127871
Contig ID	26556_1.R1010
5'-most EST	jC-atXLIB327409P4d02b1
Seq. No.	127872
Contig ID	26559_1.R1010
5'-most EST	g3868955
Method	BLASTX
NCBI GI	g4539313
BLAST score	350
E value	3.0e-52
Match length	106
% identity	99
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	127873
Contig ID	26564_1.R1010
5'-most EST	g934134
Method	BLASTN
NCBI GI	g4006885
BLAST score	436
E value	0.0e+00
Match length	531
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	127874
Contig ID	26567_1.R1010
5'-most EST	g2759417
Method	BLASTN
NCBI GI	g4757401
BLAST score	315
E value	1.0e-177
Match length	494
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	127875
Contig ID	26574_1.R1010
5'-most EST	jC-atXLIB327409P1e11b1
Method	BLASTN
NCBI GI	g4519195
BLAST score	336
E value	0.0e+00
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	127876
Contig ID	26576_1.R1010
5'-most EST	jC-atXLIB327409P1e07b1
Method	BLASTX
NCBI GI	g3980384
BLAST score	253
E value	4.0e-32
Match length	128
% identity	58
NCBI Description	(AC004561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127877
Contig ID	26578_1.R1010
5'-most EST	jC-atXLIB327409P1e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	4.0e-21
Match length	73
% identity	96

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127878
Contig ID	26580_1.R1010
5'-most EST	jC-atXLIB327409P4b04b1
Method	BLASTX
NCBI GI	g2654559
BLAST score	200
E value	2.0e-15
Match length	101
% identity	42
NCBI Description	(AF006621) embryonic lung protein [Homo sapiens]

Seq. No.	127879
Contig ID	26581_1.R1010
5'-most EST	jC-atXLIB327409P3b04b1

Seq. No.	127880
Contig ID	26582_1.R1010
5'-most EST	jC-atXLIB327409P4b05b1
Method	BLASTX
NCBI GI	g4538979
BLAST score	291
E value	4.0e-26
Match length	125
% identity	56
NCBI Description	(AL049487) putative protein [Arabidopsis thaliana]

Seq. No.	127881
Contig ID	26582_2.R1010
5'-most EST	LIB3177-077-P1-K1-H8
Method	BLASTX
NCBI GI	g4538979
BLAST score	220
E value	8.0e-18
Match length	98
% identity	58
NCBI Description	(AL049487) putative protein [Arabidopsis thaliana]

Seq. No.	127882
Contig ID	26585_1.R1010
5'-most EST	jC-atXLIB327409P3b05b1
Method	BLASTN
NCBI GI	g4455290
BLAST score	233
E value	1.0e-128
Match length	747
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	127883
Contig ID	26592_1.R1010
5'-most EST	jC-atXLIB327409P3b12b1

Seq. No.	127884

Contig ID	26598_1.R1010
5'-most EST	jC-atXLIB327409P3b10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127885
Contig ID	26600_1.R1010
5'-most EST	jC-atX35033Q1E1D11b1
Method	BLASTN
NCBI GI	g4455262
BLAST score	153
E value	2.0e-80
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	127886
Contig ID	26605_1.R1010
5'-most EST	jC-atXLIB327409P1c09b1
Method	BLASTX
NCBI GI	g2832629
BLAST score	543
E value	3.0e-55
Match length	233
% identity	46
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	127887
Contig ID	26610_1.R1010
5'-most EST	jC-atXLIB327409P1c06b1
Method	BLASTX
NCBI GI	g4220469
BLAST score	834
E value	2.0e-89
Match length	174
% identity	91
NCBI Description	(AC006069) putative receptor protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No.	127888
Contig ID	26612_1.R1010
5'-most EST	jC-atXLIB327409P1c07b1
Method	BLASTN
NCBI GI	g2760168
BLAST score	34
E value	3.0e-09
Match length	42
% identity	48
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	127889
Contig ID	26618_1.R1010
5'-most EST	LIB3175-006-P1-K1-A9
Method	BLASTN
NCBI GI	g4589412
BLAST score	33
E value	4.0e-09
Match length	61
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	127890
Contig ID	26627_1.R1010
5'-most EST	jC-atXLIB327409P4c12b1
Method	BLASTN
NCBI GI	g3128135
BLAST score	424
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	127891
Contig ID	26630_1.R1010
5'-most EST	jC-atXLIB327409P4c09b1
Method	BLASTX
NCBI GI	g1212923
BLAST score	266
E value	4.0e-23
Match length	121
% identity	23
NCBI Description	(X95951) aquaporin [Helianthus annuus]

Seq. No.	127892
Contig ID	26637_1.R1010
5'-most EST	jC-atXLIB327409P2d10b1
Method	BLASTX
NCBI GI	g4417296
BLAST score	249
E value	4.0e-21
Match length	83
% identity	59
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana] >gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	127893
Contig ID	26639_1.R1010
5'-most EST	jC-atXLIB327418P4d02b1
Method	BLASTX
NCBI GI	g4741929
BLAST score	543
E value	2.0e-55

Match length	151
% identity	67
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	127894
Contig ID	26639_3.R1010
5'-most EST	LIB3175-070-P1-K-H5
Method	BLASTX
NCBI GI	g2244806
BLAST score	198
E value	5.0e-15
Match length	119
% identity	42
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127895
Contig ID	26639_4.R1010
5'-most EST	LIB3176-008-P1-K1-D8
Method	BLASTX
NCBI GI	g2244806
BLAST score	374
E value	1.0e-35
Match length	221
% identity	38
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127896
Contig ID	26643_1.R1010
5'-most EST	jC-atXLIB327409P1d08b1
Method	BLASTX
NCBI GI	g4725942
BLAST score	888
E value	1.0e-147
Match length	289
% identity	92
NCBI Description	(AL049730) putative trehalose-6-phosphate phosphatase (AtTPPA) [Arabidopsis thaliana]

Seq. No.	127897
Contig ID	26644_1.R1010
5'-most EST	jC-atXLIB327409P4d09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127898
Contig ID	26646_1.R1010
5'-most EST	jC-atXLIB327409P3d07b1
Method	BLASTN
NCBI GI	g4519194
BLAST score	189

E value	1.0e-102
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	127899
Contig ID	26651_1.R1010
5'-most EST	jC-atXLIB327409P3d10b1
Method	BLASTX
NCBI GI	g4688596
BLAST score	601
E value	2.0e-62
Match length	144
% identity	55
NCBI Description	(AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase [Arabidopsis thaliana]

Seq. No.	127900
Contig ID	26657_1.R1010
5'-most EST	jC-atXLIB327409P1e05b1
Method	BLASTN
NCBI GI	g3046847
BLAST score	262
E value	1.0e-145
Match length	509
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	127901
Contig ID	26669_1.R1010
5'-most EST	jC-atXLIB327420P3f06b1
Method	BLASTN
NCBI GI	g3980374
BLAST score	74
E value	3.0e-33
Match length	146
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127902
Contig ID	26676_1.R1010
5'-most EST	jC-atXLIB327409P4b03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	73
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127903
Contig ID	26677_1.R1010
5'-most EST	jC-atXLIB327409P4b12b1

Method	BLASTN
NCBI GI	g2828186
BLAST score	97
E value	7.0e-47
Match length	221
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	127904
Contig ID	26683_1.R1010
5'-most EST	jC-atXLIB327409P4b11b1
Method	BLASTN
NCBI GI	g2660661
BLAST score	360
E value	0.0e+00
Match length	580
% identity	99
NCBI Description	Arabidopsis thaliana chromosome V BAC T19K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127905
Contig ID	26684_1.R1010
5'-most EST	jC-atXLIB327409P3b11b1
Method	BLASTX
NCBI GI	g3550080
BLAST score	163
E value	6.0e-11
Match length	80
% identity	34
NCBI Description	(AF071185) formin binding protein 21 [Homo sapiens]

Seq. No.	127906
Contig ID	26686_1.R1010
5'-most EST	jC-atXLIB327409P2c05b1
Method	BLASTN
NCBI GI	g4713943
BLAST score	432
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	127907
Contig ID	26687_1.R1010
5'-most EST	LIB24-136-Q1-E1-C10

Seq. No.	127908
Contig ID	26688_1.R1010
5'-most EST	LIB24-136-Q1-E1-C11
Method	BLASTX
NCBI GI	g2130442
BLAST score	284
E value	3.0e-25
Match length	161
% identity	39

NCBI Description	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment) >gi_1052534_emb_CAA91511_ (Z66569) unknown [Schizosaccharomyces pombe]
Seq. No.	127909
Contig ID	26689_1.R1010
5'-most EST	jC-atXLIB327409P2c09b1
Method	BLASTX
NCBI GI	g2160173
BLAST score	167
E value	2.0e-11
Match length	144
% identity	4
NCBI Description	(AC000132) Similar to N. tabacum salt-inducible protein (gb_U08285). [Arabidopsis thaliana]
Seq. No.	127910
Contig ID	26692_1.R1010
5'-most EST	jC-alXLIB327435P2b10b1
Method	BLASTN
NCBI GI	g3985934
BLAST score	409
E value	0.0e+00
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.	127911
Contig ID	26694_1.R1010
5'-most EST	jC-atXLIB327409P2c07b1
Method	BLASTX
NCBI GI	g3335342
BLAST score	362
E value	2.0e-34
Match length	134
% identity	52
NCBI Description	(AC004512) Similar to gb_Y08239 MADS domain transcription factor (CRM3) from Ceratopteris richardii. [Arabidopsis thaliana]
Seq. No.	127912
Contig ID	26701_1.R1010
5'-most EST	jC-atXLIB327426P3b02b1
Method	BLASTX
NCBI GI	g2842480
BLAST score	331
E value	1.0e-30
Match length	102
% identity	60
NCBI Description	(AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]
Seq. No.	127913
Contig ID	26710_1.R1010
5'-most EST	jC-atXLIB327409P3c12b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	3.0e-30
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	127914
Contig ID	26714_1.R1010
5'-most EST	jC-atXLIB327409P4c10b1
Method	BLASTX
NCBI GI	g4469009
BLAST score	545
E value	6.0e-59
Match length	145
% identity	88
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	127915
Contig ID	26715_1.R1010
5'-most EST	jC-atXLIB327409P1d07b1
Method	BLASTN
NCBI GI	g2288979
BLAST score	429
E value	0.0e+00
Match length	540
% identity	75
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127916
Contig ID	26717_1.R1010
5'-most EST	LIB3176-097-P1-K1-C10
Method	BLASTX
NCBI GI	g3334177
BLAST score	198
E value	4.0e-15
Match length	68
% identity	60
NCBI Description	GTP-BINDING PROTEIN ERA HOMOLOG >gi_1001399_dbj_BAA10021_ (D63999) GTP-binding protein Era [Synechocystis sp.]

Seq. No.	127917
Contig ID	26721_1.R1010
5'-most EST	jC-atXLIB327409P2d11b1

Seq. No.	127918
Contig ID	26726_1.R1010
5'-most EST	jC-atXLIB327409P2d08b1
Method	BLASTX
NCBI GI	g3355467
BLAST score	271
E value	1.0e-23
Match length	165
% identity	39

NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 127919
Contig ID 26727_1.R1010
5'-most EST LIB24-136-Q1-E1-G1

Seq. No. 127920
Contig ID 26733_1.R1010
5'-most EST jC-atXLIB327409P4d10b1
Method BLASTX
NCBI GI g3334276
BLAST score 637
E value 2.0e-66
Match length 209
% identity 58
NCBI Description AUTOANTIGEN NGP-1 >gi_179285 (L05425) autoantigen [Homo sapiens]

Seq. No. 127921
Contig ID 26735_1.R1010
5'-most EST jC-atXLIB327409P3d05b1
Method BLASTN
NCBI GI g2582640
BLAST score 67
E value 4.0e-29
Match length 74
% identity 99
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 127922
Contig ID 26736_1.R1010
5'-most EST jC-atXLIB327409P4d06b1
Method BLASTN
NCBI GI g2582640
BLAST score 67
E value 5.0e-29
Match length 74
% identity 99
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 127923
Contig ID 26741_1.R1010
5'-most EST LIB24-136-Q1-E1-H12
Method BLASTN
NCBI GI g2828180
BLAST score 132
E value 8.0e-68
Match length 489
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDK4, complete sequence [Arabidopsis thaliana]

Seq. No. 127924
Contig ID 26744_1.R1010
5'-most EST jC-atXLIB327409P2e05b1

Method	BLASTN
NCBI GI	g2618602
BLAST score	424
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	127925
Contig ID	26747_1.R1010
5'-most EST	LIB25-050-Q1-E1-A11
Method	BLASTX
NCBI GI	g2795805
BLAST score	1297
E value	1.0e-143
Match length	359
% identity	73
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	127926
Contig ID	26751_1.R1010
5'-most EST	jC-alXLIB327435P2e04a1
Method	BLASTN
NCBI GI	g2564050
BLAST score	317
E value	1.0e-178
Match length	840
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	127927
Contig ID	26752_1.R1010
5'-most EST	LIB25-116-Q1-E1-A12

Seq. No.	127928
Contig ID	26753_1.R1010
5'-most EST	jC-atXLIB327409P1e12b1
Method	BLASTX
NCBI GI	g2829887
BLAST score	707
E value	1.0e-123
Match length	377
% identity	63
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	127929
Contig ID	26767_1.R1010
5'-most EST	g906925
Method	BLASTX
NCBI GI	g4678332
BLAST score	610
E value	2.0e-63
Match length	184

% identity	71
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	127930
Contig ID	26769_1.R1010
5'-most EST	jC-atXP115C249L17T7014d1
Method	BLASTN
NCBI GI	g4220632
BLAST score	199
E value	1.0e-107
Match length	690
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	127931
Contig ID	26782_1.R1010
5'-most EST	LIB24-137-Q1-E1-F8
Method	BLASTN
NCBI GI	g4757414
BLAST score	248
E value	1.0e-137
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	127932
Contig ID	26784_1.R1010
5'-most EST	jC-atXLIB327409P3e07b1
Method	BLASTN
NCBI GI	g3868723
BLAST score	259
E value	1.0e-143
Match length	938
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	127933
Contig ID	26790_1.R1010
5'-most EST	jC-atXLIB327409P4e07b1
Method	BLASTN
NCBI GI	g4469002
BLAST score	422
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone. T29A15 (ESSA project)

Seq. No.	127934
Contig ID	26801_1.R1010
5'-most EST	LIB25-001-Q1-E1-A10
Method	BLASTX
NCBI GI	g3337349

BLAST score	300
E value	3.0e-27
Match length	103
% identity	62
NCBI Description	(AC004481) putative protein kinase [Arabidopsis thaliana]

Seq. No.	127935
Contig ID	26804_1.R1010
5'-most EST	LIB25-001-Q1-E1-A9
Method	BLASTX
NCBI GI	g3033388
BLAST score	188
E value	9.0e-14
Match length	111
% identity	36
NCBI Description	(AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127936
Contig ID	26805_1.R1010
5'-most EST	LIB25-001-Q1-E1-B10
Method	BLASTN
NCBI GI	g3522932
BLAST score	155
E value	1.0e-81
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127937
Contig ID	26809_1.R1010
5'-most EST	jC-atX25001Q1E1C11b1
Method	BLASTX
NCBI GI	g4559333
BLAST score	303
E value	2.0e-27
Match length	159
% identity	31
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	127938
Contig ID	26811_1.R1010
5'-most EST	LIB25-001-Q1-E1-C9
Method	BLASTX
NCBI GI	g4454038
BLAST score	498
E value	1.0e-50
Match length	118
% identity	81
NCBI Description	(AL035394) putative disease resistance response protein [Arabidopsis thaliana]

Seq. No.	127939
Contig ID	26824_1.R1010
5'-most EST	LIB25-001-Q1-E1-G11

Seq. No. 127940

Contig ID	26826_1.R1010
5'-most EST	jC-alXLIB327435P2b01b1

Seq. No.	127941
Contig ID	26836_1.R1010
5'-most EST	jC-atX25001Q1E2A03b1
Method	BLASTN
NCBI GI	g4559319
BLAST score	72
E value	3.0e-32
Match length	246
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	127942
Contig ID	26838_1.R1010
5'-most EST	jC-atX25001Q1E2A05b1
Method	BLASTN
NCBI GI	g2584827
BLAST score	384
E value	0.0e+00
Match length	425
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127943
Contig ID	26847_1.R1010
5'-most EST	jC-atXLIB327426P3h11b1
Method	BLASTX
NCBI GI	g2979565
BLAST score	652
E value	4.0e-68
Match length	124
% identity	100
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	127944
Contig ID	26848_1.R1010
5'-most EST	LIB25-101-Q1-E1-F1
Method	BLASTX
NCBI GI	g4539303
BLAST score	1197
E value	1.0e-132
Match length	234
% identity	97
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	127945
Contig ID	26849_1.R1010
5'-most EST	LIB317-021-P1-K2-G11

Seq. No.	127946
Contig ID	26856_1.R1010
5'-most EST	g1216723

Seq. No.	127947
Contig ID	26858_1.R1010
5'-most EST	jC-alXLIB327435P2a09b1
Method	BLASTX
NCBI GI	g3367593
BLAST score	233
E value	3.0e-19
Match length	96
% identity	43
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	127948
Contig ID	26861_1.R1010
5'-most EST	jC-atX25001Q1E2D02b1
Method	BLASTN
NCBI GI	g3461810
BLAST score	314
E value	1.0e-176
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127949
Contig ID	26864_1.R1010
5'-most EST	LIB3176-035-P1-K1-H11
Method	BLASTX
NCBI GI	g4587554
BLAST score	251
E value	1.0e-21
Match length	102
% identity	44
NCBI Description	(AC006577) Similar to gb_AJ005701 Na/Ca,K-exchanger from Caenorhabditis elegans. ESTs gb_T04173 and gb_AA585918 come from this gene. [Arabidopsis thaliana]

Seq. No.	127950
Contig ID	26875_1.R1010
5'-most EST	jC-alXLIB327434P4a03b1
Method	BLASTX
NCBI GI	g3540199
BLAST score	348
E value	4.0e-76
Match length	162
% identity	92
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	127951
Contig ID	26877_1.R1010
5'-most EST	LIB3234-100-P1-K1-B4
Method	BLASTX
NCBI GI	g1351135
BLAST score	918

E value	2.0e-99
Match length	190
% identity	95
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_436792_emb_CAA50317_ (X70990) sucrose synthase [Arabidopsis thaliana]

Seq. No.	127952
Contig ID	26880_1.R1010
5'-most EST	jC-atX25001Q1E2F03b1
Method	BLASTN
NCBI GI	g4115930
BLAST score	105
E value	6.0e-52
Match length	348
% identity	94
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	127953
Contig ID	26890_1.R1010
5'-most EST	jC-alXLIB327435P2b03b1
Method	BLASTX
NCBI GI	g4490721
BLAST score	297
E value	1.0e-26
Match length	67
% identity	84
NCBI Description	(AL035709) squalene epoxidase-like protein [Arabidopsis thaliana]

Seq. No.	127954
Contig ID	26896_1.R1010
5'-most EST	LIB25-001-Q1-E2-H1
Method	BLASTN
NCBI GI	g4519193
BLAST score	228
E value	1.0e-125
Match length	596
% identity	42
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	127955
Contig ID	26901_1.R1010
5'-most EST	LIB25-001-Q1-E2-H4
Method	BLASTN
NCBI GI	g4699904
BLAST score	172
E value	1.0e-91
Match length	548
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	127956
Contig ID	26908_1.R1010
5'-most EST	LIB25-002-Q1-E1-A11

Method	BLASTX
NCBI GI	g2829901
BLAST score	467
E value	1.0e-46
Match length	97
% identity	100
NCBI Description	(AC002311) putative 10kd chaperonin [Arabidopsis thaliana]

Seq. No.	127957
Contig ID	26919_1.R1010
5'-most EST	LIB3176-051-P1-K1-D11
Method	BLASTX
NCBI GI	g4406775
BLAST score	320
E value	2.0e-29
Match length	135
% identity	44
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	127958
Contig ID	26920_1.R1010
5'-most EST	jC-atX25002Q1E1B02b1

Seq. No.	127959
Contig ID	26921_1.R1010
5'-most EST	LIB25-002-Q1-E1-B3
Method	BLASTX
NCBI GI	g3377825
BLAST score	259
E value	8.0e-39
Match length	96
% identity	78
NCBI Description	(AF075598) contains similarity to fibrillins [Arabidopsis thaliana]

Seq. No.	127960
Contig ID	26922_1.R1010
5'-most EST	g936978
Method	BLASTX
NCBI GI	g3548801
BLAST score	378
E value	6.0e-36
Match length	202
% identity	39
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	127961
Contig ID	26927_1.R1010
5'-most EST	jC-atXLIB327440P1c11b1
Method	BLASTX
NCBI GI	g3004564
BLAST score	133
E value	6.0e-31
Match length	129
% identity	57

NCBI Description	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	127962
Contig ID	26929_1.R1010
5'-most EST	g2047628
Method	BLASTX
NCBI GI	g4678939
BLAST score	335
E value	3.0e-31
Match length	70
% identity	96
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]
Seq. No.	127963
Contig ID	26929_2.R1010
5'-most EST	LIB25-002-Q1-E1-C11
Method	BLASTN
NCBI GI	g4691223
BLAST score	236
E value	1.0e-130
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)
Seq. No.	127964
Contig ID	26931_1.R1010
5'-most EST	jC-alXLIB327434P4a07b1
Method	BLASTX
NCBI GI	g4510357
BLAST score	709
E value	6.0e-75
Match length	134
% identity	97
NCBI Description	(AC006921) putative invertase [Arabidopsis thaliana] >gi_4678229_gb_AAD26974.1_AC007135_10 (AC007135) putative invertase [Arabidopsis thaliana]
Seq. No.	127965
Contig ID	26934_1.R1010
5'-most EST	jC-alXLIB327434P2a02b1
Method	BLASTN
NCBI GI	g2264311
BLAST score	859
E value	0.0e+00
Match length	892
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.	127966
Contig ID	26941_1.R1010
5'-most EST	jC-alXLIB327435P2a12b1
Seq. No.	127967
Contig ID	26951_1.R1010

5'-most EST	jC-atXLIB327417P4b11a1
Method	BLASTX
NCBI GI	g1903360
BLAST score	860
E value	1.0e-129
Match length	275
% identity	86
NCBI Description	(AC000104) Similar to Arabidopsis 2A6 (gb_X83096). EST gb_T76913 comes from this gene. [Arabidopsis thaliana]

Seq. No.	127968
Contig ID	26951_2.R1010
5'-most EST	g935859
Method	BLASTX
NCBI GI	g1903360
BLAST score	650
E value	4.0e-68
Match length	127
% identity	98
NCBI Description	(AC000104) Similar to Arabidopsis 2A6 (gb_X83096). EST gb_T76913 comes from this gene. [Arabidopsis thaliana]

Seq. No.	127969
Contig ID	26956_1.R1010
5'-most EST	jC-alXLIB327434P3a06b1
Method	BLASTN
NCBI GI	g2828188
BLAST score	265
E value	1.0e-147
Match length	550
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	127970
Contig ID	26960_1.R1010
5'-most EST	jC-alXLIB327434P4a02b1
Method	BLASTX
NCBI GI	g4567197
BLAST score	332
E value	7.0e-31
Match length	140
% identity	51
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	127971
Contig ID	26963_1.R1010
5'-most EST	jC-alXLIB327434P4a10b1

Seq. No.	127972
Contig ID	26964_1.R1010
5'-most EST	jC-atXLIB327417P1g08b1
Method	BLASTX
NCBI GI	g3183185
BLAST score	579
E value	2.0e-59
Match length	173

% identity	65
NCBI Description	GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG >gi_2224766_emb_CAB09712_ (Z97025) product highly similar to elongation factor EF-G [Bacillus subtilis] >gi_2633848_emb_CAB13350_ (Z99111) similar to GTP-binding elongation factor [Bacillus subtilis]

Seq. No.	127973
Contig ID	26970_1.R1010
5'-most EST	jC-atXP85CG8A12T7b1
Method	BLASTX
NCBI GI	g3107905
BLAST score	179
E value	1.0e-12
Match length	163
% identity	7
NCBI Description	(D85101) leaf protein [Ipomoea nil]

Seq. No.	127974
Contig ID	26970_2.R1010
5'-most EST	jC-alXLIB327434P3a08b1
Method	BLASTX
NCBI GI	g4006835
BLAST score	220
E value	2.0e-17
Match length	156
% identity	10
NCBI Description	(AC005970) hypothetical protein [Arabidopsis thaliana]

Seq. No.	127975
Contig ID	26976_1.R1010
5'-most EST	jC-alXLIB327434P2b03b1
Method	BLASTX
NCBI GI	g4539423
BLAST score	696
E value	2.0e-73
Match length	159
% identity	86
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	127976
Contig ID	26982_1.R1010
5'-most EST	LIB3175-032-P1-K1-D8
Method	BLASTN
NCBI GI	g3860243
BLAST score	372
E value	0.0e+00
Match length	417
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127977
Contig ID	26991_1.R1010
5'-most EST	LIB3175-022-P1-K1-A5
Method	BLASTX

NCBI GI	g4191796
BLAST score	231
E value	7.0e-19
Match length	65
% identity	60
NCBI Description	(AC005917) putative senescence-associated protein 5 [Arabidopsis thaliana]

Seq. No.	127978
Contig ID	26991_2.R1010
5'-most EST	g2756945
Method	BLASTX
NCBI GI	g3551954
BLAST score	585
E value	3.0e-60
Match length	234
% identity	47
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	127979
Contig ID	26994_1.R1010
5'-most EST	jC-alXLIB327434P4b08b1
Method	BLASTX
NCBI GI	g3355471
BLAST score	1082
E value	1.0e-118
Match length	208
% identity	100
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	127980
Contig ID	26994_2.R1010
5'-most EST	LIB35-054-Q1-E1-B7
Method	BLASTX
NCBI GI	g3355471
BLAST score	782
E value	1.0e-83
Match length	152
% identity	97
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	127981
Contig ID	26999_1.R1010
5'-most EST	jC-alXLIB327434P3b05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 127982

Contig ID	27010_1.R1010
5'-most EST	jC-atX25003Q1E1B08b1
Method	BLASTN
NCBI GI	g3785992
BLAST score	381
E value	0.0e+00
Match length	483
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127983
Contig ID	27020_1.R1010
5'-most EST	LIB25-003-Q1-E1-C7

Seq. No.	127984
Contig ID	27021_1.R1010
5'-most EST	jC-alXLIB327434P4c01b1
Method	BLASTX
NCBI GI	g2564114
BLAST score	596
E value	2.0e-61
Match length	290
% identity	47
NCBI Description	(AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]

Seq. No.	127985
Contig ID	27024_1.R1010
5'-most EST	jC-alXLIB327434P4c12b1
Method	BLASTX
NCBI GI	g4539348
BLAST score	863
E value	5.0e-93
Match length	165
% identity	99
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	127986
Contig ID	27024_2.R1010
5'-most EST	LIB3177-064-P1-K1-F11
Method	BLASTN
NCBI GI	g4539331
BLAST score	177
E value	7.0e-95
Match length	392
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	127987
Contig ID	27038_1.R1010
5'-most EST	jC-alXLIB327434P2d11b1
Method	BLASTX
NCBI GI	g4512659
BLAST score	448
E value	2.0e-44

Match length	156
% identity	63
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	127988
Contig ID	27041_1.R1010
5'-most EST	jC-alXLIB327434P4d01b1
Method	BLASTX
NCBI GI	g4508070
BLAST score	740
E value	1.0e-78
Match length	146
% identity	97
NCBI Description	(AC005882) 24349 [Arabidopsis thaliana]

Seq. No.	127989
Contig ID	27053_1.R1010
5'-most EST	jC-alXLIB327434P4d07b1
Method	BLASTX
NCBI GI	g419760
BLAST score	817
E value	1.0e-87
Match length	177
% identity	53
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	127990
Contig ID	27061_1.R1010
5'-most EST	jC-alXLIB327435P2e07b1
Method	BLASTN
NCBI GI	g2351067
BLAST score	332
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	127991
Contig ID	27063_1.R1010
5'-most EST	LIB25-004-Q1-E1-F5

Seq. No.	127992
Contig ID	27065_1.R1010
5'-most EST	LIB25-003-Q1-E1-H1
Method	BLASTX
NCBI GI	g1929056
BLAST score	396
E value	3.0e-38
Match length	87
% identity	85
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	127993
Contig ID	27066_1.R1010
5'-most EST	LIB25-003-Q1-E1-H10
Method	BLASTN
NCBI GI	g3176693
BLAST score	248
E value	1.0e-137
Match length	478
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	127994
Contig ID	27070_1.R1010
5'-most EST	jC-alXLIB327434P4e02b1
Method	BLASTX
NCBI GI	g2127524
BLAST score	266
E value	5.0e-23
Match length	144
% identity	44
NCBI Description	hypothetical 345 protein - Streptomyces coelicolor (fragment)

Seq. No.	127995
Contig ID	27073_1.R1010
5'-most EST	LIB25-090-Q1-E1-B9
Method	BLASTX
NCBI GI	g4584523
BLAST score	837
E value	7.0e-90
Match length	177
% identity	92
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	127996
Contig ID	27083_1.R1010
5'-most EST	jC-atXLIB327420P3f11b1

Seq. No.	127997
Contig ID	27087_1.R1010
5'-most EST	jC-atXP123C117C21T7083d1
Method	BLASTX
NCBI GI	g3269288
BLAST score	518
E value	2.0e-52
Match length	134
% identity	71
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	127998
Contig ID	27087_3.R1010
5'-most EST	LIB25-004-Q1-E1-B1
Method	BLASTX
NCBI GI	g3269288
BLAST score	230

E value	2.0e-54
Match length	183
% identity	60
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	127999
Contig ID	27088_1.R1010
5'-most EST	LIB25-004-Q1-E1-B10
Method	BLASTN
NCBI GI	g4376087
BLAST score	276
E value	1.0e-154
Match length	448
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	128000
Contig ID	27091_1.R1010
5'-most EST	LIB25-004-Q1-E1-B3
Method	BLASTN
NCBI GI	g4468103
BLAST score	185
E value	1.0e-99
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	128001
Contig ID	27101_1.R1010
5'-most EST	jC-alXLIB327434P4c04b1
Method	BLASTX
NCBI GI	g4769004
BLAST score	345
E value	3.0e-46
Match length	89
% identity	97
NCBI Description	(AF140598) ring-box protein 1 [Homo sapiens] >gi_4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box protein 1 [Mus musculus]

Seq. No.	128002
Contig ID	27102_1.R1010
5'-most EST	jC-alXLIB327436P4b08b1
Method	BLASTX
NCBI GI	g2829899
BLAST score	347
E value	3.0e-32
Match length	139
% identity	50
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	128003
Contig ID	27104_1.R1010

5'-most EST	jC-alXLIB327434P3c05b1
Method	BLASTX
NCBI GI	g3149952
BLAST score	837
E value	6.0e-90
Match length	181
% identity	88
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	128004
Contig ID	27105_1.R1010
5'-most EST	jC-alXLIB327434P2c11b1
Method	BLASTN
NCBI GI	g3522932
BLAST score	399
E value	0.0e+00
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128005
Contig ID	27108_1.R1010
5'-most EST	jC-atX25004Q1E1D01a1
Method	BLASTN
NCBI GI	g217828
BLAST score	89
E value	1.0e-42
Match length	97
% identity	98
NCBI Description	Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase

Seq. No.	128006
Contig ID	27115_1.R1010
5'-most EST	jC-atXP112C129E8T7d2
Method	BLASTX
NCBI GI	g3643607
BLAST score	507
E value	4.0e-51
Match length	115
% identity	41
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	128007
Contig ID	27115_2.R1010
5'-most EST	jC-alXLIB327434P4c11b1
Method	BLASTX
NCBI GI	g1871185
BLAST score	582
E value	8.0e-60
Match length	175
% identity	59
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	128008
Contig ID	27116_1.R1010

5'-most EST	jC-alXLIB327434P3c11b1
Seq. No.	128009
Contig ID	27123_1.R1010
5'-most EST	LIB3175-035-P1-K1-G11
Method	BLASTN
NCBI GI	g3241922
BLAST score	293
E value	1.0e-164
Match length	516
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.	128010
Contig ID	27124_1.R1010
5'-most EST	jC-atXP119C195P24T7076a1
Method	BLASTX
NCBI GI	g122007
BLAST score	466
E value	2.0e-46
Match length	137
% identity	69
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]
Seq. No.	128011
Contig ID	27124_3.R1010
5'-most EST	g1053643
Method	BLASTN
NCBI GI	g3241923
BLAST score	243
E value	1.0e-134
Match length	345
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.	128012
Contig ID	27124_4.R1010
5'-most EST	g3450302
Method	BLASTX
NCBI GI	g122007
BLAST score	214
E value	4.0e-17
Match length	51
% identity	82
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]
Seq. No.	128013
Contig ID	27127_1.R1010
5'-most EST	jC-atXLIB327424P4c06b1
Method	BLASTX
NCBI GI	g2911073

BLAST score	421
E value	5.0e-41
Match length	87
% identity	99
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	128014
Contig ID	27127_2.R1010
5'-most EST	g17550
Method	BLASTX
NCBI GI	g2911073
BLAST score	46
E value	6.0e-13
Match length	40
% identity	97
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	128015
Contig ID	27128_1.R1010
5'-most EST	jC-atXLIB327418P2d05b2
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	8.0e-22
Match length	67
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	128016
Contig ID	27135_1.R1010
5'-most EST	jC-alXLIB327434P4d11b1
Method	BLASTN
NCBI GI	g2264315
BLAST score	430
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	128017
Contig ID	27142_1.R1010
5'-most EST	jC-alXLIB327435P2e05b1
Method	BLASTX
NCBI GI	g3461821
BLAST score	293
E value	3.0e-26
Match length	119
% identity	57
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	128018
Contig ID	27143_1.R1010
5'-most EST	jC-alXLIB327435P2e06b1
Method	BLASTX
NCBI GI	g3927836

BLAST score	271
E value	1.0e-23
Match length	111
% identity	53
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	128019
Contig ID	27148_1.R1010
5'-most EST	LIB25-069-Q1-E1-E2
Method	BLASTX
NCBI GI	g2190551
BLAST score	577
E value	8.0e-60
Match length	106
% identity	99
NCBI Description	(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from this gene. [Arabidopsis thaliana]

Seq. No.	128020
Contig ID	27156_1.R1010
5'-most EST	jC-atXP37C159C1T7s2

Seq. No.	128021
Contig ID	27159_1.R1010
5'-most EST	jC-atXP86CG8E1T7d2
Method	BLASTN
NCBI GI	g3643588
BLAST score	202
E value	1.0e-109
Match length	544
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128022
Contig ID	27163_1.R1010
5'-most EST	jC-alXLIB327434P4b01b1
Method	BLASTN
NCBI GI	g3869064
BLAST score	335
E value	0.0e+00
Match length	545
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1O13, complete sequence [Arabidopsis thaliana]

Seq. No.	128023
Contig ID	27177_1.R1010
5'-most EST	jC-alXLIB327434P4d04b1
Method	BLASTN
NCBI GI	g2351062
BLAST score	226
E value	1.0e-123
Match length	697
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	128024
Contig ID	27178_1.R1010
5'-most EST	jC-alXLIB327434P3d04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	2.0e-26
Match length	78
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128025
Contig ID	27185_1.R1010
5'-most EST	LIB25-006-Q1-E1-A12
Method	BLASTX
NCBI GI	g1352683
BLAST score	572
E value	8.0e-59
Match length	115
% identity	98
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]

Seq. No.	128026
Contig ID	27186_1.R1010
5'-most EST	LIB3175-068-P1-K1-E10
Method	BLASTX
NCBI GI	g1082798
BLAST score	200
E value	1.0e-15
Match length	98
% identity	42
NCBI Description	spliceosome-associated protein SAP 61 - human >gi_508723 (U08815) SAP 61 [Homo sapiens]

Seq. No.	128027
Contig ID	27193_1.R1010
5'-most EST	g2048824
Method	BLASTX
NCBI GI	g3201554
BLAST score	329
E value	2.0e-30
Match length	75
% identity	80
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	128028
Contig ID	27194_1.R1010
5'-most EST	LIB35-039-Q1-E1-G6
Method	BLASTX
NCBI GI	g2827526
BLAST score	659
E value	2.0e-69
Match length	130

% identity	98
NCBI Description	(AL021633) AIG2-like protein [Arabidopsis thaliana]

Seq. No.	128029
Contig ID	27195_1.R1010
5'-most EST	jC-atXP98CH8A9T7070d1
Method	BLASTN
NCBI GI	g4115930
BLAST score	391
E value	0.0e+00
Match length	517
% identity	98
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	128030
Contig ID	27196_1.R1010
5'-most EST	LIB25-006-Q1-E1-B2

Seq. No.	128031
Contig ID	27204_1.R1010
5'-most EST	LIB25-006-Q1-E1-C1
Method	BLASTN
NCBI GI	g4454447
BLAST score	253
E value	1.0e-140
Match length	431
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128032
Contig ID	27207_1.R1010
5'-most EST	jC-alXLIB327434P2d06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	7.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128033
Contig ID	27213_1.R1010
5'-most EST	jC-atXLIB327421P2b11b1
Method	BLASTX
NCBI GI	g473874
BLAST score	274
E value	6.0e-24
Match length	198
% identity	11
NCBI Description	(U08285) a membrane-associated salt-inducible protein [Nicotiana tabacum]

Seq. No.	128034
Contig ID	27229_1.R1010
5'-most EST	jC-alXLIB327435P2c09b1

Method	BLASTX
NCBI GI	g4204258
BLAST score	1144
E value	1.0e-125
Match length	218
% identity	100
NCBI Description	(AC005223) 14409 [Arabidopsis thaliana]

Seq. No.	128035
Contig ID	27236_1.R1010
5'-most EST	LIB25-006-Q1-E1-E8
Method	BLASTX
NCBI GI	g2827630
BLAST score	418
E value	4.0e-41
Match length	93
% identity	88
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	128036
Contig ID	27241_1.R1010
5'-most EST	LIB25-049-Q1-E1-G2

Seq. No.	128037
Contig ID	27244_1.R1010
5'-most EST	jC-atXP52C183G15T7d2

Seq. No.	128038
Contig ID	27270_1.R1010
5'-most EST	LIB25-006-Q1-E1-H8
Method	BLASTX
NCBI GI	g4539428
BLAST score	185
E value	1.0e-13
Match length	60
% identity	67
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	128039
Contig ID	27273_1.R1010
5'-most EST	jC-alXLIB327434P2b11b1

Seq. No.	128040
Contig ID	27279_1.R1010
5'-most EST	g2747975
Method	BLASTX
NCBI GI	g4467139
BLAST score	450
E value	2.0e-44
Match length	91
% identity	98
NCBI Description	(AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No.	128041
Contig ID	27280_1.R1010
5'-most EST	jC-alXLIB327435P2b11b1

Method	BLASTX
NCBI GI	g2827663
BLAST score	142
E value	2.0e-08
Match length	163
% identity	3
NCBI Description	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]

Seq. No.	128042
Contig ID	27294_1.R1010
5'-most EST	LIB25-006-Q1-E2-C1
Method	BLASTX
NCBI GI	g4587573
BLAST score	436
E value	4.0e-43
Match length	88
% identity	100
NCBI Description	(AC006550) Similar to clathrin assembly protein gb_AF041374 (CALM) from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	128043
Contig ID	27304_1.R1010
5'-most EST	jC-alXLIB327434P4c06b1
Method	BLASTN
NCBI GI	g1931636
BLAST score	501
E value	0.0e+00
Match length	534
% identity	100
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	128044
Contig ID	27310_1.R1010
5'-most EST	jC-alXLIB327434P4c10b1

Seq. No.	128045
Contig ID	27313_1.R1010
5'-most EST	jC-alXLIB327434P4c08b1
Method	BLASTX
NCBI GI	g2961346
BLAST score	940
E value	1.0e-102
Match length	189
% identity	91
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	128046
Contig ID	27323_1.R1010
5'-most EST	jC-alXLIB327434P2d05b1
Method	BLASTX
NCBI GI	g2529679
BLAST score	155
E value	7.0e-10
Match length	56
% identity	48

NCBI Description	(AC002535) hypothetical protein [Arabidopsis thaliana]
Seq. No.	128047
Contig ID	27329_1.R1010
5'-most EST	jC-alXLIB327434P4d06b1
Method	BLASTN
NCBI GI	g4467094
BLAST score	392
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)
Seq. No.	128048
Contig ID	27329_2.R1010
5'-most EST	LIB3175-043-P1-K1-C6
Method	BLASTX
NCBI GI	g4467097
BLAST score	659
E value	5.0e-69
Match length	159
% identity	87
NCBI Description	(AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]
Seq. No.	128049
Contig ID	27329_3.R1010
5'-most EST	jC-atX25056Q1E1H06a1
Method	BLASTN
NCBI GI	g4467094
BLAST score	222
E value	1.0e-121
Match length	314
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)
Seq. No.	128050
Contig ID	27331_1.R1010
5'-most EST	LIB25-019-Q1-E1-B9
Method	BLASTN
NCBI GI	g2696018
BLAST score	346
E value	0.0e+00
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.	128051
Contig ID	27337_1.R1010
5'-most EST	jC-alXLIB327435P2e02b1
Method	BLASTX
NCBI GI	g4454458
BLAST score	1221
E value	1.0e-134

Match length	287
% identity	87
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	128052
Contig ID	27337_2.R1010
5'-most EST	g2750063
Method	BLASTN
NCBI GI	g4454447
BLAST score	291
E value	1.0e-163
Match length	299
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128053
Contig ID	27346_1.R1010
5'-most EST	LIB25-006-Q1-E2-H11
Method	BLASTX
NCBI GI	g2262116
BLAST score	119
E value	3.0e-91
Match length	185
% identity	87
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	128054
Contig ID	27359_1.R1010
5'-most EST	jC-atXLIB327424P1e12b2
Method	BLASTX
NCBI GI	g1620650
BLAST score	291
E value	5.0e-26
Match length	72
% identity	78
NCBI Description	(U64561) pollen-specific pectin esterase [Brassica rapa ssp. pekinensis]

Seq. No.	128055
Contig ID	27368_1.R1010
5'-most EST	jC-alXLIB327435P2f10b1
Method	BLASTX
NCBI GI	g3128168
BLAST score	586
E value	2.0e-60
Match length	169
% identity	57
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	128056
Contig ID	27373_1.R1010
5'-most EST	jC-alXLIB327434P4f10b1
Method	BLASTX
NCBI GI	g2492513
BLAST score	419

E value	9.0e-41
Match length	166
% identity	52
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG 4 >gi_1652085_dbj_BAA17010_ (D90902) cell division protein FtsH [Synechocystis sp.]

Seq. No.	128057
Contig ID	27374_1.R1010
5'-most EST	LIB3234-052-P1-K1-B11
Method	BLASTX
NCBI GI	g4454482
BLAST score	185
E value	1.0e-36
Match length	121
% identity	67
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128058
Contig ID	27379_1.R1010
5'-most EST	jC-alXLIB327434P3f08b1
Method	BLASTN
NCBI GI	g531832
BLAST score	33
E value	1.0e-08
Match length	81
% identity	85
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	128059
Contig ID	27384_1.R1010
5'-most EST	LIB25-037-Q1-E1-D9
Method	BLASTN
NCBI GI	g4262221
BLAST score	46
E value	1.0e-16
Match length	110
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128060
Contig ID	27384_2.R1010
5'-most EST	LIB3177-077-P1-K1-G1
Method	BLASTX
NCBI GI	g4262234
BLAST score	500
E value	3.0e-50
Match length	146
% identity	68
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	128061
Contig ID	27388_1.R1010
5'-most EST	jC-alXLIB327435P2g04b1
Method	BLASTN
NCBI GI	g2924653

BLAST score	276
E value	1.0e-154
Match length	440
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	128062
Contig ID	27389_1.R1010
5'-most EST	jC-atXLIB327438P4c03a2

Seq. No.	128063
Contig ID	27390_1.R1010
5'-most EST	jC-alXLIB327435P2g05b1
Method	BLASTX
NCBI GI	g3269287
BLAST score	368
E value	4.0e-35
Match length	107
% identity	72
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	128064
Contig ID	27399_1.R1010
5'-most EST	LIB3175-032-P1-K1-B5

Seq. No.	128065
Contig ID	27404_1.R1010
5'-most EST	jC-alXLIB327435P2h01b1

Seq. No.	128066
Contig ID	27408_1.R1010
5'-most EST	LIB25-007-Q1-E1-F6
Method	BLASTN
NCBI GI	g4191771
BLAST score	173
E value	1.0e-92
Match length	221
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128067
Contig ID	27414_1.R1010
5'-most EST	jC-alXLIB327434P2h10b1
Method	BLASTN
NCBI GI	g4662609
BLAST score	654
E value	0.0e+00
Match length	718
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	128068
Contig ID	27416_1.R1010
5'-most EST	jC-alXLIB327434P2h11b1

Seq. No.	128069
Contig ID	27426_1.R1010
5'-most EST	jC-alXLIB327434P4h10b1
Method	BLASTX
NCBI GI	g4588012
BLAST score	207
E value	3.0e-78
Match length	169
% identity	85
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	128070
Contig ID	27432_1.R1010
5'-most EST	jC-alXLIB327434P4e11b1
Method	BLASTX
NCBI GI	g480725
BLAST score	602
E value	2.0e-62
Match length	168
% identity	67
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	128071
Contig ID	27434_1.R1010
5'-most EST	jC-alXLIB327435P2f01b1
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	6.0e-17
Match length	66
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	128072
Contig ID	27443_1.R1010
5'-most EST	g1158272

Seq. No.	128073
Contig ID	27449_1.R1010
5'-most EST	LIB25-008-Q1-E1-B6
Method	BLASTX
NCBI GI	g3063444
BLAST score	474
E value	4.0e-47
Match length	143
% identity	58
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	128074
Contig ID	27449_2.R1010
5'-most EST	jC-atX25023Q1E1C10b1

Method	BLASTN
NCBI GI	g2760169
BLAST score	328
E value	0.0e+00
Match length	352
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	128075
Contig ID	27450_1.R1010
5'-most EST	jC-alXLIB327434P2f09b1
Method	BLASTX
NCBI GI	g4835240
BLAST score	1262
E value	1.0e-139
Match length	249
% identity	95
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	128076
Contig ID	27452_1.R1010
5'-most EST	jC-atX25008Q1E1B09b1

Seq. No.	128077
Contig ID	27461_1.R1010
5'-most EST	jC-alXLIB327435P2g06b1
Method	BLASTN
NCBI GI	g2264321
BLAST score	434
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	128078
Contig ID	27462_1.R1010
5'-most EST	g2749043
Method	BLASTX
NCBI GI	g687844
BLAST score	491
E value	2.0e-49
Match length	221
% identity	7
NCBI Description	(U21320) contains TPR domain-like repeats [Caenorhabditis elegans]

Seq. No.	128079
Contig ID	27466_2.R1010
5'-most EST	jC-atXmonuni26Ae07b1
Method	BLASTX
NCBI GI	g2708751
BLAST score	695
E value	2.0e-73
Match length	145
% identity	89

NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128080
Contig ID	27470_1.R1010
5'-most EST	jC-alXLIB327434P4g03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	5.0e-24
Match length	82
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128081
Contig ID	27474_1.R1010
5'-most EST	jC-alXLIB327434P3g04b1
Method	BLASTX
NCBI GI	g1418319
BLAST score	1137
E value	1.0e-125
Match length	215
% identity	100
NCBI Description	(X95965) CER1-like [Arabidopsis thaliana]

Seq. No.	128082
Contig ID	27475_1.R1010
5'-most EST	jC-alXLIB327434P4g01b1
Method	BLASTX
NCBI GI	g2244871
BLAST score	80
E value	3.0e-58
Match length	144
% identity	92
NCBI Description	(Z97338) phosphocholine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	128083
Contig ID	27479_1.R1010
5'-most EST	jC-alXLIB327434P2h01b1
Method	BLASTX
NCBI GI	g1504008
BLAST score	165
E value	3.0e-11
Match length	127
% identity	34
NCBI Description	(D86967) Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [Homo sapiens]

Seq. No.	128084
Contig ID	27484_1.R1010
5'-most EST	LIB3168-037-P1-K1-C8
Method	BLASTX
NCBI GI	g4263704
BLAST score	218
E value	2.0e-17

Match length	75
% identity	49
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	128085
Contig ID	27493_1.R1010
5'-most EST	jC-alXLIB327435P2h09b1
Method	BLASTX
NCBI GI	g1170125
BLAST score	245
E value	1.0e-20
Match length	122
% identity	40
NCBI Description	GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE) >gi_2145847_pir__S72813 GMP synthase (glutamine-hydrolysing) (EC 6.3.5.2) guaA - Mycobacterium leprae >gi_466934 (U00015) guaA; B1620_C2_205 [Mycobacterium leprae]

Seq. No.	128086
Contig ID	27495_1.R1010
5'-most EST	LIB25-008-Q1-E1-H11
Method	BLASTN
NCBI GI	g3241927
BLAST score	440
E value	0.0e+00
Match length	675
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	128087
Contig ID	27499_1.R1010
5'-most EST	jC-alXLIB327434P3h09b1
Method	BLASTX
NCBI GI	g3983139
BLAST score	193
E value	2.0e-14
Match length	104
% identity	40
NCBI Description	(AF098511) Scythe [Xenopus laevis]

Seq. No.	128088
Contig ID	27504_1.R1010
5'-most EST	jC-alXLIB327434P4h06b1
Method	BLASTX
NCBI GI	g2232354
BLAST score	392
E value	8.0e-38
Match length	152
% identity	51
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	128089
Contig ID	27510_1.R1010
5'-most EST	LIB25-014-Q1-E1-F10

Method	BLASTX
NCBI GI	g3152589
BLAST score	596
E value	5.0e-62
Match length	112
% identity	100
NCBI Description	(AC002986) Strong similarity to lupeol synthase gb_U49919 from A. thaliana (second gene in a series of three with similar homologies). [Arabidopsis thaliana]

Seq. No.	128090
Contig ID	27519_1.R1010
5'-most EST	g2047526
Method	BLASTX
NCBI GI	g2160182
BLAST score	103
E value	1.0e-17
Match length	138
% identity	43
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	128091
Contig ID	27519_2.R1010
5'-most EST	jC-atXP55C187F3T7d2

Seq. No.	128092
Contig ID	27523_1.R1010
5'-most EST	g957805
Method	BLASTX
NCBI GI	g4585995
BLAST score	250
E value	3.0e-21
Match length	156
% identity	42
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	128093
Contig ID	27528_1.R1010
5'-most EST	LIB25-009-Q1-E1-C1

Seq. No.	128094
Contig ID	27532_1.R1010
5'-most EST	LIB3175-078-P1-K1-E8

Seq. No.	128095
Contig ID	27548_1.R1010
5'-most EST	LIB25-009-Q1-E1-E10
Method	BLASTX
NCBI GI	g3395431
BLAST score	423
E value	1.0e-41
Match length	92
% identity	89
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 128096

Contig ID	27553_1.R1010
5'-most EST	LIB25-046-Q1-E1-C1
Method	BLASTX
NCBI GI	g4455337
BLAST score	149
E value	2.0e-09
Match length	104
% identity	33
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	128097
Contig ID	27556_1.R1010
5'-most EST	jC-alXLIB327434P4g07b1
Method	BLASTX
NCBI GI	g4115381
BLAST score	299
E value	9.0e-27
Match length	137
% identity	49
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No.	128098
Contig ID	27559_1.R1010
5'-most EST	LIB25-009-Q1-E1-F2

Seq. No.	128099
Contig ID	27564_1.R1010
5'-most EST	jC-atXLIB327437P4a07a2
Method	BLASTX
NCBI GI	g2494275
BLAST score	245
E value	1.0e-20
Match length	85
% identity	52
NCBI Description	ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation factor P [Synechococcus PCC7942]

Seq. No.	128100
Contig ID	27567_1.R1010
5'-most EST	jC-atXP10C95K24T7d2
Method	BLASTX
NCBI GI	g4678330
BLAST score	377
E value	9.0e-36
Match length	88
% identity	85
NCBI Description	(AL049658) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128101
Contig ID	27569_1.R1010
5'-most EST	LIB3176-067-P1-K1-H3
Method	BLASTN
NCBI GI	g3810584
BLAST score	223
E value	1.0e-122
Match length	347

% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128102
Contig ID	27570_1.R1010
5'-most EST	jC-atXP50C179I19T7021d1
Method	BLASTX
NCBI GI	g2245138
BLAST score	372
E value	2.0e-35
Match length	163
% identity	43
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128103
Contig ID	27573_1.R1010
5'-most EST	LIB25-009-Q1-E1-G9

Seq. No.	128104
Contig ID	27576_1.R1010
5'-most EST	jC-alXLIB327434P4h02b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	4.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	128105
Contig ID	27579_1.R1010
5'-most EST	LIB3168-059-P1-K1-G9
Method	BLASTX
NCBI GI	g2464905
BLAST score	480
E value	2.0e-48
Match length	131
% identity	74
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	128106
Contig ID	27586_1.R1010
5'-most EST	jC-alXLIB327434P4e06b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	4.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	128107
Contig ID	27586_2.R1010
5'-most EST	LIB3176-009-P1-K2-D8
Method	BLASTN
NCBI GI	g2961335

BLAST score	29
E value	2.0e-06
Match length	171
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	128108
Contig ID	27589_1.R1010
5'-most EST	LIB3176-037-P1-K1-A4
Method	BLASTX
NCBI GI	g461550
BLAST score	542
E value	3.0e-55
Match length	157
% identity	73
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	128109
Contig ID	27596_1.R1010
5'-most EST	jC-alXLIB327435P2f07b1
Method	BLASTX
NCBI GI	g2829891
BLAST score	1007
E value	1.0e-109
Match length	205
% identity	95
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	128110
Contig ID	27596_2.R1010
5'-most EST	g2446055
Method	BLASTN
NCBI GI	g4585952
BLAST score	333
E value	0.0e+00
Match length	458
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	128111
Contig ID	27600_1.R1010
5'-most EST	jC-alXLIB327434P2f04b1
Method	BLASTX
NCBI GI	g3928097
BLAST score	658
E value	5.0e-69
Match length	159
% identity	84
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	128112
Contig ID	27614_1.R1010
5'-most EST	LIB25-010-Q1-E1-D6
Method	BLASTX
NCBI GI	g2244918
BLAST score	640
E value	1.0e-66
Match length	188
% identity	72
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128113
Contig ID	27617_1.R1010
5'-most EST	jC-alXLIB327435P2g02b1

Seq. No.	128114
Contig ID	27618_1.R1010
5'-most EST	jC-alXLIB327435P2g08b1

Seq. No.	128115
Contig ID	27631_1.R1010
5'-most EST	LIB25-010-Q1-E1-F2
Method	BLASTN
NCBI GI	g3702728
BLAST score	424
E value	0.0e+00
Match length	488
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	128116
Contig ID	27632_1.R1010
5'-most EST	jC-alXLIB327434P4g09b1
Method	BLASTX
NCBI GI	g3080414
BLAST score	692
E value	1.0e-72
Match length	201
% identity	80
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	128117
Contig ID	27637_1.R1010
5'-most EST	jC-alXLIB327435P2h04b1
Method	BLASTX
NCBI GI	g4204294
BLAST score	518
E value	1.0e-52
Match length	120
% identity	93
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	128118
Contig ID	27639_1.R1010
5'-most EST	LIB25-010-Q1-E1-G4

Method	BLASTX
NCBI GI	g1621465
BLAST score	547
E value	3.0e-56
Match length	122
% identity	76
NCBI Description	(U73105) laccase [Liriodendron tulipifera]

Seq. No.	128119
Contig ID	27645_1.R1010
5'-most EST	jC-alXLIB327435P2h12b1
Method	BLASTX
NCBI GI	g1200256
BLAST score	229
E value	9.0e-19
Match length	125
% identity	39
NCBI Description	(X90990) stpk1 protein kinase [Solanum tuberosum]

Seq. No.	128120
Contig ID	27651_1.R1010
5'-most EST	jC-alXLIB327434P3h04b1

Seq. No.	128121
Contig ID	27653_1.R1010
5'-most EST	jC-alXLIB327434P4h01b1
Method	BLASTX
NCBI GI	g404690
BLAST score	245
E value	1.0e-20
Match length	120
% identity	41
NCBI Description	(L19075) cytochrome P450 [Catharanthus roseus]

Seq. No.	128122
Contig ID	27657_1.R1010
5'-most EST	LIB317-050-P1-K2-G12
Method	BLASTX
NCBI GI	g1350680
BLAST score	1021
E value	1.0e-111
Match length	252
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	128123
Contig ID	27657_2.R1010
5'-most EST	jC-atXP100CE3F11T7b1
Method	BLASTX
NCBI GI	g1350680
BLAST score	488
E value	4.0e-56
Match length	143
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	128124

Contig ID	27659_1.R1010
5'-most EST	jC-alXLIB327435P2a08a1
Method	BLASTX
NCBI GI	g4220480
BLAST score	85
E value	6.4e-02
Match length	145
% identity	12
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	128125
Contig ID	27666_1.R1010
5'-most EST	LIB3177-097-P1-K1-D1
Method	BLASTN
NCBI GI	g3492855
BLAST score	451
E value	0.0e+00
Match length	518
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	128126
Contig ID	27666_2.R1010
5'-most EST	jC-alXLIB327435P4a06b1
Method	BLASTN
NCBI GI	g3492855
BLAST score	308
E value	1.0e-173
Match length	439
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	128127
Contig ID	27669_1.R1010
5'-most EST	LIB25-011-Q1-E1-B3
Method	BLASTN
NCBI GI	g3293581
BLAST score	160
E value	9.0e-85
Match length	336
% identity	98
NCBI Description	Arabidopsis thaliana BAC T24H24

Seq. No.	128128
Contig ID	27671_1.R1010
5'-most EST	jC-alXLIB327435P4a08b1
Method	BLASTX
NCBI GI	g2252828
BLAST score	153
E value	1.0e-09
Match length	87
% identity	39
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 128129

Contig ID	27673_1.R1010
5'-most EST	jC-alXLIB327435P4a02b1
Method	BLASTN
NCBI GI	g3641835
BLAST score	827
E value	0.0e+00
Match length	827
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	128130
Contig ID	27676_1.R1010
5'-most EST	jC-alXLIB327436P1b01b1
Method	BLASTX
NCBI GI	g3273757
BLAST score	565
E value	3.0e-58
Match length	126
% identity	85
NCBI Description	(AF061852) iron superoxide dismutase 3 [Arabidopsis thaliana]

Seq. No.	128131
Contig ID	27681_1.R1010
5'-most EST	g2758897
Method	BLASTN
NCBI GI	g4559319
BLAST score	299
E value	1.0e-167
Match length	753
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	128132
Contig ID	27684_1.R1010
5'-most EST	jC-alXLIB327435P3a12b1
Method	BLASTN
NCBI GI	g4733991
BLAST score	52
E value	5.0e-20
Match length	52
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4D8 genomic sequence, complete sequence

Seq. No.	128133
Contig ID	27687_1.R1010
5'-most EST	jC-alXLIB327436P1b09b1

Seq. No.	128134
Contig ID	27696_1.R1010
5'-most EST	jC-alXLIB327435P2b11a1
Method	BLASTN
NCBI GI	g4585890
BLAST score	341

E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	128135
Contig ID	27708_1.R1010
5'-most EST	jC-alXLIB327435P3b07b1
Method	BLASTX
NCBI GI	g2335097
BLAST score	923
E value	1.0e-100
Match length	192
% identity	94
NCBI Description	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	128136
Contig ID	27709_1.R1010
5'-most EST	g936984

Seq. No.	128137
Contig ID	27712_1.R1010
5'-most EST	LIB25-011-Q1-E1-F10
Method	BLASTN
NCBI GI	g2341023
BLAST score	185
E value	1.0e-100
Match length	185
% identity	100
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	128138
Contig ID	27721_1.R1010
5'-most EST	jC-alXLIB327435P2c05a1
Method	BLASTX
NCBI GI	g2500139
BLAST score	182
E value	3.0e-13
Match length	87
% identity	40
NCBI Description	PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) >gi_1653916_dbj_BAA18826_ (D90917) peptide chain release factor [Synechocystis sp.]

Seq. No.	128139
Contig ID	27722_1.R1010
5'-most EST	LIB3234-075-P1-K1-E4

Seq. No.	128140
Contig ID	27724_1.R1010
5'-most EST	jC-alXLIB327435P3c02b1
Method	BLASTX
NCBI GI	g2648032
BLAST score	446

E value	6.0e-44
Match length	180
% identity	52
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	128141
Contig ID	27724_2.R1010
5'-most EST	LIB3177-017-P1-K2-A3
Method	BLASTX
NCBI GI	g2648032
BLAST score	585
E value	2.0e-60
Match length	145
% identity	74
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	128142
Contig ID	27724_3.R1010
5'-most EST	jC-atXP7C91I23T7s1
Method	BLASTN
NCBI GI	g2564046
BLAST score	354
E value	0.0e+00
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	128143
Contig ID	27725_1.R1010
5'-most EST	LIB25-011-Q1-E1-G12

Seq. No.	128144
Contig ID	27727_1.R1010
5'-most EST	jC-alXLIB327435P3c04b1
Method	BLASTX
NCBI GI	g4406801
BLAST score	335
E value	4.0e-31
Match length	101
% identity	61
NCBI Description	(AC006304) unknown protein [Arabidopsis thaliana]

Seq. No.	128145
Contig ID	27729_1.R1010
5'-most EST	jC-atXP34C149K24T7d1
Method	BLASTX
NCBI GI	g4455271
BLAST score	435
E value	5.0e-71
Match length	169
% identity	82
NCBI Description	(AL035527) serine protease-like protein [Arabidopsis thaliana]

Seq. No.	128146
Contig ID	27733_1.R1010

5'-most EST	jC-alXLIB327436P1d02b1
Method	BLASTN
NCBI GI	g2264311
BLAST score	344
E value	0.0e+00
Match length	419
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	128147
Contig ID	27739_1.R1010
5'-most EST	jC-alXLIB327436P1d03b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	128148
Contig ID	27740_1.R1010
5'-most EST	jC-alXLIB327435P4c11b1
Method	BLASTN
NCBI GI	g4376087
BLAST score	424
E value	0.0e+00
Match length	535
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	128149
Contig ID	27743_1.R1010
5'-most EST	jC-alXLIB327436P1d01b1
Method	BLASTX
NCBI GI	g2979550
BLAST score	469
E value	6.0e-47
Match length	109
% identity	85
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	128150
Contig ID	27744_1.R1010
5'-most EST	LIB25-012-Q1-E1-A1
Method	BLASTX
NCBI GI	g3746071
BLAST score	380
E value	1.0e-36
Match length	122
% identity	63
NCBI Description	(AC005311) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	128151
Contig ID	27747_1.R1010
5'-most EST	jC-alXLIB327436P1a06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	6.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128152
Contig ID	27749_2.R1010
5'-most EST	jC-alXLIB327436P1a07b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	130
E value	1.0e-66
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128153
Contig ID	27755_1.R1010
5'-most EST	jC-alXLIB327436P1a05b1
Method	BLASTX
NCBI GI	g2827039
BLAST score	665
E value	6.0e-70
Match length	133
% identity	99
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	128154
Contig ID	27765_1.R1010
5'-most EST	jC-alXLIB327435P4a04b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	8.0e-10
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	128155
Contig ID	27770_1.R1010
5'-most EST	jC-alXLIB327436P1b02b1
Method	BLASTX
NCBI GI	g1705678
BLAST score	115
E value	2.0e-05
Match length	144
% identity	33
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
valosin-containing protein [Glycine max]

Seq. No.	128156
Contig *ID*	27775_1.R1010
5'-most EST	g2759931
Method	BLASTX
NCBI GI	g4455293
BLAST score	266
E value	4.0e-23
Match length	124
% identity	56
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	128157
Contig ID	27775_2.R1010
5'-most EST	jC-alXLIB327435P2b01a1
Method	BLASTX
NCBI GI	g4455293
BLAST score	182
E value	3.0e-13
Match length	51
% identity	75
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	128158
Contig ID	27777_1.R1010
5'-most EST	LIB25-012-Q1-E1-D1
Method	BLASTN
NCBI GI	g3176701
BLAST score	33
E value	7.0e-09
Match length	85
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128159
Contig ID	27782_1.R1010
5'-most EST	jC-alXLIB327434P1g01b1
Method	BLASTN
NCBI GI	g1402874
BLAST score	172
E value	9.0e-92
Match length	474
% identity	100
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	128160
Contig ID	27783_1.R1010
5'-most EST	jC-alXLIB327435P4b02a1
Method	BLASTN
NCBI GI	g2564049
BLAST score	354
E value	0.0e+00
Match length	436
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.	128161
Contig ID	27783_2.R1010
5'-most EST	jC-alXLIB327435P4b02b1
Method	BLASTX
NCBI GI	g4539330
BLAST score	226
E value	3.0e-18
Match length	169
% identity	33
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]
Seq. No.	128162
Contig ID	27793_1.R1010
5'-most EST	jC-alXLIB327435P3b10b1
Method	BLASTX
NCBI GI	g1097877
BLAST score	606
E value	1.0e-62
Match length	266
% identity	51
NCBI Description	aminolevulinate dehydratase [Lycopersicon esculentum]
Seq. No.	128163
Contig ID	27799_1.R1010
5'-most EST	jC-alXLIB327435P4b09b1
Method	BLASTX
NCBI GI	g4455015
BLAST score	166
E value	3.0e-11
Match length	179
% identity	12
NCBI Description	(AF113131) host cell factor homolog LCP [Homo sapiens]
Seq. No.	128164
Contig ID	27804_1.R1010
5'-most EST	jC-alXLIB327435P2c07a1
Method	BLASTX
NCBI GI	g4406767
BLAST score	632
E value	5.0e-66
Match length	120
% identity	100
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]
Seq. No.	128165
Contig ID	27808_1.R1010
5'-most EST	jC-alXLIB327436P1c05b1
Method	BLASTN
NCBI GI	g3241924
BLAST score	170
E value	1.0e-90
Match length	437

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	128166
Contig ID	27828_1.R1010
5'-most EST	jC-alXLIB327435P3c11b1
Method	BLASTN
NCBI GI	g3402745
BLAST score	390
E value	0.0e+00
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	128167
Contig ID	27829_1.R1010
5'-most EST	LIB25-012-Q1-E1-H7
Method	BLASTX
NCBI GI	g3096922
BLAST score	418
E value	1.0e-40
Match length	225
% identity	42
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	128168
Contig ID	27832_1.R1010
5'-most EST	LIB3176-090-P1-K1-H7
Method	BLASTX
NCBI GI	g2317725
BLAST score	147
E value	8.0e-09
Match length	180
% identity	27
NCBI Description	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]

Seq. No.	128169
Contig ID	27837_1.R1010
5'-most EST	LIB25-013-Q1-E1-A5
Method	BLASTN
NCBI GI	g3869072
BLAST score	188
E value	1.0e-101
Match length	192
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	128170
Contig ID	27840_1.R1010
5'-most EST	jC-alXLIB327434P3h12b1
Method	BLASTX
NCBI GI	g4432855
BLAST score	793

E value	1.0e-90
Match length	217
% identity	88
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	128171
Contig ID	27841_1.R1010
5'-most EST	jC-alXLIB327436P1a11b1
Method	BLASTN
NCBI GI	g3985949
BLAST score	159
E value	5.0e-84
Match length	349
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	128172
Contig ID	27842_1.R1010
5'-most EST	jC-alXLIB327435P2a12a1

Seq. No.	128173
Contig ID	27843_1.R1010
5'-most EST	g2749452
Method	BLASTN
NCBI GI	g3869067
BLAST score	326
E value	0.0e+00
Match length	429
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	128174
Contig ID	27843_2.R1010
5'-most EST	jC-alXLIB327436P1a12b1
Method	BLASTX
NCBI GI	g1651865
BLAST score	175
E value	3.0e-12
Match length	91
% identity	48
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	128175
Contig ID	27848_1.R1010
5'-most EST	LIB25-013-Q1-E1-B7
Method	BLASTN
NCBI GI	g4646215
BLAST score	102
E value	7.0e-50
Match length	657
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T22O13 genomic sequence, complete sequence

Seq. No. 128176

Contig ID	27853_1.R1010
5'-most EST	jC-alXLIB327435P4a10b1
Method	BLASTX
NCBI GI	g3135252
BLAST score	577
E value	1.0e-62
Match length	164
% identity	40
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana] >gi_3176720 (AC002392) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128177
Contig ID	27863_1.R1010
5'-most EST	jC-alXLIB327435P2b08a1
Method	BLASTX
NCBI GI	g3046705
BLAST score	709
E value	8.0e-75
Match length	159
% identity	88
NCBI Description	(AL022198) ribosomal protein S11 - like (partial) [Arabidopsis thaliana]

Seq. No.	128178
Contig ID	27877_1.R1010
5'-most EST	LIB25-013-Q1-E1-E6
Method	BLASTN
NCBI GI	g3859658
BLAST score	266
E value	1.0e-148
Match length	486
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	128179
Contig ID	27880_1.R1010
5'-most EST	jC-alXLIB327435P4b04b1
Method	BLASTX
NCBI GI	g2586083
BLAST score	212
E value	5.0e-21
Match length	151
% identity	6
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	128180
Contig ID	27884_1.R1010
5'-most EST	jC-alXLIB327436P1c01b1
Method	BLASTX
NCBI GI	g2245125
BLAST score	354
E value	4.0e-33
Match length	94
% identity	78

NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	128181
Contig ID	27892_1.R1010
5'-most EST	ARABLI-019-Q1-B1-B4
Seq. No.	128182
Contig ID	27895_1.R1010
5'-most EST	jC-alXLIB327435P2c08a1
Method	BLASTX
NCBI GI	g4512678
BLAST score	696
E value	2.0e-73
Match length	143
% identity	99
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]
Seq. No.	128183
Contig ID	27897_1.R1010
5'-most EST	jC-alXLIB327435P2c09a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	128184
Contig ID	27901_1.R1010
5'-most EST	jC-alXLIB327435P4c06b1
Method	BLASTX
NCBI GI	g3421376
BLAST score	176
E value	2.0e-12
Match length	151
% identity	30
NCBI Description	(AF080399) mitotic checkpoint control protein kinase BUB1 [Drosophila melanogaster]
Seq. No.	128185
Contig ID	27906_1.R1010
5'-most EST	jC-alXLIB327434P3h10b1
Method	BLASTX
NCBI GI	g3834316
BLAST score	1180
E value	1.0e-130
Match length	224
% identity	98
NCBI Description	(AC005679) Similar to gb_X16648 pathogenesis related protein from Hordeum vulgare. EST gb_Z18206 comes from this gene. [Arabidopsis thaliana]
Seq. No.	128186
Contig ID	27911_1.R1010
5'-most EST	jC-alXLIB327436P1a01b1

Method	BLASTX
NCBI GI	g4063749
BLAST score	177
E value	1.0e-12
Match length	95
% identity	23
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128187
Contig ID	27916_1.R1010
5'-most EST	jC-alXLIB327434P4h12b1
Method	BLASTN
NCBI GI	g4589437
BLAST score	550
E value	0.0e+00
Match length	601
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	128188
Contig ID	27917_1.R1010
5'-most EST	jC-alXLIB327435P2a01a1
Method	BLASTX
NCBI GI	g2832664
BLAST score	924
E value	1.0e-100
Match length	194
% identity	94
NCBI Description	(AL021710) pollen-specific protein - like [Arabidopsis thaliana]

Seq. No.	128189
Contig ID	27917_2.R1010
5'-most EST	jC-alX25052Q1E1B02b1
Method	BLASTX
NCBI GI	g2832664
BLAST score	434
E value	6.0e-43
Match length	85
% identity	96
NCBI Description	(AL021710) pollen-specific protein - like [Arabidopsis thaliana]

Seq. No.	128190
Contig ID	27922_1.R1010
5'-most EST	jC-alXLIB327435P2a09a1
Method	BLASTX
NCBI GI	g4263712
BLAST score	627
E value	4.0e-65
Match length	144
% identity	87
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 128191

Contig ID	27931_1.R1010
5'-most EST	jC-alXLIB327435P3a08b1
Method	BLASTX
NCBI GI	g4102839
BLAST score	358
E value	9.0e-34
Match length	148
% identity	49
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	128192
Contig ID	27932_1.R1010
5'-most EST	jC-alXLIB327435P4a09b1
Method	BLASTX
NCBI GI	g2145356
BLAST score	923
E value	1.0e-100
Match length	178
% identity	99
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	128193
Contig ID	27935_1.R1010
5'-most EST	jC-alXLIB327436P1b03b1

Seq. No.	128194
Contig ID	27938_1.R1010
5'-most EST	LIB35-042-Q1-E1-B12
Method	BLASTX
NCBI GI	g2245115
BLAST score	259
E value	3.0e-22
Match length	52
% identity	94
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	128195
Contig ID	27938_2.R1010
5'-most EST	jC-alXLIB327436P1b07b1
Method	BLASTX
NCBI GI	g2245114
BLAST score	476
E value	5.0e-62
Match length	163
% identity	82
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128196
Contig ID	27938_3.R1010
5'-most EST	jC-alXLIB327436P3f04b1
Method	BLASTX
NCBI GI	g4539454
BLAST score	273
E value	1.0e-23
Match length	108
% identity	48

NCBI Description	(AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]

Seq. No.	128197
Contig ID	27940_1.R1010
5'-most EST	jC-alXLIB327436P1b08b1
Method	BLASTX
NCBI GI	g4567282
BLAST score	559
E value	2.0e-57
Match length	128
% identity	84
NCBI Description	(AC006841) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	128198
Contig ID	27942_1.R1010
5'-most EST	LIB3168-045-P1-K1-H3
Method	BLASTX
NCBI GI	g1723275
BLAST score	281
E value	8.0e-25
Match length	111
% identity	52
NCBI Description	HYPOTHETICAL 55.6 KD PROTEIN C13F4.15C IN CHROMOSOME I >gi_2130223_pir__S67390 hypothetical protein - fission yeast (Schizosaccharomyces pombe) >gi_3451294_emb_CAA20426_ (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]

Seq. No.	128199
Contig ID	27952_1.R1010
5'-most EST	jC-atXP86CG9E12T7b1
Method	BLASTX
NCBI GI	g2580440
BLAST score	231
E value	1.0e-18
Match length	59
% identity	73
NCBI Description	(D87261) PCF2 [Oryza sativa]

Seq. No.	128200
Contig ID	27953_1.R1010
5'-most EST	jC-alXLIB327435P4b06b1
Method	BLASTX
NCBI GI	g4325351
BLAST score	124
E value	2.0e-11
Match length	116
% identity	41
NCBI Description	(AF128394) similar to Antirrhinum majus (garden snapdragon) TNP2 protein (GB:X57297) [Arabidopsis thaliana]

Seq. No.	128201
Contig ID	27962_1.R1010
5'-most EST	jC-alXLIB327436P1c02b1

Seq. No.	128202
Contig ID	27966_1.R1010

5'-most EST	jC-alXLIB327435P2c01a1
Method	BLASTN
NCBI GI	g2760169
BLAST score	651
E value	0.0e+00
Match length	675
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	128203
Contig ID	27970_2.R1010
5'-most EST	LIB3176-007-P1-K1-G1
Method	BLASTN
NCBI GI	g3810584
BLAST score	366
E value	0.0e+00
Match length	722
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128204
Contig ID	27974_1.R1010
5'-most EST	jC-alXLIB327436P1c08b1
Method	BLASTX
NCBI GI	g3193316
BLAST score	359
E value	5.0e-34
Match length	85
% identity	87
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	128205
Contig ID	27976_1.R1010
5'-most EST	jC-alXLIB327436P1c09b1
Method	BLASTX
NCBI GI	g4432844
BLAST score	666
E value	1.0e-69
Match length	179
% identity	73
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	128206
Contig ID	27980_1.R1010
5'-most EST	jC-alXLIB327435P4c08b1
Method	BLASTX
NCBI GI	g2623295
BLAST score	708
E value	8.0e-75
Match length	137
% identity	99
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 128207

Contig ID	27982_1.R1010
5'-most EST	jC-atXLIB327421P2f02b1
Method	BLASTN
NCBI GI	g4539290
BLAST score	305
E value	1.0e-171
Match length	448
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	128208
Contig ID	27989_1.R1010
5'-most EST	LIB25-015-Q1-E1-A10
Method	BLASTN
NCBI GI	g3108024
BLAST score	556
E value	0.0e+00
Match length	662
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128209
Contig ID	27992_1.R1010
5'-most EST	jC-alXLIB327436P1d10b1
Method	BLASTX
NCBI GI	g2435395
BLAST score	401
E value	2.0e-87
Match length	183
% identity	83
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	128210
Contig ID	27995_1.R1010
5'-most EST	jC-atXP53C185F10T7079d1
Method	BLASTX
NCBI GI	g3482924
BLAST score	507
E value	1.0e-59
Match length	137
% identity	88
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	128211
Contig ID	27999_1.R1010
5'-most EST	jC-alXLIB327435P2d08a1
Method	BLASTX
NCBI GI	g4406777
BLAST score	282
E value	6.0e-25
Match length	55
% identity	95
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	128212
Contig ID	28003_1.R1010
5'-most EST	jC-alXLIB327435P3d07b1
Method	BLASTX
NCBI GI	g1771162
BLAST score	673
E value	1.0e-70
Match length	196
% identity	68
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	128213
Contig ID	28004_1.R1010
5'-most EST	jC-alXLIB327435P4d05b1
Method	BLASTX
NCBI GI	g2262143
BLAST score	161
E value	2.0e-10
Match length	116
% identity	44
NCBI Description	(AC002330) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	128214
Contig ID	28004_2.R1010
5'-most EST	g2749648
Method	BLASTX
NCBI GI	g2795805
BLAST score	164
E value	4.0e-11
Match length	61
% identity	51
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	128215
Contig ID	28011_1.R1010
5'-most EST	jC-atXLIB327418P4c10b1
Method	BLASTX
NCBI GI	g400983
BLAST score	407
E value	2.0e-39
Match length	139
% identity	66
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	128216
Contig ID	28013_1.R1010
5'-most EST	jC-alXLIB327435P2e01a1

Seq. No.	128217
Contig ID	28017_1.R1010
5'-most EST	LIB3176-087-P1-K1-D2
Method	BLASTN
NCBI GI	g4757407
BLAST score	387
E value	0.0e+00
Match length	541
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	128218
Contig ID	28026_1.R1010
5'-most EST	jC-atXLIB327421P4d06b1
Method	BLASTX
NCBI GI	g4337202
BLAST score	535
E value	2.0e-54
Match length	186
% identity	63
NCBI Description	(AC006403) putative endosperm-specific protein [Arabidopsis thaliana]

Seq. No.	128219
Contig ID	28026_2.R1010
5'-most EST	jC-alXLIB327435P4f02b1
Method	BLASTX
NCBI GI	g4337202
BLAST score	871
E value	8.0e-94
Match length	217
% identity	84
NCBI Description	(AC006403) putative endosperm-specific protein [Arabidopsis thaliana]

Seq. No.	128220
Contig ID	28027_1.R1010
5'-most EST	jC-alXLIB327436P1e10b1
Method	BLASTX
NCBI GI	g3822225
BLAST score	748
E value	2.0e-79
Match length	156
% identity	91
NCBI Description	(AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]

Seq. No.	128221
Contig ID	28027_2.R1010
5'-most EST	g936788
Method	BLASTN
NCBI GI	g3822224
BLAST score	205
E value	1.0e-111
Match length	287
% identity	95

NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHG1a mRNA, partial cds
Seq. No.	128222
Contig ID	28031_1.R1010
5'-most EST	jC-alXLIB327435P2e08a1
Method	BLASTX
NCBI GI	g2464855
BLAST score	313
E value	2.0e-28
Match length	75
% identity	84
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]
Seq. No.	128223
Contig ID	28034_1.R1010
5'-most EST	jC-alXLIB327435P2e09a1
Method	BLASTN
NCBI GI	g2494106
BLAST score	422
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	128224
Contig ID	28035_1.R1010
5'-most EST	jC-alXLIB327435P4e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	65
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	128225
Contig ID	28040_1.R1010
5'-most EST	LIB25-015-Q1-E1-E3
Method	BLASTX
NCBI GI	g3618320
BLAST score	340
E value	8.0e-32
Match length	93
% identity	67
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]
Seq. No.	128226
Contig ID	28041_1.R1010
5'-most EST	jC-alXLIB327435P3e08b1
Method	BLASTN
NCBI GI	g3860243
BLAST score	325
E value	0.0e+00
Match length	579

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128227
Contig ID	28041_2.R1010
5'-most EST	LIB3177-005-P1-K2-F1
Method	BLASTN
NCBI GI	g3860243
BLAST score	382
E value	0.0e+00
Match length	782
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128228
Contig ID	28042_1.R1010
5'-most EST	jC-alXLIB327435P3e05b1
Method	BLASTX
NCBI GI	g2827039
BLAST score	900
E value	3.0e-97
Match length	199
% identity	92
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	128229
Contig ID	28045_1.R1010
5'-most EST	LIB25-015-Q1-E1-F1
Method	BLASTX
NCBI GI	g4539333
BLAST score	711
E value	5.0e-75
Match length	215
% identity	92
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No.	128230
Contig ID	28058_1.R1010
5'-most EST	jC-alXLIB327436P1f12b1
Method	BLASTN
NCBI GI	g2351071
BLAST score	268
E value	1.0e-149
Match length	738
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	128231
Contig ID	28060_1.R1010
5'-most EST	jC-alXLIB327435P3f01b1
Method	BLASTN
NCBI GI	g3513725

BLAST score	442
E value	0.0e+00
Match length	560
% identity	100
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	128232
Contig ID	28063_1.R1010
5'-most EST	jC-alXLIB327435P2f09a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128233
Contig ID	28065_1.R1010
5'-most EST	jC-atXLIB327421P3b03b1

Seq. No.	128234
Contig ID	28065_2.R1010
5'-most EST	jC-atXLIB327421P3b03a1

Seq. No.	128235
Contig ID	28068_1.R1010
5'-most EST	jC-alXLIB327435P3f09b1

Seq. No.	128236
Contig ID	28098_1.R1010
5'-most EST	LIB3176-097-P1-K1-C11
Method	BLASTX
NCBI GI	g2213602
BLAST score	1157
E value	1.0e-127
Match length	246
% identity	92
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	128237
Contig ID	28099_1.R1010
5'-most EST	jC-alXLIB327436P1e01b1
Method	BLASTN
NCBI GI	g2252848
BLAST score	543
E value	0.0e+00
Match length	575
% identity	96
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	128238
Contig ID	28110_1.R1010
5'-most EST	jC-alXLIB327436P1e09b1
Method	BLASTN
NCBI GI	g4757407

BLAST score	337
E value	0.0e+00
Match length	802
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	128239
Contig ID	28113_1.R1010
5'-most EST	jC-alXLIB327436P1e11b1

Seq. No.	128240
Contig ID	28117_1.R1010
5'-most EST	jC-alXLIB327436P1e08b1
Method	BLASTN
NCBI GI	g3449326
BLAST score	315
E value	1.0e-177
Match length	443
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	128241
Contig ID	28121_1.R1010
5'-most EST	jC-atXLIB327424P4b11b1
Method	BLASTX
NCBI GI	g4337025
BLAST score	666
E value	9.0e-70
Match length	129
% identity	100
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	128242
Contig ID	28124_1.R1010
5'-most EST	jC-alXLIB327435P4e08b1
Method	BLASTX
NCBI GI	g3292817
BLAST score	264
E value	5.0e-24
Match length	149
% identity	48
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128243
Contig ID	28125_1.R1010
5'-most EST	jC-alXLIB327435P4e09b1
Method	BLASTN
NCBI GI	g2656026
BLAST score	523
E value	0.0e+00
Match length	582
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	128244
Contig ID	28125_2.R1010
5'-most EST	g2722681
Method	BLASTN
NCBI GI	g2656026
BLAST score	126
E value	1.0e-64
Match length	223
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	128245
Contig ID	28129_1.R1010
5'-most EST	LIB25-016-Q1-E1-E8
Method	BLASTX
NCBI GI	g3901294
BLAST score	257
E value	8.0e-22
Match length	75
% identity	68
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	128246
Contig ID	28129_2.R1010
5'-most EST	jC-atXLIB327421P4e10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	6.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128247
Contig ID	28131_1.R1010
5'-most EST	jC-alXLIB327435P3e04b1
Method	BLASTX
NCBI GI	g2463509
BLAST score	595
E value	1.0e-61
Match length	163
% identity	69
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	128248
Contig ID	28139_1.R1010
5'-most EST	jC-atXLIB327438P1c08a1
Method	BLASTN
NCBI GI	g4049332
BLAST score	184
E value	5.0e-99
Match length	383
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	128249
Contig ID	28141_1.R1010
5'-most EST	jC-alXLIB327435P2f03a1
Method	BLASTN
NCBI GI	g2459406
BLAST score	330
E value	0.0e+00
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128250
Contig ID	28148_1.R1010
5'-most EST	g1520839
Method	BLASTX
NCBI GI	g3892056
BLAST score	380
E value	2.0e-36
Match length	82
% identity	96
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	128251
Contig ID	28148_2.R1010
5'-most EST	g936744
Method	BLASTX
NCBI GI	g3892056
BLAST score	635
E value	4.0e-66
Match length	128
% identity	100
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	128252
Contig ID	28148_3.R1010
5'-most EST	ARABL1-038-Q1-E1-E7
Method	BLASTX
NCBI GI	g2275216
BLAST score	206
E value	3.0e-16
Match length	52
% identity	75
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]

Seq. No.	128253
Contig ID	28149_1.R1010
5'-most EST	jC-alXLIB327436P1f08b1
Method	BLASTX
NCBI GI	g481032
BLAST score	309
E value	2.0e-31
Match length	115
% identity	67
NCBI Description	drought-induced protein BnD22 - rape

>gi_17813_emb_CAA46591_ (X65637) BnD22 drought induced protein [Brassica napus]

Seq. No.	128254
Contig ID	28155_1.R1010
5'-most EST	jC-alXLIB327435P4f09b1
Method	BLASTN
NCBI GI	g4519191
BLAST score	196
E value	1.0e-106
Match length	575
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	128255
Contig ID	28158_1.R1010
5'-most EST	jC-alXLIB327435P4f10b1
Method	BLASTN
NCBI GI	g3449330
BLAST score	518
E value	0.0e+00
Match length	564
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	128256
Contig ID	28174_1.R1010
5'-most EST	jC-atXLIB327431P3h07a1
Method	BLASTN
NCBI GI	g3406034
BLAST score	184
E value	1.0e-98
Match length	798
% identity	99
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128257
Contig ID	28181_1.R1010
5'-most EST	g2758160

Seq. No.	128258
Contig ID	28183_1.R1010
5'-most EST	LIB25-025-Q1-E1-B6
Method	BLASTN
NCBI GI	g4589421
BLAST score	156
E value	2.0e-82
Match length	352
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	128259
Contig ID	28184_1.R1010

5'-most EST	jC-alXLIB327436P2a10b1
Method	BLASTX
NCBI GI	g3805763
BLAST score	227
E value	3.0e-44
Match length	220
% identity	50
NCBI Description	(AC005693) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128260
Contig ID	28195_1.R1010
5'-most EST	LIB25-017-Q1-E1-D12
Method	BLASTX
NCBI GI	g4581116
BLAST score	301
E value	2.0e-27
Match length	92
% identity	68
NCBI Description	(AC005825) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	128261
Contig ID	28197_1.R1010
5'-most EST	LIB3176-106-P1-K1-E1

Seq. No.	128262
Contig ID	28211_1.R1010
5'-most EST	LIB25-022-Q1-E1-C11
Method	BLASTX
NCBI GI	g4115381
BLAST score	698
E value	7.0e-74
Match length	142
% identity	96
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No.	128263
Contig ID	28214_1.R1010
5'-most EST	jC-alXLIB327435P2f01a1
Method	BLASTX
NCBI GI	g1730915
BLAST score	153
E value	7.0e-10
Match length	152
% identity	19
NCBI Description	HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC REGION >gi_1146219 (L47648) similar to Escherichia coli GTP-binding protein Era; putative [Bacillus subtilis] >gi_2634702_emb_CAB14200_ (Z99115) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	128264
Contig ID	28224_1.R1010
5'-most EST	jC-alXLIB327435P4f05b1
Method	BLASTX
NCBI GI	g2911086
BLAST score	968

E value	1.0e-105
Match length	193
% identity	35
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	128265
Contig ID	28229_1.R1010
5'-most EST	jC-alXLIB327435P3f03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	71
E value	2.0e-31
Match length	71
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128266
Contig ID	28233_1.R1010
5'-most EST	jC-alXLIB327436P1d05b1

Seq. No.	128267
Contig ID	28239_1.R1010
5'-most EST	jC-alX25028Q1E1D11b1
Method	BLASTX
NCBI GI	g3309082
BLAST score	767
E value	1.0e-81
Match length	163
% identity	90
NCBI Description	(AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No.	128268
Contig ID	28240_1.R1010
5'-most EST	g2048281
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	128269
Contig ID	28242_1.R1010
5'-most EST	jC-alXLIB327436P1d12b1
Method	BLASTX
NCBI GI	g481132
BLAST score	421
E value	4.0e-41
Match length	129
% identity	66
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	128270
Contig ID	28247_1.R1010
5'-most EST	jC-alXLIB327435P3d04b1
Method	BLASTX
NCBI GI	g3850585
BLAST score	470
E value	6.0e-47
Match length	129
% identity	78
NCBI Description	(AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and gb_T20569 come from this gene. [Arabidopsis thaliana]

Seq. No.	128271
Contig ID	28253_1.R1010
5'-most EST	jC-alXLIB327435P3d10b1
Method	BLASTX
NCBI GI	g3646326
BLAST score	233
E value	4.0e-19
Match length	70
% identity	66
NCBI Description	(AJ000762) MADS-box protein [Malus domestica]

Seq. No.	128272
Contig ID	28256_1.R1010
5'-most EST	jC-alXLIB327435P4d11b1
Method	BLASTN
NCBI GI	g2924651
BLAST score	285
E value	1.0e-159
Match length	804
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	128273
Contig ID	28257_1.R1010
5'-most EST	jC-alXLIB327435P3d11b1
Method	BLASTN
NCBI GI	g2252848
BLAST score	285
E value	1.0e-159
Match length	558
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	128274
Contig ID	28258_1.R1010
5'-most EST	jC-alXLIB327435P4d12b1
Method	BLASTN
NCBI GI	g4263753
BLAST score	379
E value	0.0e+00
Match length	816
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128275
Contig ID	28268_1.R1010
5'-most EST	jC-alXLIB327435P2e07a1
Method	BLASTX
NCBI GI	g1064887
BLAST score	166
E value	2.0e-11
Match length	65
% identity	48
NCBI Description	(X92955) pollen coat protein [Brassica oleracea]

Seq. No.	128276
Contig ID	28269_1.R1010
5'-most EST	jC-alXLIB327436P1e04b1
Method	BLASTX
NCBI GI	g2894598
BLAST score	498
E value	4.0e-50
Match length	140
% identity	71
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	128277
Contig ID	28271_1.R1010
5'-most EST	jC-alXLIB327435P2e05a1
Method	BLASTN
NCBI GI	g2213606
BLAST score	463
E value	0.0e+00
Match length	791
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	128278
Contig ID	28274_1.R1010
5'-most EST	jC-alXLIB327435P4e02b1
Method	BLASTX
NCBI GI	g2832300
BLAST score	343
E value	1.0e-42
Match length	119
% identity	75
NCBI Description	(AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus roseus]

Seq. No.	128279
Contig ID	28278_1.R1010
5'-most EST	jC-alXLIB327435P4e04b1
Method	BLASTX
NCBI GI	g4006924
BLAST score	1434
E value	1.0e-160
Match length	263
% identity	99
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No.	128280
Contig ID	28282_1.R1010
5'-most EST	jC-atXLIB327427P1c02b1
Method	BLASTX
NCBI GI	g4378848
BLAST score	359
E value	5.0e-34
Match length	123
% identity	56
NCBI Description	(AF124349) hydrolase [Zymomonas mobilis]

Seq. No.	128281
Contig ID	28305_1.R1010
5'-most EST	jC-alXLIB327435P3f05b1
Method	BLASTN
NCBI GI	g4490291
BLAST score	274
E value	1.0e-152
Match length	563
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	128282
Contig ID	28312_1.R1010
5'-most EST	jC-alXLIB327435P4f04b1

Seq. No.	128283
Contig ID	28315_1.R1010
5'-most EST	LIB25-019-Q1-E1-A10
Method	BLASTX
NCBI GI	g3461828
BLAST score	414
E value	1.0e-40
Match length	110
% identity	65
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	128284
Contig ID	28317_1.R1010
5'-most EST	jC-atXLIB327430P4c11b1
Method	BLASTN
NCBI GI	g2351062
BLAST score	356
E value	0.0e+00
Match length	807
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	128285
Contig ID	28327_1.R1010
5'-most EST	LIB25-019-Q1-E1-B10
Method	BLASTX
NCBI GI	g3413717

BLAST score	761
E value	4.0e-81
Match length	165
% identity	91
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643590 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	128286
Contig ID	28334_1.R1010
5'-most EST	LIB25-019-Q1-E1-B8
Method	BLASTX
NCBI GI	g3184283
BLAST score	691
E value	2.0e-72
Match length	155
% identity	93
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	128287
Contig ID	28337_1.R1010
5'-most EST	jC-atXLIB327423P1h12b1
Method	BLASTX
NCBI GI	g3980393
BLAST score	318
E value	6.0e-29
Match length	192
% identity	36
NCBI Description	(AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	128288
Contig ID	28345_1.R1010
5'-most EST	jC-alXLIB327435P4c07b1
Method	BLASTN
NCBI GI	g2708736
BLAST score	681
E value	0.0e+00
Match length	706
% identity	99
NCBI Description	Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128289
Contig ID	28346_1.R1010
5'-most EST	jC-atXLIB327420P4g01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	6.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	128290
Contig ID	28346_2.R1010

5'-most EST	jC-atXLIB327423P3h11b1
Method	BLASTN
NCBI GI	g2494106
BLAST score	129
E value	4.0e-66
Match length	304
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128291
Contig ID	28347_1.R1010
5'-most EST	jC-atXLIB327414P3a04b1
Method	BLASTX
NCBI GI	g2827712
BLAST score	533
E value	2.0e-54
Match length	91
% identity	99
NCBI Description	(AL021684) endoxyloglucan tranferase-like protein [Arabidopsis thaliana]

Seq. No.	128292
Contig ID	28348_1.R1010
5'-most EST	jC-atXLIB327424P1a08a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	65
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128293
Contig ID	28359_1.R1010
5'-most EST	LIB3177-076-P1-K1-G4
Method	BLASTN
NCBI GI	g3241922
BLAST score	19
E value	1.2e+00
Match length	347
% identity	73
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	128294
Contig ID	28364_1.R1010
5'-most EST	jC-atX25019Q1E1E07b1
Method	BLASTX
NCBI GI	g3776577
BLAST score	255
E value	1.0e-21
Match length	124
% identity	44
NCBI Description	(AC005388) T22H22.24 [Arabidopsis thaliana]

Seq. No.	128295
Contig ID	28369_1.R1010
5'-most EST	LIB25-019-Q1-E1-F11
Method	BLASTN
NCBI GI	g3869069
BLAST score	376
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	128296
Contig ID	28375_1.R1010
5'-most EST	g4210259
Method	BLASTX
NCBI GI	g3212862
BLAST score	510
E value	2.0e-51
Match length	120
% identity	87
NCBI Description	(AC004005) putative riboflavin synthase [Arabidopsis thaliana]

Seq. No.	128297
Contig ID	28379_1.R1010
5'-most EST	jC-atX25023Q1E1H08b1
Method	BLASTN
NCBI GI	g4220510
BLAST score	279
E value	1.0e-156
Match length	295
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	128298
Contig ID	28380_1.R1010
5'-most EST	jC-atXLIB327403P3a05b2
Method	BLASTN
NCBI GI	g4580454
BLAST score	445
E value	0.0e+00
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	128299
Contig ID	28385_1.R1010
5'-most EST	jC-atXLIB327424P1b03b2
Method	BLASTX
NCBI GI	g2582351
BLAST score	299
E value	4.0e-27
Match length	103
% identity	49

NCBI Description (AF018639) unknown [Dictyostelium discoideum]

Seq. No. 128300
Contig ID 28386_1.R1010
5'-most EST LIB3176-021-P1-K1-B9
Method BLASTX
NCBI GI g1703220
BLAST score 477
E value 1.0e-47
Match length 164
% identity 53
NCBI Description AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No. 128301
Contig ID 28386_2.R1010
5'-most EST LIB25-019-Q1-E1-G5
Method BLASTX
NCBI GI g1703220
BLAST score 112
E value 1.0e-19
Match length 95
% identity 54
NCBI Description AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No. 128302
Contig ID 28386_3.R1010
5'-most EST jC-atXLIB327424P1b04a1
Method BLASTX
NCBI GI g1703220
BLAST score 210
E value 1.0e-16
Match length 66
% identity 56
NCBI Description AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No. 128303
Contig ID 28395_1.R1010
5'-most EST LIB25-105-Q1-E1-C9
Method BLASTX
NCBI GI g3980380
BLAST score 546
E value 4.0e-56
Match length 112
% identity 98
NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]

Seq. No. 128304
Contig ID 28411_1.R1010
5'-most EST jC-atXLIB327423P3g10b1
Method BLASTN
NCBI GI g2760172
BLAST score 222
E value 1.0e-121
Match length 466

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	128305
Contig ID	28413_1.R1010
5'-most EST	jC-atXLIB327423P4g11b1
Method	BLASTN
NCBI GI	g2749918
BLAST score	415
E value	0.0e+00
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128306
Contig ID	28419_1.R1010
5'-most EST	jC-atXLIB327423P4g09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	5.0e-13
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128307
Contig ID	28421_2.R1010
5'-most EST	jC-atX25020Q1E1C01b1
Method	BLASTX
NCBI GI	g3176717
BLAST score	166
E value	2.0e-11
Match length	96
% identity	36
NCBI Description	(AC002392) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	128308
Contig ID	28422_1.R1010
5'-most EST	g2393203

Seq. No.	128309
Contig ID	28427_1.R1010
5'-most EST	LIB25-020-Q1-E1-C5
Method	BLASTX
NCBI GI	g2245125
BLAST score	436
E value	4.0e-43
Match length	138
% identity	67
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128310
Contig ID	28429_1.R1010
5'-most EST	ARABL1-020-Q1-B1-H12

Method	BLASTX
NCBI GI	g3738332
BLAST score	620
E value	8.0e-65
Match length	119
% identity	100
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]

Seq. No.	128311
Contig ID	28430_1.R1010
5'-most EST	jC-alXLIB327436P3a02a1
Method	BLASTX
NCBI GI	g3874563
BLAST score	219
E value	1.0e-17
Match length	81
% identity	54
NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No.	128312
Contig ID	28442_1.R1010
5'-most EST	jC-atXLIB327423P4h10b1
Method	BLASTN
NCBI GI	g2494106
BLAST score	341
E value	0.0e+00
Match length	487
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128313
Contig ID	28443_1.R1010
5'-most EST	jC-alXLIB327436P2e03b1
Method	BLASTX
NCBI GI	g4220526
BLAST score	214
E value	5.0e-17
Match length	113
% identity	42
NCBI Description	(AL035356) Bnm1 like protein [Arabidopsis thaliana]

Seq. No.	128314
Contig ID	28447_1.R1010
5'-most EST	jC-atXLIB327403P3a09b1
Method	BLASTX
NCBI GI	g2244866
BLAST score	195

E value	8.0e-15
Match length	116
% identity	31
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128315
Contig ID	28452_1.R1010
5'-most EST	jC-atXLIB327403P3a07b1
Method	BLASTX
NCBI GI	g4580394
BLAST score	464
E value	4.0e-49
Match length	123
% identity	75
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	128316
Contig ID	28460_1.R1010
5'-most EST	jC-atXLIB327417P1d07b1
Method	BLASTX
NCBI GI	g3096944
BLAST score	531
E value	6.0e-54
Match length	106
% identity	97
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	128317
Contig ID	28461_1.R1010
5'-most EST	LIB25-020-Q1-E1-F4
Method	BLASTX
NCBI GI	g4726118
BLAST score	350
E value	3.0e-33
Match length	99
% identity	73
NCBI Description	(AC006436) putative somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]

Seq. No.	128318
Contig ID	28466_1.R1010
5'-most EST	jC-atXLIB327424P1b01b2
Method	BLASTN
NCBI GI	g4038029
BLAST score	340
E value	0.0e+00
Match length	457
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128319
Contig ID	28472_1.R1010
5'-most EST	LIB25-020-Q1-E1-G4
Method	BLASTX
NCBI GI	g4006853

BLAST score 542
E value 1.0e-55
Match length 129
% identity 84
NCBI Description (Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No. 128320
Contig ID 28477_1.R1010
5'-most EST jC-atXLIB327427P1d09b1

Seq. No. 128321
Contig ID 28486_2.R1010
5'-most EST jC-atX25020Q1E1H08b2
Method BLASTX
NCBI GI g2062169
BLAST score 288
E value 5.0e-26
Match length 108
% identity 37
NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No. 128322
Contig ID 28489_1.R1010
5'-most EST jC-atXLIB327423P1g07b1
Method BLASTX
NCBI GI g4512654
BLAST score 625
E value 8.0e-65
Match length 243
% identity 57
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 128323
Contig ID 28494_1.R1010
5'-most EST jC-atXLIB327423P1g10b1

Seq. No. 128324
Contig ID 28494_2.R1010
5'-most EST jC-alX24077Q1E1C09a1
Method BLASTN
NCBI GI g3510337
BLAST score 43
E value 2.0e-14
Match length 107
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No. 128325
Contig ID 28495_1.R1010
5'-most EST LIB3234-072-P1-K1-E7
Method BLASTX
NCBI GI g2688544
BLAST score 198
E value 4.0e-15

Match length	98
% identity	39
NCBI Description	(AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) [Borrelia burgdorferi]

Seq. No.	128326
Contig ID	28496_1.R1010
5'-most EST	jC-atXLIB327423P2g05b1
Method	BLASTN
NCBI GI	g4249393
BLAST score	234
E value	1.0e-128
Match length	476
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128327
Contig ID	28504_1.R1010
5'-most EST	LIB25-024-Q1-E1-B12
Method	BLASTN
NCBI GI	g1931636
BLAST score	217
E value	1.0e-118
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	128328
Contig ID	28506_1.R1010
5'-most EST	jC-atXP92C246M15T7065d1
Method	BLASTX
NCBI GI	g1174448
BLAST score	563
E value	1.0e-57
Match length	142
% identity	80
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	128329
Contig ID	28506_2.R1010
5'-most EST	LIB25-104-Q1-E1-C1
Method	BLASTX
NCBI GI	g1174448
BLAST score	811
E value	1.0e-86
Match length	173
% identity	93
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	128330
Contig ID	28520_1.R1010
5'-most EST	jC-atXLIB327423P1h03b1
Method	BLASTX
NCBI GI	g3292831
BLAST score	628
E value	3.0e-65
Match length	179
% identity	61
NCBI Description	(AL031018) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	128331
Contig ID	28522_1.R1010
5'-most EST	jC-alX25022Q1E1D09b1
Method	BLASTX
NCBI GI	g2529677
BLAST score	778
E value	3.0e-83
Match length	152
% identity	100
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	128332
Contig ID	28524_1.R1010
5'-most EST	jC-atXLIB327423P3h06b1
Method	BLASTN
NCBI GI	g4519194
BLAST score	225
E value	1.0e-123
Match length	370
% identity	70
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	128333
Contig ID	28525_1.R1010
5'-most EST	jC-atXLIB327423P3h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	3.0e-14
Match length	50
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128334
Contig ID	28531_1.R1010
5'-most EST	jC-atXLIB327430P1d02b1
Method	BLASTX
NCBI GI	g4678301
BLAST score	795
E value	7.0e-85
Match length	202
% identity	77

NCBI Description	(AL049655) pectate lyase-like protein [Arabidopsis thaliana]

Seq. No.	128335
Contig ID	28531_2.R1010
5'-most EST	jC-atXLIB327423P3h04b1
Method	BLASTX
NCBI GI	g4678301
BLAST score	326
E value	3.0e-64
Match length	203
% identity	66
NCBI Description	(AL049655) pectate lyase-like protein [Arabidopsis thaliana]

Seq. No.	128336
Contig ID	28533_1.R1010
5'-most EST	jC-atXLIB327424P1a03b2
Method	BLASTN
NCBI GI	g4584531
BLAST score	309
E value	1.0e-173
Match length	491
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	128337
Contig ID	28553_1.R1010
5'-most EST	ARABLI-15-Q1-B1-D10
Method	BLASTX
NCBI GI	g2505872
BLAST score	382
E value	7.0e-37
Match length	74
% identity	100
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128338
Contig ID	28560_1.R1010
5'-most EST	jC-atXLIB327425P1b03b1
Method	BLASTX
NCBI GI	g3894172
BLAST score	256
E value	7.0e-22
Match length	113
% identity	43
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	128339
Contig ID	28569_1.R1010
5'-most EST	LIB3175-065-P1-K1-E9
Method	BLASTN
NCBI GI	g4309747
BLAST score	236
E value	1.0e-130

Match length	732
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128340
Contig ID	28570_1.R1010
5'-most EST	jC-atXLIB327403P3b06b1
Method	BLASTN
NCBI GI	g2656029
BLAST score	432
E value	0.0e+00
Match length	483
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	128341
Contig ID	28574_1.R1010
5'-most EST	LIB25-022-Q1-E1-A11

Seq. No.	128342
Contig ID	28580_1.R1010
5'-most EST	jC-atXLIB327423P1g05b1

Seq. No.	128343
Contig ID	28582_1.R1010
5'-most EST	jC-atXLIB327423P2g06b1
Method	BLASTX
NCBI GI	g2842493
BLAST score	188
E value	1.0e-28
Match length	108
% identity	66
NCBI Description	(AL021749) predicted protein [Arabidopsis thaliana]

Seq. No.	128344
Contig ID	28590_1.R1010
5'-most EST	g1217352
Method	BLASTX
NCBI GI	g2117725
BLAST score	1227
E value	1.0e-135
Match length	249
% identity	93
NCBI Description	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SBE2.2 precursor - Arabidopsis thaliana (fragment) >gi_726490 (U22428) starch branching enzyme class II [Arabidopsis thaliana]

Seq. No.	128345
Contig ID	28593_2.R1010
5'-most EST	jC-atX25023Q1E1C04b1

Seq. No.	128346
Contig ID	28597_1.R1010
5'-most EST	g2581634

Method	BLASTX
NCBI GI	g4512684
BLAST score	492
E value	2.0e-49
Match length	102
% identity	98
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	128347
Contig ID	28597_2.R1010
5'-most EST	jC-atXLIB327414P2g04a1
Method	BLASTX
NCBI GI	g4512684
BLAST score	697
E value	2.0e-73
Match length	140
% identity	100
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	128348
Contig ID	28600_1.R1010
5'-most EST	jC-atXLIB327423P1h07b1
Method	BLASTN
NCBI GI	g2924651
BLAST score	391
E value	0.0e+00
Match length	506
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	128349
Contig ID	28609_1.R1010
5'-most EST	g906846
Method	BLASTX
NCBI GI	g4415931
BLAST score	669
E value	1.0e-71
Match length	146
% identity	95
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	128350
Contig ID	28610_1.R1010
5'-most EST	jC-atXLIB327423P4h08b1
Method	BLASTN
NCBI GI	g2864607
BLAST score	246
E value	1.0e-136
Match length	453
% identity	97

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	128351
Contig ID	28612_1.R1010
5'-most EST	jC-atXLIB327423P3h08b1
Method	BLASTX
NCBI GI	g2642158
BLAST score	767
E value	1.0e-81
Match length	184
% identity	86
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128352
Contig ID	28613_2.R1010
5'-most EST	jC-atX25022Q1E1D06b1
Method	BLASTX
NCBI GI	g127112
BLAST score	248
E value	3.0e-21
Match length	113
% identity	47
NCBI Description	MAK16 PROTEIN >gi_73269_pir__BVBYK6 MAK16 protein - yeast (Saccharomyces cerevisiae) >gi_171880 (J03852) MAK16 protein [Saccharomyces cerevisiae] >gi_595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]

Seq. No.	128353
Contig ID	28618_1.R1010
5'-most EST	jC-atXLIB327403P3a03b1
Method	BLASTX
NCBI GI	g4587514
BLAST score	282
E value	5.0e-25
Match length	54
% identity	100
NCBI Description	(AC007060) Similar to WO8E3.3 gi_3880615 putative GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No.	128354
Contig ID	28619_1.R1010
5'-most EST	jC-atXLIB327424P1a04b2
Method	BLASTN
NCBI GI	g166645
BLAST score	49
E value	3.0e-18
Match length	66
% identity	93
NCBI Description	Arabidopsis thaliana light-harvesting chlorophyll a/b-binding protein (Cab4) mRNA, complete cds

Seq. No.	128355
Contig ID	28620_1.R1010
5'-most EST	LIB25-022-Q1-E1-E2

Seq. No.	128356
Contig ID	28622_1.R1010
5'-most EST	g957758
Method	BLASTN
NCBI GI	g4558656
BLAST score	304
E value	1.0e-170
Match length	913
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T10F5 genomic sequence, complete sequence

Seq. No.	128357
Contig ID	28630_1.R1010
5'-most EST	LIB25-022-Q1-E1-F9
Method	BLASTN
NCBI GI	g2494106
BLAST score	434
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128358
Contig ID	28631_1.R1010
5'-most EST	LIB25-022-Q1-E1-G12
Method	BLASTX
NCBI GI	g2313304
BLAST score	185
E value	1.0e-13
Match length	76
% identity	43
NCBI Description	(AE000541) sodium-dependent transporter (huNaDC-1) [Helicobacter pylori 26695]

Seq. No.	128359
Contig ID	28643_1.R1010
5'-most EST	g2764188
Method	BLASTN
NCBI GI	g4220638
BLAST score	295
E value	1.0e-165
Match length	504
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	128360
Contig ID	28643_2.R1010
5'-most EST	LIB25-022-Q1-E1-H3
Method	BLASTN
NCBI GI	g4220638
BLAST score	556
E value	0.0e+00
Match length	580
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	128361
Contig ID	28644_1.R1010
5'-most EST	LIB3175-017-P1-K1-A1
Method	BLASTN
NCBI GI	g4263753
BLAST score	170
E value	1.0e-90
Match length	353
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128362
Contig ID	28645_1.R1010
5'-most EST	jC-atXLIB327424P1b10b2
Method	BLASTX
NCBI GI	g4220512
BLAST score	318
E value	5.0e-29
Match length	90
% identity	70
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	128363
Contig ID	28647_1.R1010
5'-most EST	jC-atXLIB327424P1b05b2
Method	BLASTN
NCBI GI	g1707006
BLAST score	298
E value	1.0e-167
Match length	468
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128364
Contig ID	28648_1.R1010
5'-most EST	jC-atXLIB327424P1b06b2
Method	BLASTN
NCBI GI	g2245073
BLAST score	333
E value	0.0e+00
Match length	345
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	128365
Contig ID	28650_1.R1010
5'-most EST	jC-atXLIB327421P3h04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	7.0e-26

Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128366
Contig ID	28651_1.R1010
5'-most EST	g2739595
Method	BLASTX
NCBI GI	g2911049
BLAST score	341
E value	6.0e-32
Match length	110
% identity	65
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	128367
Contig ID	28653_1.R1010
5'-most EST	jC-atX25023Q1E1A02b1
Method	BLASTX
NCBI GI	g728777
BLAST score	261
E value	1.0e-22
Match length	127
% identity	57
NCBI Description	ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36) >gi_1498257 (L07540) replication factor C, 36-kDa subunit [Homo sapiens]

Seq. No.	128368
Contig ID	28657_1.R1010
5'-most EST	LIB25-023-Q1-E1-A6
Method	BLASTX
NCBI GI	g1946355
BLAST score	349
E value	6.0e-33
Match length	128
% identity	50
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	128369
Contig ID	28663_1.R1010
5'-most EST	jC-atXLIB327424P1c10b2
Method	BLASTX
NCBI GI	g3702336
BLAST score	649
E value	5.0e-68
Match length	143
% identity	87
NCBI Description	(AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No.	128370

Contig ID	28670_1.R1010
5'-most EST	g2757737
Method	BLASTX
NCBI GI	g3915020
BLAST score	487
E value	8.0e-49
Match length	149
% identity	64
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE) >gi_1022365_emb_CAA91217_ (Z56278) sucrose phosphate synthase [Vicia faba]

Seq. No.	128371
Contig ID	28681_1.R1010
5'-most EST	LIB3234-080-P1-K1-E8

Seq. No.	128372
Contig ID	28686_1.R1010
5'-most EST	jC-atXP124C121B13T7d1

Seq. No.	128373
Contig ID	28695_2.R1010
5'-most EST	g2413575
Method	BLASTN
NCBI GI	g2924733
BLAST score	269
E value	1.0e-149
Match length	455
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	128374
Contig ID	28704_2.R1010
5'-most EST	jC-atXLIB327424P1e03b2
Method	BLASTX
NCBI GI	g2289010
BLAST score	356
E value	1.0e-33
Match length	71
% identity	99
NCBI Description	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	128375
Contig ID	28704_3.R1010
5'-most EST	LIB3177-038-P1-K2-A12
Method	BLASTX
NCBI GI	g2289010
BLAST score	718
E value	1.0e-76
Match length	153
% identity	98
NCBI Description	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No. 128376

Contig ID	28705_1.R1010
5'-most EST	LIB3176-030-P1-K1-B1
Method	BLASTX
NCBI GI	g4490725
BLAST score	254
E value	6.0e-22
Match length	45
% identity	100
NCBI Description	(AL035709) endo-xyloglucan transferase-like protein [Arabidopsis thaliana]

Seq. No.	128377
Contig ID	28706_2.R1010
5'-most EST	LIB3234-050-P1-K1-E7

Seq. No.	128378
Contig ID	28708_1.R1010
5'-most EST	jC-atXLIB327424P1e07b2
Method	BLASTX
NCBI GI	g3860250
BLAST score	237
E value	9.0e-20
Match length	99
% identity	47
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	128379
Contig ID	28719_1.R1010
5'-most EST	jC-atX25023Q1E1G12b1

Seq. No.	128380
Contig ID	28722_1.R1010
5'-most EST	LIB25-023-Q1-E1-G5
Method	BLASTX
NCBI GI	g1652601
BLAST score	161
E value	8.0e-11
Match length	79
% identity	44
NCBI Description	(D90906) hypothetical protein [Synechocystis sp.]

Seq. No.	128381
Contig ID	28730_1.R1010
5'-most EST	jC-atXLIB327424P1f03b2
Method	BLASTN
NCBI GI	g3449321
BLAST score	322
E value	0.0e+00
Match length	402
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	128382
Contig ID	28736_1.R1010
5'-most EST	jC-atXLIB327424P4e12b1

Method	BLASTX
NCBI GI	g322492
BLAST score	688
E value	1.0e-72
Match length	128
% identity	99
NCBI Description	photomorphogenesis repressor COP1 - Arabidopsis thaliana

Seq. No.	128383
Contig ID	28744_1.R1010
5'-most EST	jC-atXP65C207L23T7067d1
Method	BLASTN
NCBI GI	g4589427
BLAST score	553
E value	0.0e+00
Match length	597
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	128384
Contig ID	28746_2.R1010
5'-most EST	LIB25-024-Q1-E1-A7
Method	BLASTX
NCBI GI	g1076632
BLAST score	143
E value	3.0e-48
Match length	132
% identity	78
NCBI Description	protein kinase - common tobacco >gi_506534_emb_CAA50374_ (X71057) protein kinase [Nicotiana tabacum]

Seq. No.	128385
Contig ID	28755_1.R1010
5'-most EST	jC-atXLIB327424P2c08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128386
Contig ID	28758_1.R1010
5'-most EST	LIB25-024-Q1-E1-C1
Method	BLASTX
NCBI GI	g4507311
BLAST score	215
E value	4.0e-17
Match length	103
% identity	40
NCBI Description	suppressor of Ty (S.cerevisiae) 4 homolog 1 >gi_3122873_sp_Q16550_SPT4_HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi_1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential

N-terminal zinc-finger [Homo sapiens] >gi_1401053 (U38818) SUPT4H [Homo sapiens] >gi_1401055 (U38817) SUPT4H [Homo sapiens] >gi_1401066 (U43154) Supt4h [Mus musculus] >gi_3779194 (U96809) chromatin structural protein homolog [Mus musculus]

Seq. No.	128387
Contig ID	28763_1.R1010
5'-most EST	LIB25-024-Q1-E1-C5
Method	BLASTX
NCBI GI	g4559364
BLAST score	155
E value	3.0e-10
Match length	104
% identity	33
NCBI Description	(AC006585) unknown protein [Arabidopsis thaliana]

Seq. No.	128388
Contig ID	28764_1.R1010
5'-most EST	LIB25-087-Q1-E1-G1
Method	BLASTN
NCBI GI	g2264309
BLAST score	362
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	128389
Contig ID	28769_1.R1010
5'-most EST	g957704
Method	BLASTX
NCBI GI	g3540201
BLAST score	315
E value	3.0e-72
Match length	174
% identity	77
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No.	128390
Contig ID	28769_2.R1010
5'-most EST	g2446006
Method	BLASTN
NCBI GI	g3176694
BLAST score	267
E value	1.0e-148
Match length	483
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128391
Contig ID	28777_1.R1010
5'-most EST	LIB25-024-Q1-E1-D8
Method	BLASTX
NCBI GI	g3292827

BLAST score	504
E value	6.0e-51
Match length	118
% identity	79
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	128392
Contig ID	28783_1.R1010
5'-most EST	jC-atX25024Q1E1E06b1
Method	BLASTN
NCBI GI	g3985931
BLAST score	313
E value	1.0e-176
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	128393
Contig ID	28784_1.R1010
5'-most EST	jC-atXP85C241G24T7b1
Method	BLASTX
NCBI GI	g2651309
BLAST score	854
E value	7.0e-92
Match length	172
% identity	97
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	128394
Contig ID	28786_1.R1010
5'-most EST	LIB25-024-Q1-E1-F1
Method	BLASTX
NCBI GI	g4490323
BLAST score	652
E value	2.0e-68
Match length	168
% identity	77
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	128395
Contig ID	28787_1.R1010
5'-most EST	jC-atXLIB327430P4d07b1
Method	BLASTN
NCBI GI	g3860242
BLAST score	535
E value	0.0e+00
Match length	639
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence

Seq. No.	128396
Contig ID	28792_1.R1010
5'-most EST	g2445999
Method	BLASTN
NCBI GI	g2290120

BLAST score	43
E value	1.0e-14
Match length	66
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	128397
Contig ID	28792_2.R1010
5'-most EST	jC-atXLIB327424P1e04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128398
Contig ID	28793_1.R1010
5'-most EST	LIB25-024-Q1-E1-F7

Seq. No.	128399
Contig ID	28795_1.R1010
5'-most EST	LIB3234-013-P1-K1-E3
Method	BLASTX
NCBI GI	g2459432
BLAST score	418
E value	5.0e-41
Match length	81
% identity	89
NCBI Description	(AC002332) CONSTANS-like protein [Arabidopsis thaliana]

Seq. No.	128400
Contig ID	28798_1.R1010
5'-most EST	LIB25-024-Q1-E1-G2
Method	BLASTN
NCBI GI	g2088638
BLAST score	342
E value	0.0e+00
Match length	368
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128401
Contig ID	28817_1.R1010
5'-most EST	jC-atXLIB327424P4b06b1
Method	BLASTN
NCBI GI	g4559344
BLAST score	62
E value	7.0e-26
Match length	184
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	128402
Contig ID	28818_2.R1010
5'-most EST	g2764170
Method	BLASTX
NCBI GI	g4587550
BLAST score	1001
E value	1.0e-109
Match length	209
% identity	92
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	128403
Contig ID	28833_1.R1010
5'-most EST	LIB25-081-Q1-E1-D3
Method	BLASTX
NCBI GI	g2459430
BLAST score	831
E value	2.0e-89
Match length	153
% identity	100
NCBI Description	(AC002332) putative CUC2 protein [Arabidopsis thaliana]

Seq. No.	128404
Contig ID	28840_1.R1010
5'-most EST	LIB3168-067-P1-K1-H4
Method	BLASTX
NCBI GI	g4454043
BLAST score	358
E value	8.0e-34
Match length	189
% identity	42
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	128405
Contig ID	28842_1.R1010
5'-most EST	jC-atXLIB327424P1d03b2
Method	BLASTX
NCBI GI	g3328804
BLAST score	525
E value	3.0e-53
Match length	216
% identity	50
NCBI Description	(AE001311) GTP Binding Protein [Chlamydia trachomatis]

Seq. No.	128406
Contig ID	28844_1.R1010
5'-most EST	jC-atXLIB327424P4c12b1

Seq. No.	128407
Contig ID	28847_1.R1010
5'-most EST	LIB25-025-Q1-E1-E10
Method	BLASTN
NCBI GI	g4559319
BLAST score	360
E value	0.0e+00

Match length	364
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	128408
Contig ID	28853_1.R1010
5'-most EST	jC-atXLIB327425P3b12b1
Method	BLASTN
NCBI GI	g4589421
BLAST score	94
E value	3.0e-45
Match length	312
% identity	41
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	128409
Contig ID	28853_2.R1010
5'-most EST	LIB25-025-Q1-E1-E7
Method	BLASTN
NCBI GI	g4589421
BLAST score	340
E value	0.0e+00
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	128410
Contig ID	28864_1.R1010
5'-most EST	jC-atXLIB327424P3d11b1
Method	BLASTX
NCBI GI	g4510376
BLAST score	161
E value	8.0e-11
Match length	142
% identity	41
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	128411
Contig ID	28868_1.R1010
5'-most EST	ARABL1-043-Q1-B1-B2
Method	BLASTX
NCBI GI	g3004565
BLAST score	262
E value	8.0e-23
Match length	82
% identity	62
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	128412
Contig ID	28885_1.R1010
5'-most EST	jC-atXP87C244F9T7b1
Method	BLASTX
NCBI GI	g2829927
BLAST score	775

E value	9.0e-83
Match length	171
% identity	91
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	128413
Contig ID	28885_2.R1010
5'-most EST	jC-atXLIB327424P4b08b1
Method	BLASTX
NCBI GI	g2829927
BLAST score	435
E value	1.0e-42
Match length	127
% identity	73
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	128414
Contig ID	28887_1.R1010
5'-most EST	jC-atXP46C172F2T7059d1
Method	BLASTN
NCBI GI	g4096078
BLAST score	504
E value	0.0e+00
Match length	615
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128415
Contig ID	28888_1.R1010
5'-most EST	LIB25-026-Q1-E1-A7

Seq. No.	128416
Contig ID	28889_1.R1010
5'-most EST	g3868968

Seq. No.	128417
Contig ID	28894_1.R1010
5'-most EST	LIB25-026-Q1-E1-B4
Method	BLASTX
NCBI GI	g544134
BLAST score	261
E value	1.0e-22
Match length	90
% identity	51
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	128418
Contig ID	28896_1.R1010
5'-most EST	jC-atXLIB327424P2c02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	9.0e-21

Match length	73
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128419
Contig ID	28902_1.R1010
5'-most EST	jC-atX25026Q1E1F10b1
Method	BLASTN
NCBI GI	g2827644
BLAST score	158
E value	2.0e-83
Match length	471
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	128420
Contig ID	28907_1.R1010
5'-most EST	LIB25-026-Q1-E1-C5

Seq. No.	128421
Contig ID	28908_1.R1010
5'-most EST	LIB25-026-Q1-E1-C6
Method	BLASTN
NCBI GI	g2262135
BLAST score	354
E value	0.0e+00
Match length	819
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	128422
Contig ID	28915_1.R1010
5'-most EST	g2762583
Method	BLASTX
NCBI GI	g3281868
BLAST score	412
E value	2.0e-40
Match length	117
% identity	74
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	128423
Contig ID	28917_1.R1010
5'-most EST	jC-atXLIB327424P2d11b2
Method	BLASTN
NCBI GI	g3869065
BLAST score	242
E value	1.0e-133
Match length	447
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No. 128424

Contig ID	28935_1.R1010
5'-most EST	LIB3177-026-P1-K2-F3
Method	BLASTN
NCBI GI	g3849811
BLAST score	250
E value	1.0e-138
Match length	486
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128425
Contig ID	28942_1.R1010
5'-most EST	jC-atXLIB327420P1f04b1
Method	BLASTX
NCBI GI	g3885334
BLAST score	928
E value	1.0e-100
Match length	226
% identity	74
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	128426
Contig ID	28952_1.R1010
5'-most EST	jC-atXLIB327424P4e10b1
Method	BLASTN
NCBI GI	g3869068
BLAST score	223
E value	1.0e-122
Match length	530
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	128427
Contig ID	28960_1.R1010
5'-most EST	LIB3175-053-P1-K1-A4

Seq. No.	128428
Contig ID	28964_1.R1010
5'-most EST	jC-atX25027Q1E1B01b1
Method	BLASTN
NCBI GI	g3176695
BLAST score	439
E value	0.0e+00
Match length	439
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	128429
Contig ID	28966_1.R1010
5'-most EST	jC-atXLIB327422P1b09b1
Method	BLASTX
NCBI GI	g4678924

BLAST score	992
E value	1.0e-108
Match length	206
% identity	95
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	128430
Contig ID	28969_1.R1010
5'-most EST	jC-atXLIB327422P2b05b2
Method	BLASTN
NCBI GI	g2924728
BLAST score	241
E value	1.0e-133
Match length	241
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	128431
Contig ID	28970_1.R1010
5'-most EST	jC-atXLIB327422P4b03b1
Method	BLASTN
NCBI GI	g3212846
BLAST score	217
E value	1.0e-118
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128432
Contig ID	28971_1.R1010
5'-most EST	LIB3176-123-P2-K1-B9
Method	BLASTX
NCBI GI	g124226
BLAST score	739
E value	2.0e-78
Match length	158
% identity	88
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	128433
Contig ID	28984_1.R1010
5'-most EST	jC-alX25027Q1E1H11b1
Method	BLASTX
NCBI GI	g4206789
BLAST score	365
E value	8.0e-35
Match length	158
% identity	50
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	128434
Contig ID	28988_1.R1010
5'-most EST	jC-atXLIB327422P2c07b2
Method	BLASTX
NCBI GI	g3522942
BLAST score	374
E value	1.0e-35
Match length	118
% identity	63
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128435
Contig ID	28994_1.R1010
5'-most EST	jC-atXLIB327420P3a08b1
Method	BLASTN
NCBI GI	g4432829
BLAST score	456
E value	0.0e+00
Match length	492
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128436
Contig ID	29000_1.R1010
5'-most EST	jC-atXLIB327422P1d04b1
Method	BLASTN
NCBI GI	g4165340
BLAST score	609
E value	0.0e+00
Match length	633
% identity	42
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128437
Contig ID	29001_1.R1010
5'-most EST	jC-atXLIB327422P2d05b2
Method	BLASTN
NCBI GI	g4467094
BLAST score	473
E value	0.0e+00
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	128438
Contig ID	29002_1.R1010
5'-most EST	LIB25-109-Q1-E1-G7
Method	BLASTX
NCBI GI	g4262232
BLAST score	180
E value	5.0e-31
Match length	186
% identity	42
NCBI Description	(AC006200) putative ribosomal protein L7 [Arabidopsis

thaliana]

Seq. No.	128439
Contig ID	29012_1.R1010
5'-most EST	LIB25-038-Q1-E1-D10
Method	BLASTX
NCBI GI	g3242704
BLAST score	361
E value	2.0e-34
Match length	109
% identity	67
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128440
Contig ID	29016_1.R1010
5'-most EST	jC-atXLIB327422P4a09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	63
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128441
Contig ID	29018_1.R1010
5'-most EST	jC-atXLIB327422P2b08b2
Method	BLASTX
NCBI GI	g2982783
BLAST score	188
E value	8.0e-14
Match length	95
% identity	42
NCBI Description	(AE000670) 3-hydroxyisobutyrate dehydrogenase [Aquifex aeolicus]

Seq. No.	128442
Contig ID	29028_1.R1010
5'-most EST	jC-atXLIB327422P1e08b1
Method	BLASTX
NCBI GI	g4510362
BLAST score	110
E value	1.0e-49
Match length	106
% identity	94
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128443
Contig ID	29033_1.R1010
5'-most EST	jC-atXLIB327422P3b12b2
Method	BLASTX
NCBI GI	g4587574
BLAST score	160
E value	3.0e-56
Match length	150
% identity	77

NCBI Description	(AC006550) Contains PF_00010 helix-loop-helix DNA-binding domain. ESTs gb_T45640 and gb_T22783 come from this gene. [Arabidopsis thaliana]

Seq. No.	128444
Contig ID	29033_2.R1010
5'-most EST	g2763774
Method	BLASTX
NCBI GI	g4587574
BLAST score	208
E value	2.0e-16
Match length	103
% identity	50
NCBI Description	(AC006550) Contains PF_00010 helix-loop-helix DNA-binding domain. ESTs gb_T45640 and gb_T22783 come from this gene. [Arabidopsis thaliana]

Seq. No.	128445
Contig ID	29049_1.R1010
5'-most EST	jC-atXP63C205D13T7d2
Method	BLASTX
NCBI GI	g4584342
BLAST score	770
E value	7.0e-82
Match length	226
% identity	57
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	128446
Contig ID	29049_3.R1010
5'-most EST	g2446069
Method	BLASTN
NCBI GI	g4584339
BLAST score	290
E value	1.0e-162
Match length	662
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence

Seq. No.	128447
Contig ID	29050_1.R1010
5'-most EST	jC-atXLIB327422P2d04b2

Seq. No.	128448
Contig ID	29064_1.R1010
5'-most EST	LIB3177-072-P1-K1-D1
Method	BLASTX
NCBI GI	g4490725
BLAST score	787
E value	3.0e-84
Match length	150
% identity	100
NCBI Description	(AL035709) endo-xyloglucan transferase-like protein [Arabidopsis thaliana]

Seq. No.	128449
Contig ID	29066_1.R1010
5'-most EST	jC-atXLIB327422P4a06b1
Method	BLASTN
NCBI GI	g2351064
BLAST score	343
E value	0.0e+00
Match length	403
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	128450
Contig ID	29067_1.R1010
5'-most EST	LIB35-040-Q1-E1-H7
Method	BLASTX
NCBI GI	g4406770
BLAST score	1727
E value	0.0e+00
Match length	346
% identity	95
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	128451
Contig ID	29072_1.R1010
5'-most EST	LIB25-029-Q1-E1-A9
Method	BLASTX
NCBI GI	g3482979
BLAST score	154
E value	8.0e-10
Match length	121
% identity	35
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128452
Contig ID	29075_1.R1010
5'-most EST	LIB3234-026-Q1-K1-E1
Method	BLASTX
NCBI GI	g548847
BLAST score	555
E value	7.0e-57
Match length	112
% identity	96
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_1086182_pir__S39501 ribosomal protein S12 - curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	128453
Contig ID	29075_2.R1010
5'-most EST	g406825
Method	BLASTX
NCBI GI	g343503
BLAST score	392
E value	1.0e-37

Match length	77
% identity	100
NCBI Description	(L12250) ribosomal protein S12 [Nicotiana plumbaginifolia] >gi_1334367_emb_CAA27200_ (X03481) rps12-like coding sequence [Nicotiana tabacum] >gi_2924276_emb_CAA77429_ (Z00044) ribosomal protein S12 [Nicotiana tabacum] >gi_2924283_emb_CAA77436_ (Z00044) ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	128454
Contig ID	29076_1.R1010
5'-most EST	LIB25-029-Q1-E1-B2

Seq. No.	128455
Contig ID	29081_1.R1010
5'-most EST	jC-atXLIB327420P4c09a1
Method	BLASTX
NCBI GI	g2281334
BLAST score	388
E value	4.0e-37
Match length	205
% identity	43
NCBI Description	(U83619) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	128456
Contig ID	29086_1.R1010
5'-most EST	ARABL1-044-Q1-B1-A5
Method	BLASTN
NCBI GI	g4335711
BLAST score	42
E value	4.0e-14
Match length	105
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128457
Contig ID	29093_1.R1010
5'-most EST	LIB3176-037-P1-K1-C2
Method	BLASTX
NCBI GI	g4455364
BLAST score	386
E value	5.0e-37
Match length	141
% identity	64
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	128458
Contig ID	29100_1.R1010
5'-most EST	jC-atXLIB327422P4b12b1
Method	BLASTN
NCBI GI	g4662628
BLAST score	185
E value	1.0e-99
Match length	419
% identity	91

NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence
Seq. No.	128459
Contig ID	29102_1.R1010
5'-most EST	g931212
Method	BLASTN
NCBI GI	g3868723
BLAST score	410
E value	0.0e+00
Match length	541
% identity	95
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	128460
Contig ID	29102_2.R1010
5'-most EST	jC-atXLIB327422P3b08b2
Method	BLASTN
NCBI GI	g3868723
BLAST score	644
E value	0.0e+00
Match length	728
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	128461
Contig ID	29117_1.R1010
5'-most EST	jC-alX25029Q1E1E09b1
Seq. No.	128462
Contig ID	29123_1.R1010
5'-most EST	jC-atXLIB327422P1c11b1
Method	BLASTN
NCBI GI	g2760165
BLAST score	79
E value	5.0e-36
Match length	332
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.	128463
Contig ID	29123_2.R1010
5'-most EST	g2597369
Method	BLASTN
NCBI GI	g2760165
BLAST score	57
E value	5.0e-23
Match length	206
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.	128464
Contig ID	29138_1.R1010

5'-most EST	jC-atXLIB327422P2d08b2
Method	BLASTX
NCBI GI	g3021512
BLAST score	1280
E value	1.0e-141
Match length	279
% identity	85
NCBI Description	(X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]

Seq. No.	128465
Contig ID	29143_1.R1010
5'-most EST	LIB3176-083-P1-K1-H5
Method	BLASTX
NCBI GI	g3377843
BLAST score	1332
E value	1.0e-147
Match length	289
% identity	91
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	128466
Contig ID	29145_1.R1010
5'-most EST	jC-atXLIB327426P2d09b1
Method	BLASTX
NCBI GI	g2191127
BLAST score	898
E value	8.0e-97
Match length	177
% identity	100
NCBI Description	(AF007269) A_IG002N01.1 gene product [Arabidopsis thaliana]

Seq. No.	128467
Contig ID	29148_1.R1010
5'-most EST	g2722058
Method	BLASTX
NCBI GI	g3850571
BLAST score	430
E value	2.0e-42
Match length	83
% identity	100
NCBI Description	(AC005278) Similar to gb_U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb_AA612141 comes from this gene. [Arabidopsis thaliana]

Seq. No.	128468
Contig ID	29152_1.R1010
5'-most EST	jC-alXLIB327436P3h09b1
Method	BLASTN
NCBI GI	g1946354
BLAST score	215
E value	1.0e-117
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	128469
Contig ID	29152_2.R1010
5'-most EST	LIB25-064-Q1-E1-H7
Method	BLASTN
NCBI GI	g1946354
BLAST score	234
E value	1.0e-129
Match length	386
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	128470
Contig ID	29153_1.R1010
5'-most EST	LIB3177-060-P1-K1-E7
Method	BLASTX
NCBI GI	g4689034
BLAST score	164
E value	3.0e-11
Match length	39
% identity	82
NCBI Description	(AJ133751) chloroplast ribosome recycling factor protein [Spinacia oleracea]

Seq. No.	128471
Contig ID	29155_1.R1010
5'-most EST	jC-atXLIB327422P4a02b1
Method	BLASTN
NCBI GI	g4757402
BLAST score	205
E value	1.0e-111
Match length	402
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	128472
Contig ID	29160_1.R1010
5'-most EST	jC-atX25030Q1E1B11b1
Method	BLASTX
NCBI GI	g1946374
BLAST score	282
E value	4.0e-25
Match length	81
% identity	78
NCBI Description	(U93215) myb-like protein isolog [Arabidopsis thaliana] >gi_2347205 (AC002338) myb-like protein isolog [Arabidopsis thaliana]

Seq. No.	128473
Contig ID	29171_1.R1010
5'-most EST	jC-atXLIB327422P3b01b2
Method	BLASTX
NCBI GI	g4467153
BLAST score	443
E value	3.0e-45

Match length	90
% identity	87
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	128474
Contig ID	29175_1.R1010
5'-most EST	LIB25-031-Q1-E1-F10
Method	BLASTX
NCBI GI	g3608142
BLAST score	161
E value	2.0e-12
Match length	120
% identity	40
NCBI Description	(AC005314) putative hin1 [Arabidopsis thaliana]

Seq. No.	128475
Contig ID	29185_1.R1010
5'-most EST	jC-atXLIB327421P1c07b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	963
E value	1.0e-104
Match length	184
% identity	100
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	128476
Contig ID	29194_1.R1010
5'-most EST	LIB25-030-Q1-E1-F11
Method	BLASTN
NCBI GI	g3873174
BLAST score	327
E value	0.0e+00
Match length	351
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	128477
Contig ID	29197_1.R1010
5'-most EST	jC-atXLIB327422P3c02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	5.0e-16
Match length	45
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128478
Contig ID	29198_1.R1010
5'-most EST	jC-atXLIB327422P2c11b2

Seq. No.	128479
Contig ID	29202_1.R1010

5'-most EST	jC-atXLIB327422P3c09b2
Method	BLASTN
NCBI GI	g2924734
BLAST score	204
E value	1.0e-111
Match length	531
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	128480
Contig ID	29217_1.R1010
5'-most EST	LIB25-030-Q1-E1-H6
Method	BLASTN
NCBI GI	g2351068
BLAST score	668
E value	0.0e+00
Match length	708
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	128481
Contig ID	29232_1.R1010
5'-most EST	jC-atXLIB327422P1e07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	76
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128482
Contig ID	29234_1.R1010
5'-most EST	LIB3168-041-P1-K1-A9

Seq. No.	128483
Contig ID	29241_1.R1010
5'-most EST	g1158451
Method	BLASTX
NCBI GI	g2827656
BLAST score	398
E value	2.0e-46
Match length	129
% identity	78
NCBI Description	(AL021637) DAG-like protein [Arabidopsis thaliana]

Seq. No.	128484
Contig ID	29251_1.R1010
5'-most EST	jC-atXLIB327422P3e08b2
Method	BLASTN
NCBI GI	g3406034
BLAST score	221
E value	1.0e-121
Match length	391

% identity	100
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128485
Contig ID	29252_1.R1010
5'-most EST	jC-atXLIB327422P1f05b1
Method	BLASTX
NCBI GI	g4204265
BLAST score	352
E value	3.0e-33
Match length	157
% identity	48
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	128486
Contig ID	29256_1.R1010
5'-most EST	jC-atXLIB327422P2f06b2
Method	BLASTX
NCBI GI	g4335758
BLAST score	234
E value	2.0e-71
Match length	200
% identity	65
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	128487
Contig ID	29257_1.R1010
5'-most EST	LIB35-011-Q1-E1-C11

Seq. No.	128488
Contig ID	29260_1.R1010
5'-most EST	g1216556
Method	BLASTX
NCBI GI	g2190547
BLAST score	726
E value	5.0e-77
Match length	168
% identity	84
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	128489
Contig ID	29262_1.R1010
5'-most EST	jC-atXLIB327422P4f03b1
Method	BLASTX
NCBI GI	g3643611
BLAST score	577
E value	2.0e-59
Match length	134
% identity	81
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	128490
Contig ID	29268_1.R1010
5'-most EST	jC-atXP84CG2H9T7b1

Method	BLASTN
NCBI GI	g3449313
BLAST score	289
E value	1.0e-161
Match length	536
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	128491
Contig ID	29268_2.R1010
5'-most EST	g937237
Method	BLASTN
NCBI GI	g3449313
BLAST score	240
E value	1.0e-132
Match length	379
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	128492
Contig ID	29271_1.R1010
5'-most EST	jC-atXLIB327422P3f10b2
Method	BLASTN
NCBI GI	g2828181
BLAST score	220
E value	1.0e-120
Match length	375
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE8, complete sequence [Arabidopsis thaliana]

Seq. No.	128493
Contig ID	29273_1.R1010
5'-most EST	jC-atXP15C108F10T7095a1
Method	BLASTX
NCBI GI	g2586125
BLAST score	712
E value	3.0e-75
Match length	137
% identity	100
NCBI Description	(U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No.	128494
Contig ID	29279_1.R1010
5'-most EST	jC-atXP55C186L3T7d2
Method	BLASTX
NCBI GI	g4432841
BLAST score	574
E value	3.0e-66
Match length	263
% identity	52
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128495
Contig ID	29284_1.R1010

5'-most EST	jC-atXLIB327422P4d10b1
Method	BLASTX
NCBI GI	g1465770
BLAST score	224
E value	5.0e-18
Match length	197
% identity	32
NCBI Description	(U61233) cofactor D [Bos taurus]

Seq. No.	128496
Contig ID	29289_1.R1010
5'-most EST	LIB25-032-Q1-E1-A6
Method	BLASTN
NCBI GI	g4757409
BLAST score	242
E value	1.0e-133
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	128497
Contig ID	29290_1.R1010
5'-most EST	jC-atXLIB327422P3d08b2
Method	BLASTN
NCBI GI	g4589440
BLAST score	282
E value	1.0e-157
Match length	465
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	128498
Contig ID	29291_1.R1010
5'-most EST	jC-atXLIB327422P4d09b1
Method	BLASTX
NCBI GI	g3043422
BLAST score	242
E value	2.0e-20
Match length	106
% identity	46
NCBI Description	(AJ004917) endoxyloglucan transferase [Cicer arietinum]

Seq. No.	128499
Contig ID	29294_1.R1010
5'-most EST	jC-atXLIB327422P2e04b2
Method	BLASTX
NCBI GI	g4731111
BLAST score	419
E value	3.0e-44
Match length	144
% identity	65
NCBI Description	(AF064707) exhydrolase II [Zea mays]

Seq. No.	128500
Contig ID	29294_2.R1010

5'-most EST	jC-atXLIB327420P4c06b1
Method	BLASTX
NCBI GI	g3201554
BLAST score	163
E value	5.0e-11
Match length	93
% identity	43
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	128501
Contig ID	29299_1.R1010
5'-most EST	jC-atXLIB327422P1e03b1
Method	BLASTN
NCBI GI	g4678291
BLAST score	136
E value	3.0e-70
Match length	208
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	128502
Contig ID	29299_2.R1010
5'-most EST	jC-atX25032Q1E1B06b1
Method	BLASTX
NCBI GI	g4678295
BLAST score	145
E value	1.0e-08
Match length	207
% identity	5
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	128503
Contig ID	29305_1.R1010
5'-most EST	jC-atXLIB327422P3e02b2
Method	BLASTN
NCBI GI	g4678371
BLAST score	164
E value	5.0e-87
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	128504
Contig ID	29308_1.R1010
5'-most EST	jC-atX25032Q1E1C07b1
Method	BLASTX
NCBI GI	g2245094
BLAST score	418
E value	5.0e-41
Match length	77
% identity	100
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128505
Contig ID	29315_1.R1010

5'-most EST	jC-atXLIB327438P4a02a2
Method	BLASTX
NCBI GI	g2494264
BLAST score	525
E value	4.0e-53
Match length	232
% identity	49
NCBI Description	HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G [Synechocystis sp.]

Seq. No.	128506
Contig ID	29315_3.R1010
5'-most EST	jC-atXLIB327427P4a09b2
Method	BLASTX
NCBI GI	g2494264
BLAST score	279
E value	2.0e-24
Match length	121
% identity	49
NCBI Description	HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G [Synechocystis sp.]

Seq. No.	128507
Contig ID	29315_6.R1010
5'-most EST	LIB3176-098-P1-K1-G1
Method	BLASTX
NCBI GI	g2494264
BLAST score	312
E value	2.0e-28
Match length	117
% identity	54
NCBI Description	HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G [Synechocystis sp.]

Seq. No.	128508
Contig ID	29317_1.R1010
5'-most EST	LIB3175-007-P1-K1-C6
Method	BLASTX
NCBI GI	g1402916
BLAST score	303
E value	1.0e-27
Match length	139
% identity	53
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]

Seq. No.	128509
Contig ID	29319_1.R1010
5'-most EST	jC-atXLIB327422P4e08b1
Method	BLASTN
NCBI GI	g3659491
BLAST score	168
E value	2.0e-89

Match length	378
% identity	98
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	128510
Contig ID	29322_1.R1010
5'-most EST	LIB3175-045-P1-K1-A12

Seq. No.	128511
Contig ID	29324_1.R1010
5'-most EST	jC-atXLIB327422P2f05b2
Method	BLASTX
NCBI GI	g4588003
BLAST score	805
E value	6.0e-86
Match length	195
% identity	90
NCBI Description	(AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No.	128512
Contig ID	29325_1.R1010
5'-most EST	jC-atXLIB327416P2g03b1
Method	BLASTN
NCBI GI	g2760316
BLAST score	315
E value	1.0e-177
Match length	551
% identity	97
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	128513
Contig ID	29332_1.R1010
5'-most EST	jC-atXLIB327422P2f04b2
Method	BLASTX
NCBI GI	g4220474
BLAST score	604
E value	1.0e-62
Match length	168
% identity	72
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	128514
Contig ID	29344_1.R1010
5'-most EST	jC-atXLIB327422P4f02b1
Method	BLASTN
NCBI GI	g4519188
BLAST score	214
E value	1.0e-117
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No. 128515

Contig ID	29350_1.R1010
5'-most EST	jC-atXLIB327422P4f09b1
Method	BLASTN
NCBI GI	g4539402
BLAST score	262
E value	1.0e-145
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)

Seq. No.	128516
Contig ID	29358_1.R1010
5'-most EST	LIB3175-026-P1-K1-B7
Method	BLASTX
NCBI GI	g3329294
BLAST score	246
E value	1.0e-20
Match length	234
% identity	29
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	128517
Contig ID	29363_1.R1010
5'-most EST	jC-atXLIB327424P4e10a1
Method	BLASTN
NCBI GI	g3869068
BLAST score	158
E value	2.0e-83
Match length	365
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	128518
Contig ID	29364_1.R1010
5'-most EST	jC-atXLIB327422P3d04b2

Seq. No.	128519
Contig ID	29377_1.R1010
5'-most EST	LIB25-033-Q1-E1-B2
Method	BLASTX
NCBI GI	g4567273
BLAST score	548
E value	2.0e-56
Match length	126
% identity	86
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	128520
Contig ID	29384_1.R1010
5'-most EST	jC-atXLIB327422P2e08b2

Seq. No.	128521
Contig ID	29391_1.R1010

5'-most EST	jC-atXLIB327431P4h05a1
Method	BLASTX
NCBI GI	g4559369
BLAST score	664
E value	1.0e-69
Match length	156
% identity	79
NCBI Description	(AC006585) putative Rieske iron-sulfur protein [Arabidopsis thaliana]

Seq. No.	128522
Contig ID	29391_2.R1010
5'-most EST	jC-atXLIB327422P2e07b2
Method	BLASTX
NCBI GI	g4559369
BLAST score	809
E value	9.0e-87
Match length	153
% identity	98
NCBI Description	(AC006585) putative Rieske iron-sulfur protein [Arabidopsis thaliana]

Seq. No.	128523
Contig ID	29391_3.R1010
5'-most EST	jC-alXLIB327436P2a08b1
Method	BLASTX
NCBI GI	g4559369
BLAST score	523
E value	3.0e-53
Match length	122
% identity	85
NCBI Description	(AC006585) putative Rieske iron-sulfur protein [Arabidopsis thaliana]

Seq. No.	128524
Contig ID	29396_1.R1010
5'-most EST	jC-atXLIB327422P3e05b2
Method	BLASTX
NCBI GI	g2982583
BLAST score	365
E value	9.0e-35
Match length	103
% identity	69
NCBI Description	(AJ003135) polygalacturonase [Arabidopsis thaliana] >gi_3152948_emb_CAA06610_ (AJ005584) polygalacturonase [Arabidopsis thaliana]

Seq. No.	128525
Contig ID	29400_1.R1010
5'-most EST	LIB25-033-Q1-E1-D3
Method	BLASTX
NCBI GI	g2655098
BLAST score	192
E value	1.0e-14
Match length	56
% identity	59
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	128526
Contig ID	29403_1.R1010
5'-most EST	LIB3234-060-P1-K1-B12
Method	BLASTN
NCBI GI	g2696018
BLAST score	293
E value	1.0e-164
Match length	759
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	128527
Contig ID	29412_1.R1010
5'-most EST	LIB25-033-Q1-E1-E4

Seq. No.	128528
Contig ID	29413_1.R1010
5'-most EST	jC-atXLIB327422P4e11b1
Method	BLASTX
NCBI GI	g2160138
BLAST score	298
E value	6.0e-27
Match length	95
% identity	38
NCBI Description	(AC000375) No definition line found [Arabidopsis thaliana]

Seq. No.	128529
Contig ID	29416_1.R1010
5'-most EST	jC-atXLIB327422P4e12b1
Method	BLASTX
NCBI GI	g2270994
BLAST score	239
E value	6.0e-20
Match length	84
% identity	54
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	128530
Contig ID	29416_2.R1010
5'-most EST	LIB3234-008-P1-K1-D8

Seq. No.	128531
Contig ID	29424_1.R1010
5'-most EST	LIB25-033-Q1-E1-F4
Method	BLASTX
NCBI GI	g913141
BLAST score	799
E value	1.0e-85
Match length	148
% identity	95
NCBI Description	ARK3 product/receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana, Columbia, Peptide, 851 aa]

Seq. No.	128532
Contig ID	29428_1.R1010

5'-most EST	jC-atXLIB327422P1f08b1
Method	BLASTN
NCBI GI	g4544435
BLAST score	382
E value	0.0e+00
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	128533
Contig ID	29434_1.R1010
5'-most EST	jC-atXLIB327422P4f08b1
Method	BLASTN
NCBI GI	g2351064
BLAST score	220
E value	1.0e-120
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	128534
Contig ID	29436_1.R1010
5'-most EST	jC-atXLIB327422P3f05b2
Method	BLASTX
NCBI GI	g505588
BLAST score	207
E value	2.0e-18
Match length	105
% identity	44
NCBI Description	(L04680) 5-epi-aristolochene synthase [Nicotiana tabacum]

Seq. No.	128535
Contig ID	29441_1.R1010
5'-most EST	LIB25-033-Q1-E1-H1
Method	BLASTX
NCBI GI	g4572673
BLAST score	501
E value	1.0e-50
Match length	156
% identity	69
NCBI Description	(AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No.	128536
Contig ID	29443_1.R1010
5'-most EST	jC-atXLIB327422P2g05b2
Method	BLASTX
NCBI GI	g913445
BLAST score	405
E value	3.0e-39
Match length	122
% identity	65
NCBI Description	(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No.	128537
Contig ID	29444_1.R1010
5'-most EST	LIB3177-050-P1-K2-C3
Method	BLASTX
NCBI GI	g2245138
BLAST score	665
E value	8.0e-70
Match length	136
% identity	98
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128538
Contig ID	29448_1.R1010
5'-most EST	jC-atXLIB327422P1g02b1
Method	BLASTX
NCBI GI	g1172704
BLAST score	496
E value	5.0e-50
Match length	150
% identity	59
NCBI Description	PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN) >gi_633940 (L39082) transport protein [Arabidopsis thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine transport protein PTR2-B [Arabidopsis thaliana]

Seq. No.	128539
Contig ID	29452_1.R1010
5'-most EST	LIB3177-085-P1-K1-C4
Method	BLASTX
NCBI GI	g2791606
BLAST score	236
E value	1.0e-19
Match length	70
% identity	56
NCBI Description	(AL021287) gatB [Mycobacterium tuberculosis]

Seq. No.	128540
Contig ID	29453_1.R1010
5'-most EST	jC-atXLIB327422P4d05b1
Method	BLASTN
NCBI GI	g2656028
BLAST score	222
E value	1.0e-121
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	128541
Contig ID	29458_1.R1010
5'-most EST	jC-alXLIB327435P2h07b1
Method	BLASTX
NCBI GI	g3377795
BLAST score	624
E value	9.0e-65
Match length	175

% identity	78
NCBI Description	(AF075597) contains similarity to pectinesterases [Arabidopsis thaliana]

Seq. No.	128542
Contig ID	29459_1.R1010
5'-most EST	jC-atXLIB327422P3d03b2
Method	BLASTX
NCBI GI	g2435518
BLAST score	367
E value	5.0e-35
Match length	120
% identity	68
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	128543
Contig ID	29479_1.R1010
5'-most EST	jC-atXLIB327422P1e10b1
Method	BLASTX
NCBI GI	g4432839
BLAST score	570
E value	9.0e-59
Match length	141
% identity	54
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	128544
Contig ID	29480_1.R1010
5'-most EST	jC-atXLIB327422P2e10b2
Method	BLASTN
NCBI GI	g2618600
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	128545
Contig ID	29486_1.R1010
5'-most EST	jC-atXLIB327420P4f08b1
Method	BLASTN
NCBI GI	g2564049
BLAST score	392
E value	0.0e+00
Match length	559
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	128546
Contig ID	29490_1.R1010
5'-most EST	jC-atXLIB327422P3e07b2

Seq. No.	128547
Contig ID	29502_1.R1010

5'-most EST	jC-atXLIB327422P1f02b1
Method	BLASTX
NCBI GI	g4581508
BLAST score	453
E value	6.0e-45
Match length	147
% identity	59
NCBI Description	(AL049558) putative phosphatidylinositol-kinase [Schizosaccharomyces pombe]

Seq. No.	128548
Contig ID	29505_1.R1010
5'-most EST	jC-atXLIB327422P3e11b2
Method	BLASTN
NCBI GI	g3281847
BLAST score	294
E value	1.0e-164
Match length	294
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	128549
Contig ID	29510_1.R1010
5'-most EST	jC-atXLIB327420P4c05b1
Method	BLASTN
NCBI GI	g4584387
BLAST score	249
E value	1.0e-137
Match length	500
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	128550
Contig ID	29511_1.R1010
5'-most EST	jC-atXLIB327422P2f09b2
Method	BLASTX
NCBI GI	g2323410
BLAST score	150
E value	2.0e-09
Match length	94
% identity	34
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	128551
Contig ID	29513_1.R1010
5'-most EST	jC-alX25038Q1E1A08b1

Seq. No.	128552
Contig ID	29520_1.R1010
5'-most EST	jC-atXLIB327422P4f05b1
Method	BLASTN
NCBI GI	g4756963
BLAST score	363
E value	0.0e+00
Match length	447

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	128553
Contig ID	29526_1.R1010
5'-most EST	LIB25-034-Q1-E1-G5
Method	BLASTX
NCBI GI	g3269292
BLAST score	886
E value	2.0e-95
Match length	223
% identity	78
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	128554
Contig ID	29527_1.R1010
5'-most EST	jC-atXLIB327422P4f06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	1.0e-25
Match length	77
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128555
Contig ID	29528_1.R1010
5'-most EST	jC-alX25052Q1E1E01b1
Method	BLASTX
NCBI GI	g3668084
BLAST score	644
E value	1.0e-67
Match length	123
% identity	99
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	128556
Contig ID	29530_1.R1010
5'-most EST	jC-atXLIB327422P3f06b2
Method	BLASTX
NCBI GI	g2980781
BLAST score	307
E value	1.0e-27
Match length	143
% identity	44
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	128557
Contig ID	29531_1.R1010
5'-most EST	jC-atXLIB327422P3f12b2
Method	BLASTX
NCBI GI	g2465923
BLAST score	293
E value	3.0e-26
Match length	134

% identity	45
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	128558
Contig ID	29532_1.R1010
5'-most EST	LIB25-034-Q1-E1-H10
Seq. No.	128559
Contig ID	29536_1.R1010
5'-most EST	g1517275
Seq. No.	128560
Contig ID	29536_2.R1010
5'-most EST	g1269282
Seq. No.	128561
Contig ID	29538_1.R1010
5'-most EST	LIB35-003-Q1-E1-B7
Seq. No.	128562
Contig ID	29546_1.R1010
5'-most EST	jC-atXLIB327422P4g09a1
Method	BLASTX
NCBI GI	g3769673
BLAST score	394
E value	6.0e-38
Match length	103
% identity	69
NCBI Description	(AF095285) Tic20 [Pisum sativum]
Seq. No.	128563
Contig ID	29546_2.R1010
5'-most EST	jC-atXLIB327422P4g09b1
Method	BLASTX
NCBI GI	g3769673
BLAST score	581
E value	4.0e-60
Match length	141
% identity	69
NCBI Description	(AF095285) Tic20 [Pisum sativum]
Seq. No.	128564
Contig ID	29548_1.R1010
5'-most EST	jC-atXLIB327422P4g10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	3.0e-26
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	128565
Contig ID	29551_1.R1010
5'-most EST	jC-atXLIB327422P3g07b2

Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	7.0e-22
Match length	63
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128566
Contig ID	29556_1.R1010
5'-most EST	LIB25-035-Q1-E1-B2

Seq. No.	128567
Contig ID	29561_1.R1010
5'-most EST	jC-atXLIB327422P2h05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128568
Contig ID	29563_1.R1010
5'-most EST	LIB25-038-Q1-E1-C4
Method	BLASTX
NCBI GI	g2244910
BLAST score	175
E value	1.0e-12
Match length	83
% identity	40
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	128569
Contig ID	29564_1.R1010
5'-most EST	jC-atXLIB327430P1c05b1
Method	BLASTN
NCBI GI	g3065834
BLAST score	389
E value	0.0e+00
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana putative methyltransferase gene, complete cds

Seq. No.	128570
Contig ID	29565_1.R1010
5'-most EST	jC-atXLIB327422P3h04b2
Method	BLASTX
NCBI GI	g3894387
BLAST score	231
E value	6.0e-19
Match length	166
% identity	3

NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]
Seq. No.	128571
Contig ID	29569_1.R1010
5'-most EST	jC-atXP33C148D11T7s2
Method	BLASTX
NCBI GI	g4490737
BLAST score	199
E value	2.0e-15
Match length	54
% identity	69
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	128572
Contig ID	29569_2.R1010
5'-most EST	jC-atXLIB327422P4h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	78
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	128573
Contig ID	29575_1.R1010
5'-most EST	jC-atX25035Q1E1D10b1
Method	BLASTN
NCBI GI	g4522002
BLAST score	509
E value	0.0e+00
Match length	864
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T23K3 genomic sequence, complete sequence
Seq. No.	128574
Contig ID	29583_1.R1010
5'-most EST	jC-atXLIB327422P3h12b2
Seq. No.	128575
Contig ID	29585_1.R1010
5'-most EST	LIB25-035-Q1-E1-E10
Method	BLASTX
NCBI GI	g629670
BLAST score	637
E value	3.0e-66
Match length	232
% identity	53
NCBI Description	hypothetical protein - tomato
Seq. No.	128576
Contig ID	29587_1.R1010
5'-most EST	LIB3176-066-P1-K1-F7
Method	BLASTX
NCBI GI	g3402722

BLAST score	1484
E value	1.0e-165
Match length	324
% identity	90
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	128577
Contig ID	29595_1.R1010
5'-most EST	jC-atX25030Q1E1A09a1
Method	BLASTN
NCBI GI	g2760168
BLAST score	343
E value	0.0e+00
Match length	347
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	128578
Contig ID	29597_1.R1010
5'-most EST	jC-atXLIB327430P1c10b1
Method	BLASTX
NCBI GI	g4204257
BLAST score	401
E value	6.0e-39
Match length	98
% identity	71
NCBI Description	(AC005223) 5493 [Arabidopsis thaliana]

Seq. No.	128579
Contig ID	29610_1.R1010
5'-most EST	jC-atXLIB327423P3b02b1
Method	BLASTN
NCBI GI	g2739359
BLAST score	476
E value	0.0e+00
Match length	476
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128580
Contig ID	29617_1.R1010
5'-most EST	LIB25-036-Q1-E1-A12

Seq. No.	128581
Contig ID	29618_1.R1010
5'-most EST	g762898
Method	BLASTX
NCBI GI	g2760325
BLAST score	610
E value	2.0e-63
Match length	186
% identity	66
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No.	128582

Contig ID	29626_1.R1010
5'-most EST	LIB3175-056-P1-K1-F7
Method	BLASTX
NCBI GI	g4539465
BLAST score	138
E value	1.0e-31
Match length	72
% identity	91
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	128583
Contig ID	29635_1.R1010
5'-most EST	jC-atXLIB327422P1h05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	78
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128584
Contig ID	29635_2.R1010
5'-most EST	LIB3175-056-P1-K1-A1
Method	BLASTN
NCBI GI	g3449326
BLAST score	555
E value	0.0e+00
Match length	555
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	128585
Contig ID	29638_1.R1010
5'-most EST	LIB25-036-Q1-E1-C11
Method	BLASTX
NCBI GI	g461999
BLAST score	108
E value	3.0e-81
Match length	199
% identity	79
NCBI Description	ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No.	128586
Contig ID	29645_1.R1010
5'-most EST	LIB3175-052-P1-K1-B7
Method	BLASTX
NCBI GI	g4056506
BLAST score	616
E value	3.0e-64
Match length	124
% identity	99
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 128587

Contig ID	29675_1.R1010
5'-most EST	jC-atXLIB327423P1b03a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	2.0e-20
Match length	78
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128588
Contig ID	29676_1.R1010
5'-most EST	jC-atXLIB327431P4e02a1
Method	BLASTX
NCBI GI	g2914700
BLAST score	672
E value	1.0e-70
Match length	133
% identity	100
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	128589
Contig ID	29681_1.R1010
5'-most EST	jC-atXLIB327430P4c03b1
Method	BLASTN
NCBI GI	g2244991
BLAST score	296
E value	1.0e-165
Match length	570
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	128590
Contig ID	29684_1.R1010
5'-most EST	jC-atXLIB327423P4b02a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	81
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128591
Contig ID	29685_1.R1010
5'-most EST	jC-alX25036Q1E1H11b1
Method	BLASTX
NCBI GI	g2213592
BLAST score	313
E value	8.0e-29
Match length	100
% identity	31
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	128592
Contig ID	29688_1.R1010
5'-most EST	LIB25-036-Q1-E1-H4

Seq. No.	128593
Contig ID	29690_1.R1010
5'-most EST	LIB25-036-Q1-E1-H6
Method	BLASTN
NCBI GI	g3299824
BLAST score	246
E value	1.0e-136
Match length	371
% identity	98
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128594
Contig ID	29695_1.R1010
5'-most EST	jC-atXLIB327422P3g02b2
Method	BLASTX
NCBI GI	g1174621
BLAST score	344
E value	6.0e-32
Match length	135
% identity	51
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	128595
Contig ID	29701_1.R1010
5'-most EST	LIB25-037-Q1-E1-A6
Method	BLASTX
NCBI GI	g4567246
BLAST score	426
E value	6.0e-42
Match length	91
% identity	88
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	128596
Contig ID	29702_1.R1010
5'-most EST	jC-atXLIB327422P1g12b1
Method	BLASTN
NCBI GI	g2696018
BLAST score	391
E value	0.0e+00
Match length	527
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	128597
Contig ID	29704_1.R1010

5'-most EST	LIB25-037-Q1-E1-A9
Seq. No.	128598
Contig ID	29706_1.R1010
5'-most EST	LIB25-037-Q1-E1-B11
Method	BLASTX
NCBI GI	g3914403
BLAST score	377
E value	5.0e-36
Match length	94
% identity	73
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II) >gi_2370335_emb_CAA73866_ (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_ (AB020500) mitochondrial protoporphyrinogen oxidase [Nicotiana tabacum] >gi_4105188 (AF044129) protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]
Seq. No.	128599
Contig ID	29707_1.R1010
5'-most EST	LIB25-037-Q1-E1-B12
Method	BLASTX
NCBI GI	g1220453
BLAST score	1092
E value	1.0e-120
Match length	254
% identity	76
NCBI Description	(M79328) alpha-amylase [Solanum tuberosum]
Seq. No.	128600
Contig ID	29709_1.R1010
5'-most EST	LIB3168-040-P1-K1-F5
Method	BLASTN
NCBI GI	g1931636
BLAST score	458
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.	128601
Contig ID	29714_1.R1010
5'-most EST	LIB3234-020-P1-K1-B5
Method	BLASTX
NCBI GI	g2344889
BLAST score	1230
E value	1.0e-136
Match length	270
% identity	93
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.	128602
Contig ID	29728_1.R1010
5'-most EST	LIB25-037-Q1-E1-D11
Method	BLASTN
NCBI GI	g3242970

BLAST score	198
E value	1.0e-107
Match length	573
% identity	99
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128603
Contig ID	29729_1.R1010
5'-most EST	LIB3177-012-P1-K2-D1
Method	BLASTX
NCBI GI	g1652217
BLAST score	201
E value	3.0e-15
Match length	180
% identity	29
NCBI Description	(D90903) hypothetical protein [Synechocystis sp.]

Seq. No.	128604
Contig ID	29731_1.R1010
5'-most EST	LIB3175-059-P1-K1-B11
Method	BLASTX
NCBI GI	g2554767
BLAST score	248
E value	5.0e-21
Match length	68
% identity	68
NCBI Description	Chain A, EndoEXOCELLULASE:CELLOBIOSE FROM THERMOMONOSPORA >gi_2554768_pdb_1JS4_B Chain B, EndoEXOCELLULASE:CELLOBIOSE FROM THERMOMONOSPORA >gi_2554821_pdb_4TF4_A Chain A, EndoEXOCELLULASE:CELLOPENTAOSE FROM THERMOMONOSPORA >gi_2554822_pdb_4TF4_B Chain B, EndoEXOCELLULASE:CELLOPENTAOSE FROM THERMOMONOSPORA >gi_2554825_pdb_3TF4_A Chain A, EndoEXOCELLULASE:CELLOTRIOSE FROM THERMOMONOSPORA >gi_2554826_pdb_3TF4_B Chain B, EndoEXOCELLULASE:CELLOTRIOSE FROM THERMOMONOSPORA >gi_2554833_pdb_1TF4_A Chain A, EndoEXOCELLULASE FROM THERMOMONOSPORA >gi_2554834_pdb_1TF4_B Chain B, EndoEXOCELLULASE FROM THERMOMONOSPORA

Seq. No.	128605
Contig ID	29732_1.R1010
5'-most EST	LIB25-037-Q1-E1-D4
Method	BLASTX
NCBI GI	g3250677
BLAST score	694
E value	2.0e-73
Match length	134
% identity	100
NCBI Description	(AL024486) putative Fe(II) transport protein [Arabidopsis thaliana]

Seq. No.	128606
Contig ID	29739_1.R1010
5'-most EST	jC-atXLIB327423P2a07b1
Method	BLASTN

NCBI GI	g4063735
BLAST score	233
E value	1.0e-128
Match length	444
% identity	98
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128607
Contig ID	29741_1.R1010
5'-most EST	LIB25-037-Q1-E1-E2
Method	BLASTN
NCBI GI	g4159708
BLAST score	165
E value	2.0e-87
Match length	518
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	128608
Contig ID	29763_1.R1010
5'-most EST	jC-atXLIB327423P3a11b1
Method	BLASTX
NCBI GI	g4056455
BLAST score	113
E value	2.0e-54
Match length	167
% identity	71
NCBI Description	(AC005990) Similar to gb_L19255 carbonic anhydrase from Nicotiana tabacum and a member of the prokaryotic-type carbonic anhydrase family PF_00484. EST gb_Z235745 comes from this gene. [Arabidopsis thaliana]

Seq. No.	128609
Contig ID	29776_1.R1010
5'-most EST	LIB25-037-Q1-E1-H7
Method	BLASTN
NCBI GI	g4757412
BLAST score	219
E value	1.0e-120
Match length	219
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK23, complete sequence

Seq. No.	128610
Contig ID	29779_1.R1010
5'-most EST	LIB25-038-Q1-E1-A10

Seq. No.	128611
Contig ID	29782_1.R1010
5'-most EST	jC-atXLIB327422P3g04b2
Method	BLASTN
NCBI GI	g3046856
BLAST score	261
E value	1.0e-145

Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	128612
Contig ID	29787_1.R1010
5'-most EST	jC-atXLIB327430P1c03b1
Method	BLASTX
NCBI GI	g3695023
BLAST score	294
E value	2.0e-26
Match length	138
% identity	50
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	128613
Contig ID	29788_1.R1010
5'-most EST	LIB25-038-Q1-E1-A9
Method	BLASTN
NCBI GI	g4510360
BLAST score	324
E value	0.0e+00
Match length	407
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	128614
Contig ID	29794_1.R1010
5'-most EST	LIB25-069-Q1-E1-D9
Method	BLASTN
NCBI GI	g4519195
BLAST score	260
E value	1.0e-144
Match length	470
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	128615
Contig ID	29794_2.R1010
5'-most EST	jC-atXLIB327425P3b09b1
Method	BLASTN
NCBI GI	g2914688
BLAST score	243
E value	1.0e-134
Match length	243
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128616
Contig ID	29794_3.R1010
5'-most EST	jC-atXLIB327422P1h03b1
Method	BLASTN
NCBI GI	g4218109

BLAST score 531
E value 0.0e+00
Match length 568
% identity 80
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No. 128617
Contig ID 29794_4.R1010
5'-most EST g905691
Method BLASTN
NCBI GI g4218109
BLAST score 130
E value 1.0e-66
Match length 496
% identity 66
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No. 128618
Contig ID 29794_5.R1010
5'-most EST jC-atXP69C217M2T7075d1
Method BLASTN
NCBI GI g4584531
BLAST score 65
E value 1.0e-27
Match length 218
% identity 10
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No. 128619
Contig ID 29794_6.R1010
5'-most EST ARABL1-041-Q1-E1-A2
Method BLASTN
NCBI GI g4519195
BLAST score 265
E value 1.0e-147
Match length 281
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No. 128620
Contig ID 29794_8.R1010
5'-most EST g460455
Method BLASTN
NCBI GI g2914688
BLAST score 266
E value 1.0e-148
Match length 286
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 128621
Contig ID 29794_10.R1010

5'-most EST	LIB3177-008-P1-K2-E11
Method	BLASTN
NCBI GI	g4220627
BLAST score	113
E value	1.0e-56
Match length	395
% identity	5
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	128622
Contig ID	29795_1.R1010
5'-most EST	jC-atXLIB327422P1h04b1
Method	BLASTX
NCBI GI	g4585993
BLAST score	162
E value	6.0e-11
Match length	40
% identity	75
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	128623
Contig ID	29800_1.R1010
5'-most EST	jC-atXLIB327422P1h08b1
Method	BLASTX
NCBI GI	g4467135
BLAST score	360
E value	4.0e-34
Match length	110
% identity	60
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	128624
Contig ID	29802_1.R1010
5'-most EST	jC-atXLIB327422P2h11b2
Method	BLASTX
NCBI GI	g2494144
BLAST score	359
E value	5.0e-34
Match length	159
% identity	54
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	128625
Contig ID	29807_1.R1010
5'-most EST	LIB25-038-Q1-E1-C5
Method	BLASTX
NCBI GI	g4263821
BLAST score	184
E value	2.0e-13
Match length	76
% identity	51
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No. 128626

Contig ID	29808_1.R1010
5'-most EST	jC-atXLIB327422P1h09b1
Method	BLASTX
NCBI GI	g3582333
BLAST score	797
E value	2.0e-85
Match length	148
% identity	100
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128627
Contig ID	29810_1.R1010
5'-most EST	g2759825
Method	BLASTX
NCBI GI	g4585972
BLAST score	231
E value	7.0e-23
Match length	89
% identity	66
NCBI Description	(AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No.	128628
Contig ID	29812_1.R1010
5'-most EST	jC-atXLIB327422P3h06b2
Method	BLASTX
NCBI GI	g3036796
BLAST score	584
E value	2.0e-60
Match length	137
% identity	81
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805858_emb_CAA21478_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	128629
Contig ID	29812_2.R1010
5'-most EST	g2048204
Method	BLASTN
NCBI GI	g3805839
BLAST score	258
E value	1.0e-143
Match length	428
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	128630
Contig ID	29823_1.R1010
5'-most EST	jC-atXLIB327423P1a07b1
Method	BLASTX
NCBI GI	g1549376
BLAST score	172
E value	9.0e-12
Match length	117
% identity	42
NCBI Description	(U62616) putative protein [Synechococcus PCC7942]

Seq. No.	128631
Contig ID	29824_1.R1010
5'-most EST	jC-atXLIB327423P1a08b1

Seq. No.	128632
Contig ID	29825_1.R1010
5'-most EST	jC-atXLIB327416P2h03b1
Method	BLASTX
NCBI GI	g4191784
BLAST score	1373
E value	1.0e-152
Match length	267
% identity	97
NCBI Description	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	128633
Contig ID	29825_2.R1010
5'-most EST	g3449462
Method	BLASTN
NCBI GI	g4191771
BLAST score	273
E value	1.0e-152
Match length	315
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128634
Contig ID	29831_1.R1010
5'-most EST	jC-atXP118C155I23T7064d2
Method	BLASTX
NCBI GI	g4585879
BLAST score	1015
E value	1.0e-110
Match length	224
% identity	83
NCBI Description	(AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

Seq. No.	128635
Contig ID	29834_1.R1010
5'-most EST	jC-atXLIB327423P1d04b1
Method	BLASTN
NCBI GI	g3063690
BLAST score	248
E value	1.0e-137
Match length	623
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	128636
Contig ID	29844_1.R1010
5'-most EST	jC-alX24001Q1E1A05b1
Method	BLASTN
NCBI GI	g4589424

BLAST score	316
E value	1.0e-178
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No.	128637
Contig ID	29852_1.R1010
5'-most EST	jC-atXLIB327423P1b09b1
Method	BLASTX
NCBI GI	g4512675
BLAST score	900
E value	4.0e-97
Match length	173
% identity	100
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	128638
Contig ID	29858_1.R1010
5'-most EST	jC-atXLIB327427P3a09b2
Method	BLASTN
NCBI GI	g4662609
BLAST score	152
E value	1.0e-79
Match length	463
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	128639
Contig ID	29864_1.R1010
5'-most EST	jC-atXLIB327430P3d09b1

Seq. No.	128640
Contig ID	29872_1.R1010
5'-most EST	jC-atX25039Q1E1B11b1
Method	BLASTN
NCBI GI	g2739359
BLAST score	299
E value	1.0e-167
Match length	409
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128641
Contig ID	29874_1.R1010
5'-most EST	g2748704
Method	BLASTN
NCBI GI	g4490734
BLAST score	215
E value	1.0e-117
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	128642
Contig ID	29876_1.R1010
5'-most EST	jC-atXLIB327424P4f09b1
Method	BLASTN
NCBI GI	g4490734
BLAST score	134
E value	6.0e-69
Match length	511
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	128643
Contig ID	29882_1.R1010
5'-most EST	jC-atXLIB327424P1g01b2
Method	BLASTX
NCBI GI	g3850823
BLAST score	134
E value	3.0e-11
Match length	67
% identity	67
NCBI Description	(Y18351) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]

Seq. No.	128644
Contig ID	29885_1.R1010
5'-most EST	jC-atXLIB327403P3g04b1

Seq. No.	128645
Contig ID	29886_1.R1010
5'-most EST	jC-atXLIB327424P1g05b2
Method	BLASTN
NCBI GI	g2656027
BLAST score	250
E value	1.0e-138
Match length	790
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJH22

Seq. No.	128646
Contig ID	29889_1.R1010
5'-most EST	LIB25-039-Q1-E1-C5
Method	BLASTX
NCBI GI	g2252841
BLAST score	555
E value	6.0e-57
Match length	140
% identity	76
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	128647
Contig ID	29891_1.R1010
5'-most EST	jC-atXLIB327424P1g02b2
Method	BLASTX
NCBI GI	g4581146

BLAST score	485
E value	8.0e-49
Match length	133
% identity	74
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	128648
Contig ID	29892_2.R1010
5'-most EST	jC-atXLIB327403P3g02b1
Method	BLASTX
NCBI GI	g2642157
BLAST score	528
E value	6.0e-54
Match length	124
% identity	80
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	128649
Contig ID	29896_1.R1010
5'-most EST	LIB3234-038-P1-K1-G9
Method	BLASTX
NCBI GI	g1174583
BLAST score	241
E value	4.0e-20
Match length	140
% identity	36
NCBI Description	TRANSALDOLASE >gi_1074653_pir__D64167 hypothetical protein HI1125 - Haemophilus influenzae (strain Rd KW20) >gi_1574680 (U32792) transaldolase B (talB) [Haemophilus influenzae Rd]

Seq. No.	128650
Contig ID	29897_1.R1010
5'-most EST	LIB25-039-Q1-E1-D12
Method	BLASTX
NCBI GI	g3096928
BLAST score	397
E value	1.0e-38
Match length	83
% identity	98
NCBI Description	(AL023094) bZIP transcription factor ATB2 [Arabidopsis thaliana]

Seq. No.	128651
Contig ID	29910_1.R1010
5'-most EST	jC-atXLIB327424P1h08b2
Method	BLASTN
NCBI GI	g4587641
BLAST score	118
E value	1.0e-59
Match length	368
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No. 128652

Contig ID	29919_1.R1010
5'-most EST	jC-atXLIB327424P1h03b2

Seq. No.	128653
Contig ID	29927_1.R1010
5'-most EST	LIB25-039-Q1-E1-G12
Method	BLASTX
NCBI GI	g2833375
BLAST score	364
E value	9.0e-35
Match length	71
% identity	96
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	128654
Contig ID	29933_1.R1010
5'-most EST	jC-alXLIB327436P3e12b1
Method	BLASTX
NCBI GI	g3128186
BLAST score	165
E value	3.0e-11
Match length	77
% identity	45
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128655
Contig ID	29942_1.R1010
5'-most EST	jC-atXLIB327430P2e06b1
Method	BLASTX
NCBI GI	g2281101
BLAST score	489
E value	3.0e-49
Match length	92
% identity	100
NCBI Description	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	128656
Contig ID	29950_1.R1010
5'-most EST	LIB25-040-Q1-E1-A6
Method	BLASTX
NCBI GI	g4731167
BLAST score	228
E value	2.0e-18
Match length	108
% identity	40
NCBI Description	(AF108357) c-myc binding protein MM-1 [Mus musculus]

Seq. No.	128657
Contig ID	29952_1.R1010
5'-most EST	LIB25-040-Q1-E1-A8
Method	BLASTN
NCBI GI	g4587986

BLAST score	58
E value	6.0e-24
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	128658
Contig ID	29962_1.R1010
5'-most EST	jC-alXLIB327436P2b04b1
Method	BLASTX
NCBI GI	g3461821
BLAST score	831
E value	3.0e-89
Match length	196
% identity	85
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	128659
Contig ID	29965_1.R1010
5'-most EST	LIB25-040-Q1-E1-C4
Method	BLASTX
NCBI GI	g4218535
BLAST score	471
E value	5.0e-47
Match length	150
% identity	59
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	128660
Contig ID	29970_1.R1010
5'-most EST	jC-atXLIB327424P1g10b2
Method	BLASTN
NCBI GI	g3046855
BLAST score	167
E value	9.0e-89
Match length	437
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	128661
Contig ID	29972_1.R1010
5'-most EST	jC-atXLIB327424P1g12b2
Method	BLASTX
NCBI GI	g3269287
BLAST score	389
E value	3.0e-39
Match length	114
% identity	68
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	128662
Contig ID	29974_1.R1010
5'-most EST	jC-atXLIB327424P3g01b1
Method	BLASTX

NCBI GI	g4581148
BLAST score	489
E value	4.0e-51
Match length	139
% identity	84
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128663
Contig ID	29979_1.R1010
5'-most EST	LIB25-040-Q1-E1-E1
Method	BLASTX
NCBI GI	g3892047
BLAST score	905
E value	7.0e-98
Match length	173
% identity	98
NCBI Description	(AC002330) putative bZIP-like DNA binding protein [Arabidopsis thaliana]

Seq. No.	128664
Contig ID	29985_1.R1010
5'-most EST	jC-atXLIB327430P2e09b1
Method	BLASTX
NCBI GI	g3482925
BLAST score	703
E value	2.0e-74
Match length	140
% identity	100
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	128665
Contig ID	29986_1.R1010
5'-most EST	LIB25-040-Q1-E1-E7

Seq. No.	128666
Contig ID	29992_1.R1010
5'-most EST	jC-atXLIB327426P3h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	61
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128667
Contig ID	29994_1.R1010
5'-most EST	g2445916
Method	BLASTN
NCBI GI	g2924734
BLAST score	332
E value	0.0e+00
Match length	496
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	128668
Contig ID	29994_2.R1010
5'-most EST	jC-atXLIB327424P1h02b2
Method	BLASTN
NCBI GI	g2924734
BLAST score	208
E value	1.0e-113
Match length	396
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	128669
Contig ID	30005_1.R1010
5'-most EST	LIB35-055-Q1-E2-E11
Method	BLASTX
NCBI GI	g4093169
BLAST score	244
E value	2.0e-52
Match length	162
% identity	65
NCBI Description	(AF095933) p20-Arc [Dictyostelium discoideum]

Seq. No.	128670
Contig ID	30009_1.R1010
5'-most EST	jC-atXLIB327424P3h01b1
Method	BLASTX
NCBI GI	g4455364
BLAST score	527
E value	2.0e-53
Match length	120
% identity	80
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	128671
Contig ID	30010_1.R1010
5'-most EST	LIB35-027-Q1-E1-E6
Method	BLASTN
NCBI GI	g4220633
BLAST score	311
E value	1.0e-175
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	128672
Contig ID	30013_1.R1010
5'-most EST	jC-atXLIB327424P1h11b2
Method	BLASTX
NCBI GI	g3367536
BLAST score	508
E value	5.0e-55
Match length	132

% identity	90
NCBI Description	(AC004392) Contains similarity to symbiosis-related like protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene. [Arabidopsis thaliana]

Seq. No.	128673
Contig ID	30016_1.R1010
5'-most EST	LIB25-040-Q1-E1-H9
Method	BLASTX
NCBI GI	g4220485
BLAST score	629
E value	1.0e-65
Match length	163
% identity	84
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	128674
Contig ID	30022_1.R1010
5'-most EST	LIB3176-106-P1-K1-D7
Method	BLASTX
NCBI GI	g4559334
BLAST score	871
E value	8.0e-94
Match length	181
% identity	90
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	128675
Contig ID	30023_1.R1010
5'-most EST	jC-atXLIB327424P1f07b2
Method	BLASTX
NCBI GI	g4417300
BLAST score	621
E value	9.0e-65
Match length	121
% identity	100
NCBI Description	(AC006446) hypothetical protein [Arabidopsis thaliana] >gi_4733990_gb_AAD28670.1_AC007209_6 (AC007209) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128676
Contig ID	30025_1.R1010
5'-most EST	jC-atXLIB327424P1f04b2
Method	BLASTX
NCBI GI	g4455363
BLAST score	101
E value	2.0e-13
Match length	163
% identity	35
NCBI Description	(AL035524) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	128677
Contig ID	30032_1.R1010
5'-most EST	jC-atXLIB327424P3f04b1

Method	BLASTN
NCBI GI	g2924729
BLAST score	278
E value	1.0e-155
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	128678
Contig ID	30033_1.R1010
5'-most EST	jC-atXLIB327424P4f05b1
Method	BLASTN
NCBI GI	g3702729
BLAST score	69
E value	5.0e-30
Match length	285
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A11, complete sequence [Arabidopsis thaliana]

Seq. No.	128679
Contig ID	30033_2.R1010
5'-most EST	LIB3175-056-P1-K1-F6
Method	BLASTX
NCBI GI	g3025194
BLAST score	167
E value	2.0e-11
Match length	75
% identity	43
NCBI Description	HYPOTHETICAL PROTEIN IN HYDROGENASE 1 5'REGION >gi_481588_pir__S38903 hypothetical protein 1 - Clostridium pasteurianum (fragment) >gi_431947_emb_CAA82208_ (Z28353) Similar to ABC1 gene of yeast (SW: ABC1_Yeast) [Clostridium pasteurianum]

Seq. No.	128680
Contig ID	30034_1.R1010
5'-most EST	LIB25-041-Q1-E1-B3
Method	BLASTX
NCBI GI	g4587530
BLAST score	394
E value	3.0e-38
Match length	111
% identity	66
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	128681
Contig ID	30036_1.R1010
5'-most EST	LIB25-041-Q1-E1-B5
Method	BLASTN
NCBI GI	g1871173
BLAST score	303
E value	1.0e-170
Match length	324

% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	128682
Contig ID	30037_1.R1010
5'-most EST	jC-atXP95CG12C7T7034d1
Method	BLASTN
NCBI GI	g1871173
BLAST score	301
E value	1.0e-168
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	128683
Contig ID	30040_1.R1010
5'-most EST	LIB25-041-Q1-E1-B9
Method	BLASTN
NCBI GI	g4585952
BLAST score	404
E value	0.0e+00
Match length	436
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	128684
Contig ID	30041_1.R1010
5'-most EST	jC-atXLIB327424P3f10b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	128685
Contig ID	30042_1.R1010
5'-most EST	jC-atXLIB327424P4f11b1

Seq. No.	128686
Contig ID	30046_1.R1010
5'-most EST	jC-atXLIB327424P4f12b1
Method	BLASTN
NCBI GI	g4678219
BLAST score	375
E value	0.0e+00
Match length	450
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	128687

Contig ID	30057_1.R1010
5'-most EST	jC-atXLIB327420P4b03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128688
Contig ID	30057_2.R1010
5'-most EST	jC-atXLIB327402P1g06b1

Seq. No.	128689
Contig ID	30067_1.R1010
5'-most EST	LIB25-041-Q1-E1-E4
Method	BLASTN
NCBI GI	g3402671
BLAST score	147
E value	6.0e-77
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128690
Contig ID	30082_1.R1010
5'-most EST	jC-atXLIB327424P3g09b1
Method	BLASTN
NCBI GI	g2760173
BLAST score	306
E value	1.0e-172
Match length	435
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	128691
Contig ID	30083_1.R1010
5'-most EST	jC-atXLIB327424P4g10b1
Method	BLASTX
NCBI GI	g4115922
BLAST score	592
E value	3.0e-65
Match length	130
% identity	87
NCBI Description	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]

Seq. No.	128692
Contig ID	30090_1.R1010
5'-most EST	jC-atXLIB327424P2h03b2
Method	BLASTX

NCBI GI	g1695882
BLAST score	362
E value	7.0e-38
Match length	182
% identity	51
NCBI Description	(U63743) mitotic centromere-associated kinesin [Homo sapiens]

Seq. No.	128693
Contig ID	30092_1.R1010
5'-most EST	jC-atXLIB327424P1h04b2
Method	BLASTN
NCBI GI	g2264306
BLAST score	172
E value	9.0e-92
Match length	355
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	128694
Contig ID	30093_1.R1010
5'-most EST	LIB25-041-Q1-E1-G8

Seq. No.	128695
Contig ID	30100_1.R1010
5'-most EST	jC-atXLIB327424P1h10b2
Method	BLASTN
NCBI GI	g3894179
BLAST score	450
E value	0.0e+00
Match length	601
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128696
Contig ID	30106_1.R1010
5'-most EST	LIB3176-067-P1-K1-B1

Seq. No.	128697
Contig ID	30106_2.R1010
5'-most EST	jC-atXLIB327430P1e07b1

Seq. No.	128698
Contig ID	30112_1.R1010
5'-most EST	jC-atXLIB327421P4c11b1
Method	BLASTX
NCBI GI	g1172538
BLAST score	1092
E value	1.0e-119
Match length	237
% identity	86
NCBI Description	PROBABLE PECTINESTERASE PRECURSOR (PECTIN METHYLESTERASE) (PE) >gi_99823_pir__S14952 pectinesterase homolog - rape >gi_17784_emb_CAA39658_ (X56195) Bp19 [Brassica napus]

Seq. No.	128699
Contig ID	30118_1.R1010
5'-most EST	LIB25-042-Q1-E1-B10
Method	BLASTX
NCBI GI	g2224899
BLAST score	50
E value	2.0e-11
Match length	73
% identity	45
NCBI Description	(U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No.	128700
Contig ID	30121_1.R1010
5'-most EST	jC-alX25045Q1E1D09b1
Method	BLASTX
NCBI GI	g4572680
BLAST score	558
E value	2.0e-57
Match length	137
% identity	18
NCBI Description	(AC006954) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128701
Contig ID	30124_1.R1010
5'-most EST	jC-atXmonuni25Ba03b1
Method	BLASTX
NCBI GI	g3608145
BLAST score	166
E value	2.0e-11
Match length	41
% identity	71
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128702
Contig ID	30125_1.R1010
5'-most EST	jC-atXP11C97O20T7s1

Seq. No.	128703
Contig ID	30128_1.R1010
5'-most EST	jC-atXLIB327404P3c01a1
Method	BLASTX
NCBI GI	g2827546
BLAST score	307
E value	9.0e-28
Match length	91
% identity	59
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	128704
Contig ID	30135_1.R1010
5'-most EST	jC-atXLIB327430P2e11b1
Method	BLASTX
NCBI GI	g3860163
BLAST score	364
E value	1.0e-34
Match length	137

% identity	55
NCBI Description	(AF098962) disease resistance protein RPP1-WsA [Arabidopsis thaliana]

Seq. No.	128705
Contig ID	30137_1.R1010
5'-most EST	LIB25-042-Q1-E1-C8
Method	BLASTN
NCBI GI	g3046847
BLAST score	255
E value	1.0e-141
Match length	328
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	128706
Contig ID	30138_1.R1010
5'-most EST	LIB25-097-Q1-E1-F11
Method	BLASTX
NCBI GI	g4406764
BLAST score	561
E value	9.0e-58
Match length	146
% identity	26
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	128707
Contig ID	30145_1.R1010
5'-most EST	LIB3168-005-P1-K1-G12
Method	BLASTN
NCBI GI	g3449330
BLAST score	439
E value	0.0e+00
Match length	607
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	128708
Contig ID	30148_1.R1010
5'-most EST	jC-atXLIB327430P4e02b1
Method	BLASTN
NCBI GI	g2244950
BLAST score	164
E value	5.0e-87
Match length	335
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	128709
Contig ID	30157_1.R1010
5'-most EST	jC-atXLIB327430P4e03b1
Method	BLASTN
NCBI GI	g3176701

BLAST score	189
E value	1.0e-102
Match length	499
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128710
Contig ID	30160_1.R1010
5'-most EST	g2749664
Method	BLASTX
NCBI GI	g3850584
BLAST score	535
E value	1.0e-54
Match length	136
% identity	79
NCBI Description	(AC005278) ESTs gb_H37641 and gb_AA651422 come from this gene. [Arabidopsis thaliana]

Seq. No.	128711
Contig ID	30160_2.R1010
5'-most EST	jC-atXLIB327425P3b11b1
Method	BLASTX
NCBI GI	g3850584
BLAST score	647
E value	8.0e-68
Match length	135
% identity	95
NCBI Description	(AC005278) ESTs gb_H37641 and gb_AA651422 come from this gene. [Arabidopsis thaliana]

Seq. No.	128712
Contig ID	30165_1.R1010
5'-most EST	LIB3176-061-P1-K1-A2
Method	BLASTN
NCBI GI	g4753195
BLAST score	62
E value	8.0e-26
Match length	596
% identity	84
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	128713
Contig ID	30169_1.R1010
5'-most EST	jC-alX25044Q1E1D09b1
Method	BLASTN
NCBI GI	g2623294
BLAST score	366
E value	0.0e+00
Match length	492
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128714
Contig ID	30170_1.R1010

5'-most EST	jC-atXmonuni25Ac11b1

Seq. No.	128715
Contig ID	30171_1.R1010
5'-most EST	LIB35-027-Q1-E1-H3
Method	BLASTX
NCBI GI	g3176676
BLAST score	430
E value	6.0e-42
Match length	214
% identity	40
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	128716
Contig ID	30171_2.R1010
5'-most EST	jC-atXmonuni25Ac12b1
Method	BLASTX
NCBI GI	g1168745
BLAST score	173
E value	3.0e-12
Match length	66
% identity	48
NCBI Description	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi_1084443_pir__S48675 carbonic anhydrase - Flaveria bidentis >gi_1089983_prf__2018192A carbonic anhydrase [Flaveria bidentis]

Seq. No.	128717
Contig ID	30174_1.R1010
5'-most EST	LIB25-043-Q1-E1-E8
Method	BLASTX
NCBI GI	g3236476
BLAST score	399
E value	8.0e-39
Match length	84
% identity	96
NCBI Description	(AF071195) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	128718
Contig ID	30175_1.R1010
5'-most EST	jC-alX25045Q1E1G01b1
Method	BLASTX
NCBI GI	g3445212
BLAST score	95
E value	9.0e-45
Match length	146
% identity	64
NCBI Description	(AC004786) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	128719
Contig ID	30176_1.R1010
5'-most EST	jC-atXmonuni25Ac10b1
Method	BLASTX

NCBI GI	g3600039
BLAST score	423
E value	1.0e-41
Match length	166
% identity	49
NCBI Description	(AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No.	128720
Contig ID	30180_1.R1010
5'-most EST	jC-atXmonuni25Cc12a1
Method	BLASTX
NCBI GI	g3548810
BLAST score	191
E value	2.0e-14
Match length	108
% identity	40
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	128721
Contig ID	30182_1.R1010
5'-most EST	jC-atXmonuni25Ad01b1

Seq. No.	128722
Contig ID	30183_2.R1010
5'-most EST	jC-atXP124C122B23T7d1
Method	BLASTN
NCBI GI	g2651294
BLAST score	303
E value	1.0e-169
Match length	903
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128723
Contig ID	30184_1.R1010
5'-most EST	jC-alX25043Q1E1G05b1
Method	BLASTN
NCBI GI	g4757403
BLAST score	120
E value	8.0e-61
Match length	451
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	128724
Contig ID	30185_1.R1010
5'-most EST	jC-atXmonuni25Cc11a1
Method	BLASTN
NCBI GI	g4220468
BLAST score	370
E value	0.0e+00
Match length	378
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	128725
Contig ID	30186_1.R1010
5'-most EST	LIB25-043-Q1-E1-A1
Method	BLASTX
NCBI GI	g3047125
BLAST score	931
E value	1.0e-101
Match length	180
% identity	99
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	128726
Contig ID	30186_2.R1010
5'-most EST	g315479
Method	BLASTX
NCBI GI	g3047125
BLAST score	381
E value	6.0e-65
Match length	132
% identity	96
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	128727
Contig ID	30190_1.R1010
5'-most EST	LIB25-043-Q1-E1-A2
Method	BLASTX
NCBI GI	g3915030
BLAST score	434
E value	1.0e-42
Match length	104
% identity	78
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_629712_pir__S44202 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) - Commerson's wild potato >gi_474833_emb_CAA55535_ (X78935) stearoyl-acyl carrier protein desaturase [Solanum commersonii]
Seq. No.	128728
Contig ID	30193_1.R1010
5'-most EST	jC-atXLIB327424P4h09b1
Method	BLASTX
NCBI GI	g3451068
BLAST score	589
E value	8.0e-61
Match length	191
% identity	71
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]
Seq. No.	128729
Contig ID	30194_1.R1010
5'-most EST	jC-atXLIB327424P3h09b1
Method	BLASTX
NCBI GI	g3885341

BLAST score	249
E value	3.0e-21
Match length	106
% identity	42
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	128730
Contig ID	30196_1.R1010
5'-most EST	jC-atXLIB327424P4h11b1

Seq. No.	128731
Contig ID	30215_1.R1010
5'-most EST	jC-atXLIB327430P1e11b1
Method	BLASTN
NCBI GI	g3228389
BLAST score	245
E value	1.0e-135
Match length	466
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	128732
Contig ID	30223_1.R1010
5'-most EST	g2749337
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	128733
Contig ID	30223_2.R1010
5'-most EST	jC-alX25042Q1E1E05b1

Seq. No.	128734
Contig ID	30239_1.R1010
5'-most EST	jC-alX25043Q1E1F03b1
Method	BLASTX
NCBI GI	g2160185
BLAST score	349
E value	8.0e-33
Match length	125
% identity	48
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	128735
Contig ID	30240_1.R1010
5'-most EST	LIB25-043-Q1-E1-E6
Method	BLASTX
NCBI GI	g730456
BLAST score	563
E value	7.0e-58
Match length	138

% identity	73
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	128736
Contig ID	30243_1.R1010
5'-most EST	jC-atXLIB327431P3e05a1
Method	BLASTX
NCBI GI	g4539359
BLAST score	434
E value	2.0e-42
Match length	165
% identity	53
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	128737
Contig ID	30243_2.R1010
5'-most EST	jC-alXLIB327436P3f08b1
Method	BLASTX
NCBI GI	g4539359
BLAST score	254
E value	1.0e-21
Match length	94
% identity	52
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	128738
Contig ID	30251_1.R1010
5'-most EST	LIB25-043-Q1-E1-F6
Method	BLASTN
NCBI GI	g4585891
BLAST score	323
E value	0.0e+00
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1O3 genomic sequence, complete sequence

Seq. No.	128739
Contig ID	30262_1.R1010
5'-most EST	jC-alX25042Q1E1H07b1

Seq. No.	128740
Contig ID	30265_1.R1010
5'-most EST	LIB25-043-Q1-E1-G8
Method	BLASTX
NCBI GI	g1707019
BLAST score	620
E value	1.0e-64
Match length	156
% identity	80
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128741
Contig ID	30267_1.R1010
5'-most EST	jC-atXLIB327425P3c11b1
Method	BLASTN
NCBI GI	g3860242

BLAST score	236
E value	1.0e-130
Match length	447
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence

Seq. No.	128742
Contig ID	30269_1.R1010
5'-most EST	jC-atXLIB327425P3c12b1
Method	BLASTX
NCBI GI	g3687301
BLAST score	181
E value	4.0e-13
Match length	109
% identity	39
NCBI Description	(AJ006376) subtilisin-like protease [Lycopersicon esculentum] >gi_3687309_emb_CAA07001_ (AJ006380) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	128743
Contig ID	30272_1.R1010
5'-most EST	jC-atXmonuni25Cc09a1
Method	BLASTN
NCBI GI	g2623294
BLAST score	181
E value	3.0e-97
Match length	181
% identity	50
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128744
Contig ID	30273_1.R1010
5'-most EST	jC-atXmonuni25Cc10a1
Method	BLASTX
NCBI GI	g4262239
BLAST score	347
E value	1.0e-32
Match length	123
% identity	62
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	128745
Contig ID	30280_1.R1010
5'-most EST	jC-atXLIB327418P3d12b1
Method	BLASTX
NCBI GI	g2431771
BLAST score	236
E value	2.0e-19
Match length	74
% identity	62
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	128746
Contig ID	30280_2.R1010

5'-most EST	jC-atXLIB327418P3d12a2
Method	BLASTN
NCBI GI	g4159711
BLAST score	34
E value	2.0e-09
Match length	126
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD12, complete sequence

Seq. No.	128747
Contig ID	30282_1.R1010
5'-most EST	jC-atXP64C206G6T7d1
Method	BLASTN
NCBI GI	g4582444
BLAST score	949
E value	0.0e+00
Match length	953
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	128748
Contig ID	30292_1.R1010
5'-most EST	LIB317S-029-P1-K1-D10
Method	BLASTX
NCBI GI	g2924512
BLAST score	61
E value	6.0e-65
Match length	225
% identity	50
NCBI Description	(AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No.	128749
Contig ID	30302_1.R1010
5'-most EST	jC-atX25044Q1E1C07b1
Method	BLASTX
NCBI GI	g3367596
BLAST score	455
E value	2.0e-45
Match length	115
% identity	78
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	128750
Contig ID	30305_1.R1010
5'-most EST	jC-atXLIB327425P1b02b1
Method	BLASTX
NCBI GI	g3355490
BLAST score	573
E value	4.0e-59
Match length	134
% identity	86
NCBI Description	(AC004218) putative dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	128751
Contig ID	30318_1.R1010
5'-most EST	LIB25-044-Q1-E1-E12
Method	BLASTX
NCBI GI	g2244781
BLAST score	310
E value	3.0e-28
Match length	118
% identity	30
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128752
Contig ID	30322_1.R1010
5'-most EST	LIB25-044-Q1-E1-E5
Method	BLASTX
NCBI GI	g2827655
BLAST score	293
E value	2.0e-26
Match length	135
% identity	27
NCBI Description	(AL021637) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128753
Contig ID	30325_1.R1010
5'-most EST	LIB3175-021-P1-K1-A12
Method	BLASTX
NCBI GI	g3157931
BLAST score	1283
E value	1.0e-142
Match length	248
% identity	100
NCBI Description	(AC002131) Similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come from this gene. [Arabidopsis thaliana]

Seq. No.	128754
Contig ID	30349_1.R1010
5'-most EST	jC-alX25051Q1E1E11b1

Seq. No.	128755
Contig ID	30349_2.R1010
5'-most EST	LIB25-044-Q1-E1-H6

Seq. No.	128756
Contig ID	30355_1.R1010
5'-most EST	jC-atX25045Q1E1A03b1
Method	BLASTX
NCBI GI	g4544438
BLAST score	467
E value	6.0e-47
Match length	108
% identity	87
NCBI Description	(AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128757
Contig ID	30357_1.R1010

5'-most EST	LIB25-045-Q1-E1-A5
Method	BLASTX
NCBI GI	g3142294
BLAST score	598
E value	3.0e-69
Match length	145
% identity	92
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	128758
Contig ID	30366_1.R1010
5'-most EST	jC-atXLIB327425P1a08b1
Method	BLASTN
NCBI GI	g2351069
BLAST score	233
E value	1.0e-128
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	128759
Contig ID	30371_1.R1010
5'-most EST	LIB25-045-Q1-E1-C10

Seq. No.	128760
Contig ID	30373_1.R1010
5'-most EST	jC-alX25044Q1E1C12a1
Method	BLASTN
NCBI GI	g4490717
BLAST score	75
E value	5.0e-34
Match length	157
% identity	32
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	128761
Contig ID	30375_1.R1010
5'-most EST	LIB25-045-Q1-E1-C3
Method	BLASTX
NCBI GI	g2827549
BLAST score	473
E value	1.0e-47
Match length	90
% identity	100
NCBI Description	(AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	128762
Contig ID	30392_1.R1010
5'-most EST	LIB25-045-Q1-E1-E11
Method	BLASTN
NCBI GI	g4454004
BLAST score	432

E value	0.0e+00
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	128763
Contig ID	30394_1.R1010
5'-most EST	jC-atXmonuni25Ab11b1
Method	BLASTX
NCBI GI	g416652
BLAST score	554
E value	1.0e-56
Match length	181
% identity	59
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PCNT107) >gi_19793_emb_CAA39707_ (X56266) auxin-induced protein [Nicotiana tabacum]

Seq. No.	128764
Contig ID	30398_2.R1010
5'-most EST	jC-atXmonuni25Ab09b1
Method	BLASTN
NCBI GI	g3046853
BLAST score	468
E value	0.0e+00
Match length	468
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	128765
Contig ID	30403_1.R1010
5'-most EST	LIB25-045-Q1-E1-F11

Seq. No.	128766
Contig ID	30405_1.R1010
5'-most EST	LIB25-045-Q1-E1-F4
Method	BLASTN
NCBI GI	g4734003
BLAST score	200
E value	1.0e-108
Match length	442
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F3L12 genomic sequence, complete sequence

Seq. No.	128767
Contig ID	30406_1.R1010
5'-most EST	jC-atXLIB327423P4f12b1
Method	BLASTX
NCBI GI	g132724
BLAST score	363
E value	3.0e-34
Match length	114
% identity	66
NCBI Description	50S RIBOSOMAL PROTEIN L18 >gi_71259_pir__R5BS8F ribosomal

protein L18 - Bacillus stearothermophilus

Seq. No.	128768
Contig ID	30412_1.R1010
5'-most EST	g1054394

Seq. No.	128769
Contig ID	30415_1.R1010
5'-most EST	g1033250
Method	BLASTX
NCBI GI	g3258238
BLAST score	225
E value	4.0e-18
Match length	148
% identity	34
NCBI Description	(AP000007) 224aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No.	128770
Contig ID	30416_1.R1010
5'-most EST	LIB25-045-Q1-E1-G5
Method	BLASTN
NCBI GI	g2656026
BLAST score	75
E value	7.0e-34
Match length	269
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	128771
Contig ID	30421_1.R1010
5'-most EST	jC-atXLIB327430P4e10b1
Method	BLASTX
NCBI GI	g2194132
BLAST score	453
E value	5.0e-45
Match length	166
% identity	58
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	128772
Contig ID	30422_1.R1010
5'-most EST	LIB25-045-Q1-E1-H11

Seq. No.	128773
Contig ID	30425_1.R1010
5'-most EST	jC-atXLIB327430P4e08b1
Method	BLASTN
NCBI GI	g4490734
BLAST score	211
E value	1.0e-115
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	128774
Contig ID	30430_1.R1010
5'-most EST	g3450282
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	1.0e-20
Match length	72
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	128775
Contig ID	30430_3.R1010
5'-most EST	LIB3176-036-P1-K1-D7

Seq. No.	128776
Contig ID	30443_1.R1010
5'-most EST	LIB3176-002-Q1-K1-B6
Method	BLASTX
NCBI GI	g2495179
BLAST score	571
E value	6.0e-59
Match length	116
% identity	100
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	128777
Contig ID	30445_1.R1010
5'-most EST	jC-atXLIB327425P3d08b1
Method	BLASTN
NCBI GI	g3785968
BLAST score	152
E value	7.0e-80
Match length	382
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128778
Contig ID	30447_1.R1010
5'-most EST	jC-atXmonuni25Cd05a1
Method	BLASTN
NCBI GI	g3046853
BLAST score	407
E value	0.0e+00
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	128779
Contig ID	30449_1.R1010
5'-most EST	LIB25-059-Q1-E1-G6
Method	BLASTX
NCBI GI	g3885513
BLAST score	362
E value	3.0e-34
Match length	80
% identity	81
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	128780
Contig ID	30449_2.R1010
5'-most EST	g2412908
Method	BLASTX
NCBI GI	g3885513
BLAST score	231
E value	3.0e-19
Match length	52
% identity	83
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	128781
Contig ID	30459_1.R1010
5'-most EST	LIB25-046-Q1-E1-C8
Method	BLASTX
NCBI GI	g3877256
BLAST score	246
E value	2.0e-20
Match length	119
% identity	43
NCBI Description	(Z50177) similar to lipase [Caenorhabditis elegans]

Seq. No.	128782
Contig ID	30460_1.R1010
5'-most EST	g2596323

Seq. No.	128783
Contig ID	30464_1.R1010
5'-most EST	jC-alX25048Q1E1C02b1
Method	BLASTX
NCBI GI	g3128172
BLAST score	511
E value	6.0e-52
Match length	143
% identity	68
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128784
Contig ID	30467_1.R1010
5'-most EST	jC-atX24042Q1E1G03a1
Method	BLASTX
NCBI GI	g3600047
BLAST score	584
E value	2.0e-60

Match length	139
% identity	89
NCBI Description	(AF080120) similar to elongation factor EF-Ts [Arabidopsis thaliana]

Seq. No.	128785
Contig ID	30471_1.R1010
5'-most EST	LIB25-046-Q1-E1-D8
Method	BLASTN
NCBI GI	g2656029
BLAST score	195
E value	1.0e-105
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	128786
Contig ID	30478_1.R1010
5'-most EST	jC-atXmonuni25Ce11a1
Method	BLASTN
NCBI GI	g3386593
BLAST score	439
E value	0.0e+00
Match length	439
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128787
Contig ID	30481_1.R1010
5'-most EST	jC-atXmonuni25Ce09a1
Method	BLASTN
NCBI GI	g3702736
BLAST score	417
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	128788
Contig ID	30484_1.R1010
5'-most EST	jC-atXP69C219J10T7078d1
Method	BLASTX
NCBI GI	g1208468
BLAST score	156
E value	7.0e-10
Match length	153
% identity	27
NCBI Description	(D64004) hypothetical protein [Synechocystis sp.]

Seq. No.	128789
Contig ID	30484_2.R1010
5'-most EST	g1159272

Seq. No.	128790

Contig ID	30501_1.R1010
5'-most EST	g572553
Method	BLASTX
NCBI GI	g2160176
BLAST score	542
E value	2.0e-55
Match length	203
% identity	57
NCBI Description	(AC000132) F21M12.25 gene product [Arabidopsis thaliana]

Seq. No.	128791
Contig ID	30503_1.R1010
5'-most EST	LIB3176-110-P1-K1-E12

Seq. No.	128792
Contig ID	30504_1.R1010
5'-most EST	LIB3175-080-P1-K1-G10

Seq. No.	128793
Contig ID	30505_1.R1010
5'-most EST	jC-atXmonuni25Cf11a1

Seq. No.	128794
Contig ID	30508_1.R1010
5'-most EST	LIB3176-008-P1-K2-B2
Method	BLASTX
NCBI GI	g3582340
BLAST score	164
E value	5.0e-11
Match length	125
% identity	43
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	128795
Contig ID	30514_1.R1010
5'-most EST	LIB3176-021-P1-K1-C7
Method	BLASTN
NCBI GI	g3399678
BLAST score	221
E value	1.0e-120
Match length	1486
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128796
Contig ID	30519_1.R1010
5'-most EST	LIB25-047-Q1-E1-A9
Method	BLASTX
NCBI GI	g3377844
BLAST score	212
E value	7.0e-17
Match length	67
% identity	76
NCBI Description	(AF076274) contains similarity to DNA (cytosine-5-)-methyltransferases [Arabidopsis thaliana]

Seq. No.	128797
Contig ID	30522_1.R1010
5'-most EST	jC-atXP29C135K20T7002d1

Seq. No.	128798
Contig ID	30522_2.R1010
5'-most EST	jC-atXP29C137L10T7003d1

Seq. No.	128799
Contig ID	30524_1.R1010
5'-most EST	jC-atXmonuni25Cd09a1

Seq. No.	128800
Contig ID	30526_1.R1010
5'-most EST	jC-atXLIB327425P3d04b1
Method	BLASTX
NCBI GI	g4038055
BLAST score	163
E value	3.0e-38
Match length	108
% identity	80
NCBI Description	(AC005897) putative cytochrome P450 [Arabidopsis thaliana] >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	128801
Contig ID	30529_1.R1010
5'-most EST	LIB25-047-Q1-E1-B9
Method	BLASTN
NCBI GI	g2656026
BLAST score	217
E value	1.0e-118
Match length	349
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	128802
Contig ID	30538_1.R1010
5'-most EST	jC-alX25048Q1E1F08b1
Method	BLASTX
NCBI GI	g3355471
BLAST score	369
E value	3.0e-35
Match length	110
% identity	56
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	128803
Contig ID	30546_1.R1010
5'-most EST	jC-alX25046Q1E1E05b1
Method	BLASTN
NCBI GI	g3738313
BLAST score	116
E value	2.0e-58
Match length	458

% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128804
Contig ID	30551_1.R1010
5'-most EST	LIB25-047-Q1-E1-E12
Method	BLASTX
NCBI GI	g3122601
BLAST score	93
E value	9.0e-03
Match length	165
% identity	11
NCBI Description	FLAGELLAR WD-REPEAT PROTEIN PF20 >gi_1813638 (U78547) PF20 [Chlamydomonas reinhardtii]

Seq. No.	128805
Contig ID	30553_1.R1010
5'-most EST	jC-atXLIB327425P3e10b1
Method	BLASTX
NCBI GI	g1079136
BLAST score	248
E value	5.0e-21
Match length	88
% identity	49
NCBI Description	RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) >gi_532788 (U13178) RNA binding protein [Drosophila melanogaster] >gi_567106 (L37083) RNA binding protein [Drosophila melanogaster]

Seq. No.	128806
Contig ID	30556_1.R1010
5'-most EST	jC-atXLIB327425P3e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128807
Contig ID	30558_1.R1010
5'-most EST	jC-atXLIB327425P3e09b1
Method	BLASTX
NCBI GI	g4584525
BLAST score	527
E value	1.0e-87
Match length	168
% identity	98
NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	128808
Contig ID	30558_2.R1010
5'-most EST	g2048359

Method	BLASTX
NCBI GI	g4584525
BLAST score	537
E value	6.0e-55
Match length	112
% identity	92
NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	128809
Contig ID	30560_1.R1010
5'-most EST	jC-alX25049Q1E1E12b1
Method	BLASTN
NCBI GI	g2760173
BLAST score	448
E value	0.0e+00
Match length	456
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	128810
Contig ID	30560_2.R1010
5'-most EST	jC-atXLIB327411P1f01b1
Method	BLASTN
NCBI GI	g2760173
BLAST score	219
E value	1.0e-119
Match length	632
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	128811
Contig ID	30563_1.R1010
5'-most EST	jC-atXLIB327419P4h08b1
Method	BLASTX
NCBI GI	g2342735
BLAST score	534
E value	3.0e-54
Match length	114
% identity	94
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	128812
Contig ID	30563_2.R1010
5'-most EST	g936287
Method	BLASTN
NCBI GI	g2342717
BLAST score	174
E value	5.0e-93
Match length	475
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 128813

Contig ID	30563_3.R1010
5'-most EST	jC-atXLIB327421P2c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128814
Contig ID	30566_1.R1010
5'-most EST	jC-atXP5C90E24T7d1
Method	BLASTX
NCBI GI	g2827621
BLAST score	642
E value	3.0e-67
Match length	174
% identity	78
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	128815
Contig ID	30577_1.R1010
5'-most EST	jC-atXLIB327425P3f02b1
Method	BLASTN
NCBI GI	g4689466
BLAST score	311
E value	1.0e-174
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	128816
Contig ID	30592_1.R1010
5'-most EST	jC-alX25047Q1E1B06b1
Method	BLASTX
NCBI GI	g4538941
BLAST score	499
E value	1.0e-50
Match length	109
% identity	92
NCBI Description	(AL049483) NPR1 like protein [Arabidopsis thaliana]

Seq. No.	128817
Contig ID	30594_1.R1010
5'-most EST	jC-alX25046Q1E1B08b1
Method	BLASTN
NCBI GI	g2275194
BLAST score	285
E value	1.0e-159
Match length	769
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128818
Contig ID	30594_2.R1010
5'-most EST	g1269507
Method	BLASTX
NCBI GI	g2275216
BLAST score	274
E value	4.0e-24
Match length	64
% identity	84
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]

Seq. No.	128819
Contig ID	30600_1.R1010
5'-most EST	LIB25-048-Q1-E1-B11
Method	BLASTN
NCBI GI	g2645198
BLAST score	370
E value	0.0e+00
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128820
Contig ID	30614_1.R1010
5'-most EST	jC-atXmonuni25Ae02b1
Method	BLASTX
NCBI GI	g3980412
BLAST score	577
E value	1.0e-59
Match length	159
% identity	15
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	128821
Contig ID	30625_1.R1010
5'-most EST	LIB25-048-Q1-E1-D7

Seq. No.	128822
Contig ID	30628_1.R1010
5'-most EST	jC-atXmonuni25Ce05a1
Method	BLASTN
NCBI GI	g4589427
BLAST score	198
E value	1.0e-107
Match length	466
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	128823
Contig ID	30641_1.R1010
5'-most EST	jC-atXLIB327430P1f07b1

Seq. No.	128824
Contig ID	30644_1.R1010

5'-most EST	jC-atXLIB327420P1b08b1
Seq. No.	128825
Contig ID	30652_1.R1010
5'-most EST	jC-atXLIB327425P1f11b1
Method	BLASTX
NCBI GI	g4539459
BLAST score	243
E value	2.0e-20
Match length	115
% identity	47
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]
Seq. No.	128826
Contig ID	30652_2.R1010
5'-most EST	jC-alXLIB327436P3h01b1
Method	BLASTX
NCBI GI	g4539459
BLAST score	384
E value	5.0e-37
Match length	138
% identity	59
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]
Seq. No.	128827
Contig ID	30659_1.R1010
5'-most EST	jC-atXLIB327425P3f07b1
Method	BLASTX
NCBI GI	g2842496
BLAST score	498
E value	3.0e-50
Match length	102
% identity	90
NCBI Description	(AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]
Seq. No.	128828
Contig ID	30662_1.R1010
5'-most EST	jC-atXmonuni25Cf05a1
Seq. No.	128829
Contig ID	30667_1.R1010
5'-most EST	g2763601
Method	BLASTN
NCBI GI	g4753645
BLAST score	164
E value	4.0e-87
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)
Seq. No.	128830
Contig ID	30670_1.R1010
5'-most EST	jC-atXLIB327425P1d05b1
Method	BLASTN
NCBI GI	g3510338
BLAST score	110

E value	9.0e-55
Match length	466
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21I16, complete sequence [Arabidopsis thaliana]

Seq. No.	128831
Contig ID	30672_1.R1010
5'-most EST	jC-atXLIB327425P1d02b1
Method	BLASTN
NCBI GI	g4335744
BLAST score	685
E value	0.0e+00
Match length	911
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128832
Contig ID	30677_1.R1010
5'-most EST	jC-atXP24C122L23T7014a1
Method	BLASTN
NCBI GI	g4580744
BLAST score	297
E value	1.0e-166
Match length	545
% identity	100
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	128833
Contig ID	30679_1.R1010
5'-most EST	g2597247
Method	BLASTX
NCBI GI	g4006829
BLAST score	257
E value	9.0e-22
Match length	161
% identity	40
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	128834
Contig ID	30683_1.R1010
5'-most EST	jC-atXLIB327425P3d03b1
Method	BLASTX
NCBI GI	g4567256
BLAST score	194
E value	1.0e-14
Match length	44
% identity	84
NCBI Description	(AC007070) putative 60S ribosomal protein L39 [Arabidopsis thaliana]

Seq. No.	128835
Contig ID	30684_1.R1010
5'-most EST	jC-atXmonuni25Ad11b1
Method	BLASTX

NCBI GI	g2827469
BLAST score	401
E value	1.0e-38
Match length	191
% identity	45
NCBI Description	(AF044255) NOSA [Dictyostelium discoideum]

Seq. No.	128836
Contig ID	30685_1.R1010
5'-most EST	jC-atXLIB327430P1f02b1
Method	BLASTX
NCBI GI	g2160148
BLAST score	1082
E value	1.0e-118
Match length	209
% identity	100
NCBI Description	(AC000375) EST gb_H37044 comes from this gene. [Arabidopsis thaliana]

Seq. No.	128837
Contig ID	30685_3.R1010
5'-most EST	LIB25-116-Q1-E1-F1
Method	BLASTN
NCBI GI	g2160132
BLAST score	237
E value	1.0e-130
Match length	598
% identity	97
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	128838
Contig ID	30686_1.R1010
5'-most EST	jC-alX25049Q1E1C12b1
Method	BLASTX
NCBI GI	g3367568
BLAST score	533
E value	2.0e-54
Match length	117
% identity	87
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	128839
Contig ID	30687_1.R1010
5'-most EST	jC-atXLIB327425P3d09b1
Method	BLASTX
NCBI GI	g4582489
BLAST score	99
E value	1.0e-03
Match length	146
% identity	25
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	128840
Contig ID	30694_1.R1010
5'-most EST	jC-atXLIB327425P3d10b1

Method	BLASTN
NCBI GI	g2264316
BLAST score	451
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	128841
Contig ID	30695_1.R1010
5'-most EST	jC-atXmonuni25Cd11a1
Method	BLASTX
NCBI GI	g3292831
BLAST score	187
E value	2.0e-56
Match length	179
% identity	59
NCBI Description	(AL031018) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	128842
Contig ID	30696_1.R1010
5'-most EST	jC-alX25048Q1E1B06b1
Method	BLASTX
NCBI GI	g4309732
BLAST score	144
E value	6.0e-09
Match length	39
% identity	72
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128843
Contig ID	30699_1.R1010
5'-most EST	jC-atXmonuni25Ae09b1
Method	BLASTX
NCBI GI	g3892708
BLAST score	774
E value	8.0e-83
Match length	145
% identity	100
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	128844
Contig ID	30703_1.R1010
5'-most EST	jC-atXmonuni25Ae10b1
Method	BLASTX
NCBI GI	g4455293
BLAST score	228
E value	7.0e-19
Match length	60
% identity	75
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	128845
Contig ID	30708_1.R1010
5'-most EST	jC-atXLIB327425P1e08b1

Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	128846
Contig ID	30710_1.R1010
5'-most EST	jC-atXLIB327425P3e04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128847
Contig ID	30711_1.R1010
5'-most EST	LIB3176-038-P1-K1-C6
Method	BLASTX
NCBI GI	g4538920
BLAST score	489
E value	2.0e-50
Match length	145
% identity	74
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	128848
Contig ID	30711_3.R1010
5'-most EST	LIB35-036-Q1-E2-H8
Method	BLASTX
NCBI GI	g4538920
BLAST score	250
E value	2.0e-21
Match length	58
% identity	41
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	128849
Contig ID	30713_1.R1010
5'-most EST	LIB3176-064-P1-K1-H2

Seq. No.	128850
Contig ID	30717_1.R1010
5'-most EST	jC-atXLIB327416P1h07b1
Method	BLASTX
NCBI GI	g4455206
BLAST score	469
E value	7.0e-47
Match length	133
% identity	70

NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	128851
Contig ID	30719_1.R1010
5'-most EST	LIB25-049-Q1-E1-E9
Method	BLASTN
NCBI GI	g3980374
BLAST score	282
E value	1.0e-157
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128852
Contig ID	30721_1.R1010
5'-most EST	jC-atXLIB327430P2f07b1
Method	BLASTX
NCBI GI	g3329294
BLAST score	212
E value	9.0e-17
Match length	139
% identity	39
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	128853
Contig ID	30723_1.R1010
5'-most EST	jC-atX25048Q1E1F03b1
Method	BLASTN
NCBI GI	g3241926
BLAST score	348
E value	0.0e+00
Match length	475
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	128854
Contig ID	30726_1.R1010
5'-most EST	g2597805
Method	BLASTX
NCBI GI	g4507711
BLAST score	290
E value	1.0e-25
Match length	160
% identity	41
NCBI Description	tetratricopeptide repeat domain 1 >gi_1688074 (U46570) tetratricopeptide repeat protein [Homo sapiens]

Seq. No.	128855
Contig ID	30729_1.R1010
5'-most EST	jC-atX25109Q1E1H12b1
Method	BLASTN
NCBI GI	g1209632
BLAST score	251

E value	1.0e-139
Match length	267
% identity	99
NCBI Description	Arabidopsis thaliana pattern-formation (GNOM) gene, complete cds

Seq. No.	128856
Contig ID	30731_1.R1010
5'-most EST	jC-atXLIB327430P1f11b1
Method	BLASTX
NCBI GI	g1705658
BLAST score	164
E value	4.0e-11
Match length	61
% identity	52
NCBI Description	CCAAT-BINDING FACTOR (CBF) >gi_107937_pir__A36368 transcription factor CBF, CCAAT-binding - human >gi_179969 (M37197) CCAAT-box-binding factor [Homo sapiens]

Seq. No.	128857
Contig ID	30734_1.R1010
5'-most EST	jC-atXLIB327430P2f11b1

Seq. No.	128858
Contig ID	30740_1.R1010
5'-most EST	g906161
Method	BLASTN
NCBI GI	g4581084
BLAST score	443
E value	0.0e+00
Match length	489
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	128859
Contig ID	30740_2.R1010
5'-most EST	jC-atXLIB327437P4e01a2
Method	BLASTN
NCBI GI	g4581084
BLAST score	212
E value	1.0e-115
Match length	470
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	128860
Contig ID	30747_1.R1010
5'-most EST	jC-atXmonuni25Cf07a1
Method	BLASTN
NCBI GI	g4006815
BLAST score	418
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128861
Contig ID	30749_1.R1010
5'-most EST	jC-atXLIB327425P3f09b1
Method	BLASTN
NCBI GI	g3510347
BLAST score	35
E value	5.0e-10
Match length	109
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	128862
Contig ID	30753_1.R1010
5'-most EST	jC-atXLIB327430P4f03b1
Method	BLASTN
NCBI GI	g3510341
BLAST score	41
E value	1.0e-13
Match length	269
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	128863
Contig ID	30762_1.R1010
5'-most EST	LIB25-050-Q1-E1-A9

Seq. No.	128864
Contig ID	30766_1.R1010
5'-most EST	jC-atXmonuni25Cg11a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	224
E value	1.0e-123
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	128865
Contig ID	30773_1.R1010
5'-most EST	g2597567

Seq. No.	128866
Contig ID	30774_1.R1010
5'-most EST	jC-alX25052Q1E1E02b1
Method	BLASTX
NCBI GI	g4589961
BLAST score	125
E value	1.0e-12
Match length	153
% identity	6
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	128867
Contig ID	30775_1.R1010
5'-most EST	jC-atXLIB327430P4f09b1

Seq. No.	128868
Contig ID	30781_1.R1010
5'-most EST	LIB25-050-Q1-E1-C8

Seq. No.	128869
Contig ID	30804_1.R1010
5'-most EST	jC-atXP74C225F18T7070d1
Method	BLASTX
NCBI GI	g3121825
BLAST score	576
E value	3.0e-59
Match length	116
% identity	95
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	128870
Contig ID	30804_2.R1010
5'-most EST	jC-atXmonuni25Ch09a1
Method	BLASTX
NCBI GI	g3121825
BLAST score	262
E value	9.0e-23
Match length	57
% identity	91
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	128871
Contig ID	30805_1.R1010
5'-most EST	jC-atXLIB327426P2a05b1

Seq. No.	128872
Contig ID	30808_1.R1010
5'-most EST	jC-atXLIB327426P3b09b1
Method	BLASTX
NCBI GI	g3540185
BLAST score	680
E value	4.0e-74
Match length	154
% identity	88
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	128873
Contig ID	30808_2.R1010
5'-most EST	LIB25-110-Q1-E1-E2
Method	BLASTN
NCBI GI	g3176693
BLAST score	223
E value	1.0e-122

Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128874
Contig ID	30809_1.R1010
5'-most EST	jC-atXLIB327426P2a09b1
Method	BLASTN
NCBI GI	g2191181
BLAST score	282
E value	1.0e-157
Match length	467
% identity	99
NCBI Description	Arabidopsis thaliana BAC TM021B04

Seq. No.	128875
Contig ID	30815_1.R1010
5'-most EST	jC-atXP32C147M12T7d2
Method	BLASTX
NCBI GI	g3327957
BLAST score	140
E value	7.0e-16
Match length	105
% identity	47
NCBI Description	(AF060490) TLS-associated protein TASR-2 [Mus musculus] >gi_3327976 (AF067730) TLS-associated protein TASR-2 [Homo sapiens]

Seq. No.	128876
Contig ID	30822_1.R1010
5'-most EST	jC-atXmonuni26Ca04b1
Method	BLASTX
NCBI GI	g2583116
BLAST score	233
E value	2.0e-19
Match length	45
% identity	100
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	128877
Contig ID	30824_1.R1010
5'-most EST	g2748543
Method	BLASTX
NCBI GI	g3256068
BLAST score	486
E value	5.0e-49
Match length	99
% identity	88
NCBI Description	(Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]

Seq. No.	128878
Contig ID	30826_1.R1010
5'-most EST	jC-atXLIB327426P1b02b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	45

E value	6.0e-16
Match length	49
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	128879
Contig ID	30827_1.R1010
5'-most EST	jC-atXLIB327426P2b02b1
Method	BLASTX
NCBI GI	g2634023
BLAST score	163
E value	6.0e-11
Match length	116
% identity	39
NCBI Description	(Z99112) uridylate kinase [Bacillus subtilis]

Seq. No.	128880
Contig ID	30829_1.R1010
5'-most EST	jC-atXLIB327426P2b04b1
Method	BLASTN
NCBI GI	g3869071
BLAST score	298
E value	1.0e-167
Match length	494
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	128881
Contig ID	30830_1.R1010
5'-most EST	jC-atXLIB327426P2b05b1
Method	BLASTN
NCBI GI	g2832639
BLAST score	565
E value	0.0e+00
Match length	586
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	128882
Contig ID	30832_1.R1010
5'-most EST	jC-atXLIB327426P2b01b1
Method	BLASTX
NCBI GI	g3241945
BLAST score	412
E value	4.0e-40
Match length	122
% identity	61
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	128883
Contig ID	30837_1.R1010
5'-most EST	LIB25-051-Q1-E1-A3
Method	BLASTN
NCBI GI	g4580454

BLAST score 145
E value 1.0e-75
Match length 567
% identity 97
NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No. 128884
Contig ID 30838_1.R1010
5'-most EST jC-alX25053Q1E1A01b1
Method BLASTX
NCBI GI g3953467
BLAST score 632
E value 3.0e-66
Match length 134
% identity 49
NCBI Description (AC002328) F20N2.12 [Arabidopsis thaliana]

Seq. No. 128885
Contig ID 30839_1.R1010
5'-most EST jC-atXLIB327425P1g09b1
Method BLASTN
NCBI GI g4589423
BLAST score 466
E value 0.0e+00
Match length 477
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence

Seq. No. 128886
Contig ID 30840_1.R1010
5'-most EST jC-alX25051Q1E1B11b1
Method BLASTX
NCBI GI g131754
BLAST score 235
E value 1.0e-19
Match length 110
% identity 51
NCBI Description PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_ (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

Seq. No. 128887
Contig ID 30843_1.R1010
5'-most EST jC-atXLIB327420P3h06b1
Method BLASTX
NCBI GI g4191774
BLAST score 228
E value 2.0e-20
Match length 103
% identity 55
NCBI Description (AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 128888

Contig ID	30848_1.R1010
5'-most EST	LIB3177-098-P1-K1-G11
Method	BLASTX
NCBI GI	g3927830
BLAST score	88
E value	5.0e-89
Match length	228
% identity	28
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128889
Contig ID	30848_2.R1010
5'-most EST	jC-atXmonuni25Cg12b1

Seq. No.	128890
Contig ID	30849_1.R1010
5'-most EST	jC-alX25053Q1E1A04b1
Method	BLASTX
NCBI GI	g4455308
BLAST score	481
E value	3.0e-48
Match length	92
% identity	100
NCBI Description	(AL035528) SAUR-AC-like protein (small auxin up RNA) [Arabidopsis thaliana]

Seq. No.	128891
Contig ID	30850_1.R1010
5'-most EST	jC-alXLIB327435P3b08a1

Seq. No.	128892
Contig ID	30851_1.R1010
5'-most EST	jC-alX25050Q1E1A01b1

Seq. No.	128893
Contig ID	30854_1.R1010
5'-most EST	LIB3234-054-P1-K1-F11

Seq. No.	128894
Contig ID	30861_1.R1010
5'-most EST	jC-atXLIB327425P1h04b1
Method	BLASTN
NCBI GI	g3510337
BLAST score	356
E value	0.0e+00
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	128895
Contig ID	30862_1.R1010
5'-most EST	jC-atXLIB327417P1b07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27

Match length	68
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128896
Contig ID	30873_1.R1010
5'-most EST	jC-atXmonuni25Ch10a1
Method	BLASTX
NCBI GI	g2058456
BLAST score	273
E value	4.0e-24
Match length	104
% identity	57
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	128897
Contig ID	30874_1.R1010
5'-most EST	g906706
Method	BLASTX
NCBI GI	g4557495
BLAST score	148
E value	2.0e-09
Match length	81
% identity	40
NCBI Description	cleavage stimulation factor subunit 3 >gi_1082704_pir__S50852 cleavage stimulation factor 77K chain - human >gi_632498 (U15782) cleavage stimulation factor 77kDa subunit [Homo sapiens] >gi_1092656_prf__2024339A cleavage stimulation factor [Homo sapiens]

Seq. No.	128898
Contig ID	30876_1.R1010
5'-most EST	jC-atXmonuni25Ch12a1
Method	BLASTX
NCBI GI	g2244914
BLAST score	251
E value	5.0e-21
Match length	98
% identity	64
NCBI Description	(Z97339) similarity to probable splicing factor Ceprp21 [Arabidopsis thaliana]

Seq. No.	128899
Contig ID	30878_1.R1010
5'-most EST	LIB3176-035-P1-K1-G4
Method	BLASTX
NCBI GI	g2213591
BLAST score	812
E value	8.0e-87
Match length	171
% identity	95
NCBI Description	(AC000348) T7N9.11 [Arabidopsis thaliana]

Seq. No.	128900
Contig ID	30878_2.R1010
5'-most EST	g2048677
Method	BLASTN
NCBI GI	g2182287
BLAST score	177
E value	1.0e-94
Match length	364
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	128901
Contig ID	30888_1.R1010
5'-most EST	g3449453
Method	BLASTX
NCBI GI	g3176676
BLAST score	386
E value	5.0e-37
Match length	94
% identity	79
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	128902
Contig ID	30889_1.R1010
5'-most EST	jC-atXmonuni26Da04b1
Method	BLASTN
NCBI GI	g3341671
BLAST score	352
E value	0.0e+00
Match length	388
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128903
Contig ID	30890_1.R1010
5'-most EST	jC-atXLIB327420P1f01b1
Method	BLASTN
NCBI GI	g4220510
BLAST score	231
E value	1.0e-127
Match length	737
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	128904
Contig ID	30892_1.R1010
5'-most EST	jC-atX25051Q1E1G12b1
Method	BLASTX
NCBI GI	g2827141
BLAST score	426
E value	4.0e-42
Match length	122

% identity	66
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	128905
Contig ID	30910_1.R1010
5'-most EST	LIB25-105-Q1-E1-E10
Method	BLASTX
NCBI GI	g3297815
BLAST score	470
E value	7.0e-47
Match length	120
% identity	81
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	128906
Contig ID	30916_1.R1010
5'-most EST	g1054484
Method	BLASTX
NCBI GI	g2275219
BLAST score	1006
E value	1.0e-110
Match length	191
% identity	99
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	128907
Contig ID	30918_1.R1010
5'-most EST	jC-atXLIB327430P4f02b1
Method	BLASTN
NCBI GI	g4165340
BLAST score	55
E value	7.0e-22
Match length	119
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128908
Contig ID	30921_1.R1010
5'-most EST	g453945
Method	BLASTX
NCBI GI	g2160185
BLAST score	295
E value	2.0e-26
Match length	92
% identity	60
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	128909
Contig ID	30922_1.R1010
5'-most EST	jC-atXLIB327425P3g05b1
Method	BLASTX
NCBI GI	g3912997
BLAST score	281
E value	8.0e-25

Match length	83
% identity	64
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL15 >gi_2129535_pir__S71200 AGL15 protein - Arabidopsis thaliana >gi_790635 (U22528) AGL15 [Arabidopsis thaliana]

Seq. No.	128910
Contig ID	30922_2.R1010
5'-most EST	g853724
Method	BLASTX
NCBI GI	g3114586
BLAST score	144
E value	4.0e-09
Match length	33
% identity	85
NCBI Description	(AF029976) MADS box protein [Eucalyptus grandis]

Seq. No.	128911
Contig ID	30934_1.R1010
5'-most EST	LIB25-052-Q1-E1-C2
Method	BLASTX
NCBI GI	g4678386
BLAST score	257
E value	4.0e-22
Match length	93
% identity	49
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	128912
Contig ID	30939_1.R1010
5'-most EST	g905540
Method	BLASTX
NCBI GI	g1171870
BLAST score	152
E value	1.0e-09
Match length	88
% identity	33
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (COMPLEX I-19KD) (CI-19KD) (COMPLEX I-PGIV) (CI-PGIV) >gi_89670_pir__S16208 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 19K chain - bovine >gi_599681_emb_CAA42218_ (X59697) 19 kDa subunit of NADH:ubiquinone oxidoreductase complex (complex I) [Bos taurus]

Seq. No.	128913
Contig ID	30943_1.R1010
5'-most EST	jC-atXLIB327427P4e03b2
Method	BLASTX
NCBI GI	g2739381
BLAST score	636
E value	1.0e-104
Match length	239
% identity	86
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	128914
Contig ID	30943_2.R1010

5'-most EST	jC-atXmonuni27Ce03b1
Method	BLASTX
NCBI GI	g2739381
BLAST score	1056
E value	1.0e-115
Match length	207
% identity	100
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	128915
Contig ID	30951_1.R1010
5'-most EST	jC-atXP15C107N16T7072a1
Method	BLASTX
NCBI GI	g2253411
BLAST score	197
E value	7.0e-15
Match length	105
% identity	43
NCBI Description	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]

Seq. No.	128916
Contig ID	30956_1.R1010
5'-most EST	jC-atXLIB327425P3h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	68
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128917
Contig ID	30967_1.R1010
5'-most EST	LIB25-052-Q1-E1-F3

Seq. No.	128918
Contig ID	30968_1.R1010
5'-most EST	jC-atXmonuni26Aa05b1
Method	BLASTX
NCBI GI	g2129640
BLAST score	842
E value	1.0e-90
Match length	160
% identity	98
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	128919
Contig ID	30973_1.R1010
5'-most EST	jC-atXmonuni26Ca01b1
Method	BLASTN
NCBI GI	g4589437
BLAST score	289
E value	1.0e-161
Match length	447

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence
Seq. No.	128920
Contig ID	30977_1.R1010
5'-most EST	LIB25-052-Q1-E1-G3
Seq. No.	128921
Contig ID	30980_1.R1010
5'-most EST	jC-atXLIB327426P2a10b1
Method	BLASTN
NCBI GI	g4584519
BLAST score	155
E value	2.0e-81
Match length	380
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)
Seq. No.	128922
Contig ID	30984_1.R1010
5'-most EST	jC-atXmonuni26Ca09b1
Method	BLASTN
NCBI GI	g3241917
BLAST score	244
E value	1.0e-134
Match length	519
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.	128923
Contig ID	30985_1.R1010
5'-most EST	jC-atXmonuni26Da09b1
Method	BLASTX
NCBI GI	g3548802
BLAST score	443
E value	6.0e-44
Match length	132
% identity	74
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.	128924
Contig ID	30987_1.R1010
5'-most EST	g1103364
Seq. No.	128925
Contig ID	30991_1.R1010
5'-most EST	jC-atX25052Q1E1H05b1
Method	BLASTX
NCBI GI	g3128187
BLAST score	454
E value	3.0e-45
Match length	143

% identity	56
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	128926
Contig ID	30995_1.R1010
5'-most EST	jC-atXmonuni26Da08b1
Method	BLASTX
NCBI GI	g3386546
BLAST score	285
E value	3.0e-25
Match length	92
% identity	71
NCBI Description	(AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]

Seq. No.	128927
Contig ID	31000_1.R1010
5'-most EST	g2758097
Method	BLASTX
NCBI GI	g123178
BLAST score	554
E value	7.0e-57
Match length	160
% identity	73
NCBI Description	HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi_99844_pir__A39358 histidinol dehydrogenase (EC 1.1.1.23) precursor, chloroplast - cabbage >gi_167142 (M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No.	128928
Contig ID	31002_1.R1010
5'-most EST	jC-alX25052Q1E1B03b1
Method	BLASTX
NCBI GI	g1362060
BLAST score	543
E value	1.0e-55
Match length	143
% identity	76
NCBI Description	dehydroquinase-shikimate dehydrogenase - garden pea

Seq. No.	128929
Contig ID	31003_1.R1010
5'-most EST	jC-atXP108C166H5T7s1
Method	BLASTX
NCBI GI	g1935914
BLAST score	597
E value	6.0e-62
Match length	135
% identity	84
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	128930
Contig ID	31004_1.R1010
5'-most EST	jC-atXLIB327425P1g03b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	254

E value	1.0e-140
Match length	456
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	128931
Contig ID	31008_1.R1010
5'-most EST	jC-atXLIB327425P3g03b1
Method	BLASTN
NCBI GI	g4585918
BLAST score	175
E value	2.0e-93
Match length	424
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O13 genomic sequence, complete sequence

Seq. No.	128932
Contig ID	31011_1.R1010
5'-most EST	LIB25-053-Q1-E1-B3
Method	BLASTN
NCBI GI	g2104523
BLAST score	379
E value	0.0e+00
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	128933
Contig ID	31015_1.R1010
5'-most EST	LIB25-053-Q1-E1-B7

Seq. No.	128934
Contig ID	31018_1.R1010
5'-most EST	jC-atXmonuni25Bh01b1
Method	BLASTN
NCBI GI	g2264319
BLAST score	20
E value	4.9e-01
Match length	49
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	128935
Contig ID	31022_1.R1010
5'-most EST	jC-atXLIB327425P3g12b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	76
E value	2.0e-34
Match length	296
% identity	88
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128936
Contig ID	31024_1.R1010
5'-most EST	LIB25-057-Q1-E1-A6
Method	BLASTN
NCBI GI	g2760316
BLAST score	366
E value	0.0e+00
Match length	577
% identity	100
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	128937
Contig ID	31036_1.R1010
5'-most EST	LIB25-053-Q1-E1-E11
Method	BLASTN
NCBI GI	g3510336
BLAST score	264
E value	1.0e-147
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	128938
Contig ID	31037_1.R1010
5'-most EST	g509442
Method	BLASTX
NCBI GI	g2642446
BLAST score	297
E value	0.0e+00
Match length	397
% identity	98
NCBI Description	(AC002391) similar to auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	128939
Contig ID	31040_1.R1010
5'-most EST	jC-atXmonuni25Ch06a1
Method	BLASTN
NCBI GI	g4589446
BLAST score	126
E value	2.0e-64
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	128940
Contig ID	31051_1.R1010
5'-most EST	LIB25-053-Q1-E1-G11
Method	BLASTX
NCBI GI	g4585991
BLAST score	637
E value	8.0e-67
Match length	117

% identity	100
NCBI Description	(AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]

Seq. No.	128941
Contig ID	31053_1.R1010
5'-most EST	jC-atXmonuni26Aa01b1
Method	BLASTN
NCBI GI	g4589950
BLAST score	344
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	128942
Contig ID	31068_1.R1010
5'-most EST	LIB3234-052-P1-K1-C1
Method	BLASTN
NCBI GI	g4454587
BLAST score	68
E value	9.0e-30
Match length	186
% identity	87
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	128943
Contig ID	31072_1.R1010
5'-most EST	jC-atXLIB327426P1b07b1
Method	BLASTX
NCBI GI	g4006909
BLAST score	555
E value	5.0e-57
Match length	113
% identity	91
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	128944
Contig ID	31076_1.R1010
5'-most EST	LIB3177-081-P1-K1-A4
Method	BLASTX
NCBI GI	g4587595
BLAST score	247
E value	7.0e-21
Match length	96
% identity	52
NCBI Description	(AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	128945
Contig ID	31081_1.R1010
5'-most EST	g2414149
Method	BLASTN
NCBI GI	g3849811
BLAST score	314

E value	1.0e-176
Match length	441
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128946
Contig ID	31081_2.R1010
5'-most EST	jC-atX25054Q1E1B11b1
Method	BLASTN
NCBI GI	g3849811
BLAST score	552
E value	0.0e+00
Match length	610
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128947
Contig ID	31086_1.R1010
5'-most EST	jC-atXP8C92G17T7s1

Seq. No.	128948
Contig ID	31095_1.R1010
5'-most EST	jC-atXmonuni26Ab10b1
Method	BLASTX
NCBI GI	g2828292
BLAST score	794
E value	4.0e-85
Match length	155
% identity	99
NCBI Description	(AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No.	128949
Contig ID	31096_1.R1010
5'-most EST	jC-atXLIB327426P2b10b1

Seq. No.	128950
Contig ID	31096_2.R1010
5'-most EST	jC-atXP121C120C20T7071d1
Method	BLASTN
NCBI GI	g2343110
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds

Seq. No.	128951
Contig ID	31099_1.R1010
5'-most EST	jC-atXmonuni26Ab11b1
Method	BLASTX
NCBI GI	g3252805
BLAST score	340
E value	5.0e-32

Match length	66
% identity	100
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana] >gi_3650027 (AC005396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	128952
Contig ID	31101_1.R1010
5'-most EST	g2759127
Method	BLASTX
NCBI GI	g2213586
BLAST score	203
E value	7.0e-24
Match length	209
% identity	30
NCBI Description	(AC000348) T7N9.6 [Arabidopsis thaliana]

Seq. No.	128953
Contig ID	31106_1.R1010
5'-most EST	jC-atXLIB327426P2b11b1
Method	BLASTX
NCBI GI	g3176678
BLAST score	618
E value	3.0e-64
Match length	139
% identity	88
NCBI Description	(AC003671) Contains similarity to MYB transcription factor isolog T01024.1 from A. thaliana BAC gb_AC002335. [Arabidopsis thaliana]

Seq. No.	128954
Contig ID	31117_1.R1010
5'-most EST	LIB25-054-Q1-E1-G10

Seq. No.	128955
Contig ID	31120_1.R1010
5'-most EST	LIB3175-035-P1-K1-G4
Method	BLASTN
NCBI GI	g4734003
BLAST score	33
E value	1.0e-08
Match length	89
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F3L12 genomic sequence, complete sequence

Seq. No.	128956
Contig ID	31131_1.R1010
5'-most EST	jC-alXLIB327436P1h10b1
Method	BLASTN
NCBI GI	g2252823
BLAST score	81
E value	2.0e-37
Match length	260
% identity	92
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	128957
Contig ID	31133_1.R1010
5'-most EST	jC-alXLIB327435P2h12a1
Method	BLASTX
NCBI GI	g1938549
BLAST score	176
E value	2.0e-12
Match length	65
% identity	52
NCBI Description	(U97016) similar to drosophila Rlc1 gene product (NID:g563361) and S. cerevisiae mitochondrial 60S ribosomal protein L4 (YML4) (NID:g459259) [Caenorhabditis elegans]

Seq. No.	128958
Contig ID	31135_1.R1010
5'-most EST	jC-alXLIB327435P3h06b1
Method	BLASTX
NCBI GI	g2947062
BLAST score	509
E value	3.0e-51
Match length	161
% identity	71
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	128959
Contig ID	31143_1.R1010
5'-most EST	g2749498
Method	BLASTN
NCBI GI	g3128141
BLAST score	368
E value	0.0e+00
Match length	579
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	128960
Contig ID	31147_1.R1010
5'-most EST	LIB25-055-P1-E1-E5
Method	BLASTX
NCBI GI	g4468984
BLAST score	446
E value	3.0e-44
Match length	161
% identity	53
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	128961
Contig ID	31150_1.R1010
5'-most EST	LIB25-114-Q1-E1-F8
Method	BLASTX
NCBI GI	g2252833
BLAST score	262
E value	1.0e-22
Match length	115
% identity	56
NCBI Description	(AF013293) A_IG005I10.12 gene product [Arabidopsis

thaliana]

Seq. No.	128962
Contig ID	31153_1.R1010
5'-most EST	jC-atXmonuni27Bc12a1
Method	BLASTN
NCBI GI	g3449331
BLAST score	302
E value	1.0e-169
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	128963
Contig ID	31155_1.R1010
5'-most EST	LIB25-055-P1-E1-G3
Method	BLASTN
NCBI GI	g2335089
BLAST score	330
E value	0.0e+00
Match length	499
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128964
Contig ID	31160_1.R1010
5'-most EST	jC-atXLIB327409P1d03a1
Method	BLASTX
NCBI GI	g3757516
BLAST score	155
E value	9.0e-10
Match length	59
% identity	54
NCBI Description	(AC005167) putative TMV resistance protein [Arabidopsis thaliana]

Seq. No.	128965
Contig ID	31168_1.R1010
5'-most EST	LIB35-031-Q1-E1-G5
Method	BLASTX
NCBI GI	g4371282
BLAST score	753
E value	4.0e-80
Match length	157
% identity	95
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	128966
Contig ID	31171_1.R1010
5'-most EST	jC-alXLIB327436P1h08b1
Method	BLASTX
NCBI GI	g3063465
BLAST score	665
E value	6.0e-70

Match length	135
% identity	100
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	128967
Contig ID	31173_1.R1010
5'-most EST	jC-alXLIB327436P1h09b1

Seq. No.	128968
Contig ID	31174_1.R1010
5'-most EST	LIB25-112-Q1-E1-G10

Seq. No.	128969
Contig ID	31178_1.R1010
5'-most EST	jC-alXLIB327435P4h05b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	387
E value	0.0e+00
Match length	542
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	128970
Contig ID	31180_1.R1010
5'-most EST	jC-alXLIB327435P4h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128971
Contig ID	31183_1.R1010
5'-most EST	jC-alXLIB327435P3h04b1
Method	BLASTX
NCBI GI	g4512697
BLAST score	286
E value	2.0e-25
Match length	185
% identity	46
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	128972
Contig ID	31187_1.R1010
5'-most EST	jC-alXLIB327436P2a02b1
Method	BLASTN
NCBI GI	g3172156
BLAST score	256
E value	1.0e-142
Match length	525
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No.	128973
Contig ID	31191_1.R1010
5'-most EST	jC-alXLIB327435P3h12b1

Seq. No.	128974
Contig ID	31196_1.R1010
5'-most EST	jC-alXLIB327434P1h03b1
Method	BLASTX
NCBI GI	g3005576
BLAST score	441
E value	1.0e-43
Match length	122
% identity	72
NCBI Description	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No.	128975
Contig ID	31199_1.R1010
5'-most EST	LIB25-056-Q1-E1-D6
Method	BLASTX
NCBI GI	g4678333
BLAST score	280
E value	6.0e-25
Match length	88
% identity	64
NCBI Description	(AL049658) H+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	128976
Contig ID	31202_1.R1010
5'-most EST	jC-alXLIB327434P1h05b1
Method	BLASTX
NCBI GI	g4376815
BLAST score	192
E value	2.0e-14
Match length	138
% identity	33
NCBI Description	(AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia pneumoniae]

Seq. No.	128977
Contig ID	31221_1.R1010
5'-most EST	jC-alXLIB327436P3a10b1

Seq. No.	128978
Contig ID	31226_1.R1010
5'-most EST	jC-alXLIB327434P1g07b1
Method	BLASTN
NCBI GI	g3128166
BLAST score	564
E value	0.0e+00
Match length	585
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	128979
Contig ID	31231_1.R1010
5'-most EST	jC-alXLIB327436P2b08b1
Method	BLASTX
NCBI GI	g3297810
BLAST score	515
E value	2.0e-52
Match length	97
% identity	98
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	128980
Contig ID	31245_1.R1010
5'-most EST	LIB3175-001-Q1-K1-H3
Method	BLASTX
NCBI GI	g4262186
BLAST score	781
E value	1.0e-83
Match length	152
% identity	99
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	128981
Contig ID	31249_1.R1010
5'-most EST	jC-alXLIB327436P3b08b1
Method	BLASTX
NCBI GI	g2191171
BLAST score	190
E value	3.0e-14
Match length	32
% identity	97
NCBI Description	(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) [Arabidopsis thaliana]

Seq. No.	128982
Contig ID	31270_1.R1010
5'-most EST	jC-atXLIB327422P2g04b2
Method	BLASTN
NCBI GI	g4757396
BLAST score	63
E value	1.0e-26
Match length	342
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8A10, complete sequence

Seq. No.	128983
Contig ID	31278_2.R1010
5'-most EST	LIB25-057-Q1-E1-D2
Method	BLASTN
NCBI GI	g4455168
BLAST score	324
E value	0.0e+00
Match length	340
% identity	99

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)
Seq. No.	128984
Contig ID	31287_1.R1010
5'-most EST	LIB25-057-Q1-E1-E2
Method	BLASTX
NCBI GI	g2632252
BLAST score	446
E value	3.0e-44
Match length	137
% identity	61
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.	128985
Contig ID	31296_1.R1010
5'-most EST	jC-atX25062Q1E1F03b1
Method	BLASTN
NCBI GI	g2262135
BLAST score	613
E value	0.0e+00
Match length	685
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence
Seq. No.	128986
Contig ID	31318_1.R1010
5'-most EST	jC-alXLIB327436P1h05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	128987
Contig ID	31320_1.R1010
5'-most EST	jC-alXLIB327436P1h06b1
Method	BLASTX
NCBI GI	g1169867
BLAST score	165
E value	3.0e-11
Match length	123
% identity	19
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_881422 (U27537) G beta like protein [Dictyostelium discoideum]
Seq. No.	128988
Contig ID	31323_2.R1010
5'-most EST	jC-alXLIB327436P1h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62

E value	4.0e-26
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128989
Contig ID	31331_1.R1010
5'-most EST	jC-alXLIB327435P4h03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	70
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	128990
Contig ID	31336_1.R1010
5'-most EST	jC-alXLIB327435P3h01b1
Method	BLASTX
NCBI GI	g4582488
BLAST score	169
E value	3.0e-12
Match length	64
% identity	66
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	128991
Contig ID	31338_1.R1010
5'-most EST	jC-alXLIB327435P4h02b1
Method	BLASTN
NCBI GI	g4468103
BLAST score	977
E value	0.0e+00
Match length	1009
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	128992
Contig ID	31340_1.R1010
5'-most EST	jC-atX25065Q1E1B04b1
Method	BLASTX
NCBI GI	g2088651
BLAST score	576
E value	2.0e-59
Match length	163
% identity	66
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	128993
Contig ID	31342_1.R1010
5'-most EST	jC-alXLIB327435P3h08b1
Method	BLASTX

NCBI GI	g3033396
BLAST score	890
E value	6.0e-96
Match length	194
% identity	90
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	128994
Contig ID	31343_1.R1010
5'-most EST	jC-alXLIB327435P4h09b1
Method	BLASTX
NCBI GI	g2501021
BLAST score	360
E value	2.0e-43
Match length	158
% identity	61
NCBI Description	LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	128995
Contig ID	31344_1.R1010
5'-most EST	jC-alXLIB327435P3h09b1
Method	BLASTX
NCBI GI	g3790575
BLAST score	210
E value	4.0e-16
Match length	105
% identity	45
NCBI Description	(AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]

Seq. No.	128996
Contig ID	31347_1.R1010
5'-most EST	jC-atXP121C118D8T7039d1
Method	BLASTN
NCBI GI	g4757402
BLAST score	265
E value	1.0e-147
Match length	613
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	128997
Contig ID	31351_1.R1010
5'-most EST	LIB3176-088-P1-K1-H9
Method	BLASTX
NCBI GI	g4539007
BLAST score	606
E value	6.0e-63
Match length	112
% identity	100
NCBI Description	(AL049481) cytochrome c [Arabidopsis thaliana]

Seq. No.	128998
Contig ID	31356_1.R1010

5'-most EST	jC-alXLIB327436P2a04b1
Method	BLASTX
NCBI GI	g4587547
BLAST score	232
E value	4.0e-19
Match length	90
% identity	52
NCBI Description	(AC006577) Contains similarity to DNA-binding protein Gt-2 gb_X68261 from Oryza sativa. [Arabidopsis thaliana]

Seq. No.	128999
Contig ID	31360_1.R1010
5'-most EST	jC-atXP73C224B10T7b1
Method	BLASTX
NCBI GI	g2497281
BLAST score	591
E value	5.0e-61
Match length	205
% identity	56
NCBI Description	TRANSLATION INITIATION FACTOR IF-2 >gi_1651769_dbj_BAA16696_ (D90900) initiation factor IF-2 [Synechocystis sp.]

Seq. No.	129000
Contig ID	31360_2.R1010
5'-most EST	jC-alXLIB327436P2a03b1
Method	BLASTX
NCBI GI	g2497281
BLAST score	376
E value	8.0e-36
Match length	181
% identity	43
NCBI Description	TRANSLATION INITIATION FACTOR IF-2 >gi_1651769_dbj_BAA16696_ (D90900) initiation factor IF-2 [Synechocystis sp.]

Seq. No.	129001
Contig ID	31361_1.R1010
5'-most EST	LIB25-058-P1-E1-D8
Method	BLASTX
NCBI GI	g4336426
BLAST score	155
E value	3.0e-10
Match length	39
% identity	72
NCBI Description	(AF090835) Ca2+-dependent protein kinase [Mesembryanthemum crystallinum]

Seq. No.	129002
Contig ID	31370_1.R1010
5'-most EST	jC-alXLIB327436P3a01b1
Method	BLASTX
NCBI GI	g4455210
BLAST score	587
E value	1.0e-60
Match length	153
% identity	75

NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	129003
Contig ID	31372_1.R1010
5'-most EST	jC-alXLIB327434P1h02b1
Method	BLASTN
NCBI GI	g3399678
BLAST score	424
E value	0.0e+00
Match length	482
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129004
Contig ID	31381_1.R1010
5'-most EST	jC-alXLIB327436P4a10b1

Seq. No.	129005
Contig ID	31382_1.R1010
5'-most EST	jC-alXLIB327436P3a06b1

Seq. No.	129006
Contig ID	31385_1.R1010
5'-most EST	jC-alXLIB327436P4a07b1
Method	BLASTN
NCBI GI	g2252848
BLAST score	344
E value	0.0e+00
Match length	617
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	129007
Contig ID	31387_1.R1010
5'-most EST	jC-alXLIB327436P4b02b1
Method	BLASTX
NCBI GI	g4539301
BLAST score	440
E value	2.0e-43
Match length	128
% identity	73
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	129008
Contig ID	31392_1.R1010
5'-most EST	jC-alXLIB327436P2b01b1
Method	BLASTX
NCBI GI	g2252847
BLAST score	719
E value	3.0e-76
Match length	132
% identity	100
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	129009
Contig ID	31405_1.R1010
5'-most EST	LIB25-059-Q1-E1-A1
Method	BLASTX
NCBI GI	g2191132
BLAST score	453
E value	4.0e-45
Match length	140
% identity	74
NCBI Description	(AF007269) contains weak similarity to nebulin [Arabidopsis thaliana]

Seq. No.	129010
Contig ID	31409_1.R1010
5'-most EST	jC-atXLIB327420P4h04b1

Seq. No.	129011
Contig ID	31411_1.R1010
5'-most EST	jC-alXLIB327435P2h08a1
Method	BLASTN
NCBI GI	g4581103
BLAST score	241
E value	1.0e-133
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	129012
Contig ID	31414_1.R1010
5'-most EST	jC-alXLIB327436P1h04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	8.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129013
Contig ID	31420_1.R1010
5'-most EST	jC-alXLIB327436P2c03b1
Method	BLASTX
NCBI GI	g3894198
BLAST score	309
E value	4.0e-28
Match length	118
% identity	58
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129014
Contig ID	31430_1.R1010
5'-most EST	jC-alXLIB327436P4c07b1
Method	BLASTX
NCBI GI	g4115922
BLAST score	728

E value	3.0e-77
Match length	154
% identity	93
NCBI Description	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]

Seq. No.	129015
Contig ID	31431_1.R1010
5'-most EST	g1217472
Method	BLASTX
NCBI GI	g3096935
BLAST score	249
E value	4.0e-21
Match length	91
% identity	56
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	129016
Contig ID	31434_1.R1010
5'-most EST	jC-alXLIB327436P2d04b1
Method	BLASTN
NCBI GI	g2244788
BLAST score	114
E value	6.0e-57
Match length	420
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129017
Contig ID	31443_1.R1010
5'-most EST	g2763586
Method	BLASTN
NCBI GI	g4519195
BLAST score	407
E value	0.0e+00
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	129018
Contig ID	31460_1.R1010
5'-most EST	jC-alXLIB327436P4b12b1
Method	BLASTX
NCBI GI	g4103635
BLAST score	359
E value	7.0e-34
Match length	138
% identity	54
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	129019
Contig ID	31463_1.R1010
5'-most EST	jC-alXLIB327436P3b10b1

Method	BLASTX
NCBI GI	g2244973
BLAST score	350
E value	6.0e-33
Match length	146
% identity	53
NCBI Description	(Z97340) similarity to extensin class 1 protein [Arabidopsis thaliana]

Seq. No.	129020
Contig ID	31473_1.R1010
5'-most EST	jC-alXLIB327434P1f08b1
Method	BLASTX
NCBI GI	g3341679
BLAST score	526
E value	2.0e-53
Match length	149
% identity	70
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	129021
Contig ID	31476_1.R1010
5'-most EST	jC-alXLIB327434P1f07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129022
Contig ID	31480_1.R1010
5'-most EST	jC-alXLIB327436P4c04b1
Method	BLASTN
NCBI GI	g2252639
BLAST score	226
E value	1.0e-124
Match length	438
% identity	98
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	129023
Contig ID	31485_1.R1010
5'-most EST	LIB25-060-Q1-E1-C8
Method	BLASTX
NCBI GI	g3510264
BLAST score	477
E value	5.0e-48
Match length	130
% identity	72
NCBI Description	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]

Seq. No.	129024
Contig ID	31488_1.R1010
5'-most EST	g2047848

Seq. No.	129025
Contig ID	31492_1.R1010
5'-most EST	jC-alXLIB327434P1e10b1
Method	BLASTN
NCBI GI	g4691223
BLAST score	177
E value	1.0e-94
Match length	418
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	129026
Contig ID	31496_1.R1010
5'-most EST	jC-alXLIB327436P4c10b1
Method	BLASTX
NCBI GI	g3402690
BLAST score	654
E value	2.0e-68
Match length	132
% identity	97
NCBI Description	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	129027
Contig ID	31504_1.R1010
5'-most EST	jC-alXLIB327434P1e06b1
Method	BLASTX
NCBI GI	g3201994
BLAST score	803
E value	1.0e-85
Match length	253
% identity	62
NCBI Description	(AF068483) chaperonin Cct6 [Oryctolagus cuniculus]

Seq. No.	129028
Contig ID	31505_1.R1010
5'-most EST	jC-alXLIB327436P2d07b1
Method	BLASTN
NCBI GI	g4092472
BLAST score	224
E value	1.0e-123
Match length	405
% identity	97
NCBI Description	Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	129029
Contig ID	31519_1.R1010
5'-most EST	jC-alXLIB327434P1d10b1
Method	BLASTX
NCBI GI	g3386622
BLAST score	745

E value	3.0e-79
Match length	150
% identity	98
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	129030
Contig ID	31521_1.R1010
5'-most EST	jC-alXLIB327434P1d09b1
Method	BLASTN
NCBI GI	g3128166
BLAST score	235
E value	1.0e-129
Match length	707
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129031
Contig ID	31522_1.R1010
5'-most EST	jC-alXLIB327436P4d12b1
Method	BLASTX
NCBI GI	g2245030
BLAST score	289
E value	1.0e-73
Match length	193
% identity	80
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	129032
Contig ID	31524_1.R1010
5'-most EST	jC-atXLIB327417P2d10b1
Method	BLASTX
NCBI GI	g3152599
BLAST score	767
E value	3.0e-98
Match length	233
% identity	36
NCBI Description	(AC002986) Strong similarity to lupeol synthase gb_U49919 and cycloartenol synthase gb_U02555 from A. thaliana (the third gene with similar homology). [Arabidopsis thaliana]

Seq. No.	129033
Contig ID	31526_1.R1010
5'-most EST	g2393510
Method	BLASTX
NCBI GI	g4468813
BLAST score	63
E value	1.0e-61
Match length	127
% identity	98
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	129034
Contig ID	31527_1.R1010
5'-most EST	jC-alXLIB327436P2e10b1
Method	BLASTN

NCBI GI	g2494106
BLAST score	168
E value	2.0e-89
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129035
Contig ID	31531_1.R1010
5'-most EST	jC-alXLIB327436P2e08b1
Method	BLASTX
NCBI GI	g3193300
BLAST score	657
E value	1.0e-68
Match length	179
% identity	76
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	129036
Contig ID	31535_1.R1010
5'-most EST	jC-alXLIB327434P1d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129037
Contig ID	31555_1.R1010
5'-most EST	jC-alXLIB327436P2c02b1
Method	BLASTN
NCBI GI	g4220510
BLAST score	46
E value	2.0e-16
Match length	170
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	129038
Contig ID	31561_1.R1010
5'-most EST	jC-atXP85C241I6T7b1
Method	BLASTX
NCBI GI	g499068
BLAST score	782
E value	3.0e-83
Match length	216
% identity	74
NCBI Description	(X77301) GTPase [Glycine max]

Seq. No.	129039
Contig ID	31562_1.R1010
5'-most EST	jC-alXLIB327436P3c01b1

Method	BLASTN
NCBI GI	g4262221
BLAST score	172
E value	9.0e-92
Match length	208
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129040
Contig ID	31562_2.R1010
5'-most EST	g1216072
Method	BLASTN
NCBI GI	g4262221
BLAST score	415
E value	0.0e+00
Match length	681
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129041
Contig ID	31565_1.R1010
5'-most EST	jC-alXLIB327434P1f04b1
Method	BLASTN
NCBI GI	g4589421
BLAST score	338
E value	0.0e+00
Match length	856
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	129042
Contig ID	31570_1.R1010
5'-most EST	LIB25-061-Q1-E1-D11
Method	BLASTX
NCBI GI	g1708464
BLAST score	225
E value	2.0e-18
Match length	62
% identity	66
NCBI Description	PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD) (2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_ (Z69795) unknown [Schizosaccharomyces pombe]

Seq. No.	129043
Contig ID	31572_1.R1010
5'-most EST	jC-alXLIB327436P4c09b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	129044
Contig ID	31574_1.R1010
5'-most EST	jC-alXLIB327436P3c09b1
Method	BLASTX
NCBI GI	g3874440
BLAST score	169
E value	2.0e-11
Match length	121
% identity	34
NCBI Description	(Z81038) Similarity to Bovine NADH-ubiquinone oxidoreducatse B8 subunit (SW:Q02370) [Caenorhabditis elegans]

Seq. No.	129045
Contig ID	31576_1.R1010
5'-most EST	jC-alXLIB327436P4c05b1
Method	BLASTX
NCBI GI	g4539002
BLAST score	364
E value	2.0e-34
Match length	82
% identity	82
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	129046
Contig ID	31583_1.R1010
5'-most EST	jC-alXLIB327436P2d05b1

Seq. No.	129047
Contig ID	31592_1.R1010
5'-most EST	jC-alXLIB327436P4e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129048
Contig ID	31595_1.R1010
5'-most EST	jC-alXLIB327436P3d01b1
Method	BLASTN
NCBI GI	g2827644
BLAST score	230
E value	1.0e-126
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	129049
Contig ID	31607_1.R1010
5'-most EST	jC-alXLIB327436P3d09b1
Method	BLASTX
NCBI GI	g4510348

BLAST score	281
E value	7.0e-25
Match length	72
% identity	71
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	129050
Contig ID	31615_1.R1010
5'-most EST	jC-atXP20C114A20T7091a1
Method	BLASTX
NCBI GI	g2497540
BLAST score	546
E value	9.0e-56
Match length	164
% identity	63
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No.	129051
Contig ID	31615_2.R1010
5'-most EST	jC-atXP110CG4A2T7094a1
Method	BLASTX
NCBI GI	g2497540
BLAST score	521
E value	8.0e-53
Match length	156
% identity	63
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No.	129052
Contig ID	31615_4.R1010
5'-most EST	g2446019
Method	BLASTX
NCBI GI	g2497542
BLAST score	156
E value	4.0e-10
Match length	70
% identity	47
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	129053
Contig ID	31622_1.R1010
5'-most EST	jC-atXLIB327431P3c12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	9.0e-16
Match length	88
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129054
Contig ID	31623_1.R1010
5'-most EST	ARABL1-02-Q1-B1-H3
Method	BLASTX

NCBI GI	g2213592
BLAST score	553
E value	1.0e-56
Match length	143
% identity	39
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	129055
Contig ID	31626_1.R1010
5'-most EST	jC-alXLIB327436P3b09b1
Method	BLASTX
NCBI GI	g544184
BLAST score	798
E value	3.0e-85
Match length	198
% identity	75
NCBI Description	4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No.	129056
Contig ID	31635_1.R1010
5'-most EST	jC-alXLIB327436P4b10b1
Method	BLASTX
NCBI GI	g4432854
BLAST score	183
E value	2.0e-13
Match length	87
% identity	32
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129057
Contig ID	31636_1.R1010
5'-most EST	g1217001

Seq. No.	129058
Contig ID	31641_1.R1010
5'-most EST	jC-alXLIB327436P2c07b1
Method	BLASTX
NCBI GI	g4204271
BLAST score	488
E value	3.0e-49
Match length	131
% identity	66
NCBI Description	(AC005223) Unknown protein [Arabidopsis thaliana]

Seq. No.	129059
Contig ID	31658_1.R1010
5'-most EST	LIB3234-049-P1-K1-E5
Method	BLASTX
NCBI GI	g4503269
BLAST score	318
E value	3.0e-29
Match length	150
% identity	47

NCBI Description	deoxycytidine kinase >gi_118447_sp_P27707_DCK_HUMAN DEOXYCYTIDINE KINASE (DCK) >gi_105829_pir__A38585 deoxycytidine kinase (EC 2.7.1.74) - human >gi_181510 (M60527) deoxycytidine kinase [Homo sapiens]
Seq. No.	129060
Contig ID	31663_1.R1010
5'-most EST	jC-atX25059Q1E1D10b1
Method	BLASTX
NCBI GI	g2252863
BLAST score	444
E value	4.0e-44
Match length	153
% identity	31
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]
Seq. No.	129061
Contig ID	31672_1.R1010
5'-most EST	jC-atX25059Q1E1D09b1
Method	BLASTN
NCBI GI	g2494106
BLAST score	355
E value	0.0e+00
Match length	392
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	129062
Contig ID	31674_1.R1010
5'-most EST	LIB3234-084-Q1-K1-G2
Seq. No.	129063
Contig ID	31675_1.R1010
5'-most EST	jC-alXLIB327434P1e04b1
Method	BLASTN
NCBI GI	g3985934
BLAST score	371
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.	129064
Contig ID	31683_1.R1010
5'-most EST	LIB25-062-Q1-E1-E8
Method	BLASTX
NCBI GI	g3763916
BLAST score	152
E value	6.0e-10
Match length	83
% identity	35
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	129065
Contig ID	31689_1.R1010
5'-most EST	jC-atX25059Q1E1F03b1
Method	BLASTX
NCBI GI	g4580461
BLAST score	300
E value	8.0e-34
Match length	100
% identity	67
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	129066
Contig ID	31693_1.R1010
5'-most EST	LIB25-062-Q1-E1-F7
Method	BLASTX
NCBI GI	g1351630
BLAST score	184
E value	1.0e-13
Match length	102
% identity	35
NCBI Description	PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE) >gi_2130253_pir__S62537 hypothetical protein SPAC12G12.06c - fission yeast (Schizosaccharomyces pombe) >gi_1052524_emb_CAA91501_ (Z66568) SPAC12G12.06c, unknown, len: 363 [Schizosaccharomyces pombe]

Seq. No.	129067
Contig ID	31695_1.R1010
5'-most EST	LIB25-062-Q1-E1-F9
Method	BLASTX
NCBI GI	g4539329
BLAST score	600
E value	2.0e-62
Match length	115
% identity	100
NCBI Description	(AL035679) ES43 like protein [Arabidopsis thaliana]

Seq. No.	129068
Contig ID	31701_1.R1010
5'-most EST	LIB3176-115-P2-K1-C9
Method	BLASTN
NCBI GI	g4159706
BLAST score	381
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	129069
Contig ID	31712_1.R1010
5'-most EST	jC-atXLIB327406P4b12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63

E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129070
Contig ID	31712_2.R1010
5'-most EST	LIB25-062-Q1-E1-H4
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	9.0e-09
Match length	33
% identity	58
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	129071
Contig ID	31714_1.R1010
5'-most EST	LIB25-062-Q1-E1-H6
Method	BLASTX
NCBI GI	g3249077
BLAST score	406
E value	3.0e-39
Match length	140
% identity	56
NCBI Description	(AC004473) Similar to prunasin hydrolase precursor gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]

Seq. No.	129072
Contig ID	31716_1.R1010
5'-most EST	jC-atXLIB327416P3g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129073
Contig ID	31717_1.R1010
5'-most EST	g931181
Method	BLASTX
NCBI GI	g3450842
BLAST score	330
E value	1.0e-30
Match length	89
% identity	64
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	129074
Contig ID	31720_1.R1010
5'-most EST	LIB25-063-Q1-E1-A11

Seq. No.	129075
Contig ID	31722_1.R1010
5'-most EST	jC-atXLIB327418P4d07b1
Method	BLASTN
NCBI GI	g4733953
BLAST score	337
E value	0.0e+00
Match length	615
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	129076
Contig ID	31723_1.R1010
5'-most EST	jC-alXLIB327436P4e10b1
Method	BLASTX
NCBI GI	g3643599
BLAST score	402
E value	4.0e-39
Match length	78
% identity	100
NCBI Description	(AC005395) putative trytophanyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	129077
Contig ID	31724_1.R1010
5'-most EST	jC-alXLIB327436P3e10b1
Method	BLASTX
NCBI GI	g1946355
BLAST score	458
E value	2.0e-45
Match length	152
% identity	58
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	129078
Contig ID	31728_1.R1010
5'-most EST	jC-alXLIB327436P3e07b1
Method	BLASTX
NCBI GI	g4567249
BLAST score	581
E value	5.0e-60
Match length	125
% identity	88
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129079
Contig ID	31731_1.R1010
5'-most EST	LIB3175-035-P1-K1-C5
Method	BLASTN
NCBI GI	g4325340
BLAST score	247
E value	1.0e-136
Match length	444

% identity 100
NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 129080
Contig ID 31736_1.R1010
5'-most EST g2446075

Seq. No. 129081
Contig ID 31739_1.R1010
5'-most EST jC-alXLIB327436P4f02b1
Method BLASTX
NCBI GI g4006855
BLAST score 732
E value 9.0e-78
Match length 149
% identity 97
NCBI Description (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No. 129082
Contig ID 31744_1.R1010
5'-most EST jC-atX25063Q1E1C03b1
Method BLASTN
NCBI GI g3600062
BLAST score 114
E value 3.0e-57
Match length 396
% identity 99
NCBI Description Arabidopsis thaliana BAC T25C13

Seq. No. 129083
Contig ID 31746_1.R1010
5'-most EST jC-alXLIB327436P4f07b1
Method BLASTX
NCBI GI g3123712
BLAST score 315
E value 7.0e-29
Match length 145
% identity 41
NCBI Description (D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No. 129084
Contig ID 31752_1.R1010
5'-most EST LIB25-070-Q1-E1-G4
Method BLASTX
NCBI GI g4193382
BLAST score 339
E value 1.0e-31
Match length 86
% identity 76
NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No. 129085
Contig ID 31752_3.R1010
5'-most EST g493404

Method	BLASTX
NCBI GI	g4704730
BLAST score	235
E value	2.0e-19
Match length	85
% identity	59
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	129086
Contig ID	31758_1.R1010
5'-most EST	jC-alXLIB327436P2g05b1
Method	BLASTN
NCBI GI	g3702733
BLAST score	162
E value	8.0e-86
Match length	202
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJP23, complete sequence [Arabidopsis thaliana]

Seq. No.	129087
Contig ID	31762_1.R1010
5'-most EST	jC-alXLIB327436P2g07b1
Method	BLASTX
NCBI GI	g2252841
BLAST score	289
E value	1.0e-25
Match length	123
% identity	49
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	129088
Contig ID	31772_1.R1010
5'-most EST	ARABL1-08-Q1-B1-B9
Method	BLASTN
NCBI GI	g3341671
BLAST score	178
E value	2.0e-95
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129089
Contig ID	31773_1.R1010
5'-most EST	jC-alXLIB327436P4g02b1
Method	BLASTX
NCBI GI	g4204315
BLAST score	469
E value	8.0e-47
Match length	187
% identity	49
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	129090
Contig ID	31781_1.R1010
5'-most EST	jC-alXLIB327436P4g09b1

Method	BLASTN
NCBI GI	g4220635
BLAST score	394
E value	0.0e+00
Match length	676
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	129091
Contig ID	31786_1.R1010
5'-most EST	jC-alXLIB327436P4g07b1
Method	BLASTX
NCBI GI	g3367591
BLAST score	248
E value	8.0e-24
Match length	120
% identity	48
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	129092
Contig ID	31789_1.R1010
5'-most EST	jC-alXLIB327434P1a10b1
Method	BLASTX
NCBI GI	g1771160
BLAST score	373
E value	1.0e-35
Match length	156
% identity	49
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	129093
Contig ID	31789_2.R1010
5'-most EST	LIB3176-015-P1-K1-G4
Method	BLASTX
NCBI GI	g4539414
BLAST score	178
E value	6.0e-13
Match length	100
% identity	41
NCBI Description	(AL049524) putative subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	129094
Contig ID	31790_1.R1010
5'-most EST	jC-atXL1030Q1B1D05a1
Method	BLASTX
NCBI GI	g2245144
BLAST score	331
E value	1.0e-30
Match length	79
% identity	80
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No. 129095

Contig ID	31802_1.R1010
5'-most EST	jC-alXLIB327436P3e09b1
Method	BLASTX
NCBI GI	g3024697
BLAST score	856
E value	1.0e-136
Match length	250
% identity	96
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	129096
Contig ID	31810_1.R1010
5'-most EST	jC-alXLIB327436P2f07b1
Method	BLASTX
NCBI GI	g2499535
BLAST score	332
E value	7.0e-31
Match length	139
% identity	49
NCBI Description	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]

Seq. No.	129097
Contig ID	31812_1.R1010
5'-most EST	jC-alXLIB327434P1c04b1
Method	BLASTX
NCBI GI	g2501646
BLAST score	556
E value	9.0e-57
Match length	197
% identity	50
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE (UPD) >gi_1362169_pir__S55733 uroporphyrinogen decarboxylase - barley >gi_1016347_emb_CAA58039_ (X82832) uroporphyrinogen decarboxylase [Hordeum vulgare]

Seq. No.	129098
Contig ID	31816_1.R1010
5'-most EST	jC-alXLIB327436P2f04b1
Method	BLASTX
NCBI GI	g1706186
BLAST score	226
E value	2.0e-18
Match length	144
% identity	42
NCBI Description	HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR) >gi_110721_pir__A32742 murine ecotropic retrovirus receptor protein - mouse >gi_532612 (M26687) ecotropic retrovirus receptor [Mus musculus]

Seq. No.	129099
Contig ID	31820_1.R1010

5'-most EST	jC-alXLIB327434P1c06b1
Method	BLASTX
NCBI GI	g3885328
BLAST score	354
E value	3.0e-33
Match length	74
% identity	93
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	129100
Contig ID	31824_1.R1010
5'-most EST	jC-alXLIB327436P4f04b1
Method	BLASTX
NCBI GI	g2982462
BLAST score	368
E value	8.0e-35
Match length	82
% identity	46
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	129101
Contig ID	31825_1.R1010
5'-most EST	jC-alXLIB327436P4f05b1
Method	BLASTX
NCBI GI	g3779028
BLAST score	533
E value	2.0e-54
Match length	102
% identity	100
NCBI Description	(AC005171) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	129102
Contig ID	31836_1.R1010
5'-most EST	jC-alXLIB327436P4f12b1
Method	BLASTN
NCBI GI	g3746057
BLAST score	380
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129103
Contig ID	31846_1.R1010
5'-most EST	jC-alXLIB327436P2g06b1
Method	BLASTN
NCBI GI	g3702731
BLAST score	399
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	129104

Contig ID	31848_1.R1010
5'-most EST	jC-alXLIB327436P2g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129105
Contig ID	31860_1.R1010
5'-most EST	jC-alXLIB327434P1b01b1
Method	BLASTX
NCBI GI	g4406764
BLAST score	424
E value	1.0e-41
Match length	149
% identity	60
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	129106
Contig ID	31864_1.R1010
5'-most EST	jC-alXLIB327436P3g08b1
Method	BLASTX
NCBI GI	g4490751
BLAST score	764
E value	2.0e-81
Match length	143
% identity	100
NCBI Description	(AL035708) proliferating-cell nucleolar antigen-like protein [Arabidopsis thaliana]

Seq. No.	129107
Contig ID	31871_1.R1010
5'-most EST	jC-alXLIB327436P3g07b1
Method	BLASTN
NCBI GI	g1707006
BLAST score	447
E value	0.0e+00
Match length	447
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129108
Contig ID	31876_1.R1010
5'-most EST	jC-atXP8C92G8T7s1
Method	BLASTX
NCBI GI	g1750376
BLAST score	1058
E value	1.0e-116
Match length	220
% identity	93
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana]

>gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	129109
Contig ID	31880_1.R1010
5'-most EST	jC-atXP82CG2F5T7b1
Method	BLASTX
NCBI GI	g2213590
BLAST score	261
E value	3.0e-22
Match length	186
% identity	35
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	129110
Contig ID	31880_2.R1010
5'-most EST	jC-alXLIB327434P1a11b1
Method	BLASTX
NCBI GI	g4322327
BLAST score	282
E value	8.0e-25
Match length	174
% identity	37
NCBI Description	(AF080545) peptide transporter [Nepenthes alata]

Seq. No.	129111
Contig ID	31884_1.R1010
5'-most EST	jC-alXLIB327436P2e11b1
Method	BLASTX
NCBI GI	g586021
BLAST score	175
E value	2.0e-12
Match length	68
% identity	50
NCBI Description	PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION PROTEIN C) >gi_2127242_pir__S66083 stage V sporulation protein - Bacillus subtilis >gi_467442_dbj_BAA05288_ (D26185) stage V sporulation [Bacillus subtilis] >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [Bacillus subtilis]

Seq. No.	129112
Contig ID	31885_1.R1010
5'-most EST	g2749017
Method	BLASTX
NCBI GI	g3885329
BLAST score	558
E value	4.0e-57
Match length	151
% identity	79
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	129113
Contig ID	31889_1.R1010
5'-most EST	g3719128
Method	BLASTX

NCBI GI	g4539435
BLAST score	308
E value	5.0e-28
Match length	94
% identity	59
NCBI Description	(AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	129114
Contig ID	31889_3.R1010
5'-most EST	jC-alXLIB327436P2f03b1

Seq. No.	129115
Contig ID	31895_1.R1010
5'-most EST	jC-alXLIB327434P1c01b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	274
E value	1.0e-152
Match length	396
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	129116
Contig ID	31902_1.R1010
5'-most EST	jC-alXLIB327436P2f11b1
Method	BLASTX
NCBI GI	g4406820
BLAST score	468
E value	8.0e-47
Match length	89
% identity	100
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis thaliana]

Seq. No.	129117
Contig ID	31911_1.R1010
5'-most EST	jC-alXLIB327436P3f07b1
Method	BLASTN
NCBI GI	g4539378
BLAST score	333
E value	0.0e+00
Match length	460
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	129118
Contig ID	31915_1.R1010
5'-most EST	LIB25-065-Q1-E1-E1
Method	BLASTN
NCBI GI	g4220643
BLAST score	609
E value	0.0e+00
Match length	625
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	129119
Contig ID	31919_1.R1010
5'-most EST	jC-alXLIB327436P2g02b1
Method	BLASTX
NCBI GI	g4539344
BLAST score	733
E value	7.0e-78
Match length	139
% identity	97
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	129120
Contig ID	31920_1.R1010
5'-most EST	jC-alXLIB327434P1b10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129121
Contig ID	31921_1.R1010
5'-most EST	jC-alXLIB327434P1b09b1
Method	BLASTN
NCBI GI	g3366536
BLAST score	273
E value	1.0e-152
Match length	468
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	129122
Contig ID	31942_1.R1010
5'-most EST	jC-alXLIB327436P4g03b1
Method	BLASTN
NCBI GI	g4678258
BLAST score	265
E value	1.0e-147
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	129123
Contig ID	31943_1.R1010
5'-most EST	jC-alXLIB327436P3g03b1
Method	BLASTX
NCBI GI	g4678209
BLAST score	529
E value	6.0e-54
Match length	154

% identity	68
NCBI Description	(AC007134) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	129124
Contig ID	31949_1.R1010
5'-most EST	jC-atXP98CH8B9T7055d1
Method	BLASTX
NCBI GI	g3337361
BLAST score	328
E value	3.0e-30
Match length	119
% identity	59
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	129125
Contig ID	31949_2.R1010
5'-most EST	jC-atXLIB327411P1g04b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	315
E value	1.0e-28
Match length	152
% identity	51
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	129126
Contig ID	31951_1.R1010
5'-most EST	jC-alXLIB327436P4g12b1
Method	BLASTX
NCBI GI	g4586055
BLAST score	447
E value	2.0e-44
Match length	142
% identity	59
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129127
Contig ID	31958_1.R1010
5'-most EST	LIB25-066-Q1-E1-A11
Method	BLASTN
NCBI GI	g3402745
BLAST score	352
E value	0.0e+00
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	129128
Contig ID	31960_1.R1010
5'-most EST	jC-alXLIB327436P3e03b1
Method	BLASTX
NCBI GI	g4200325
BLAST score	157
E value	3.0e-10
Match length	61

% identity	46
NCBI Description	(Z98885) dJ522J7.2 (Peregrin (BR140) LIKE protein) [Homo sapiens]

Seq. No.	129129
Contig ID	31965_1.R1010
5'-most EST	jC-alXLIB327436P4e01b1
Method	BLASTX
NCBI GI	g1173194
BLAST score	267
E value	6.0e-23
Match length	111
% identity	47
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi_2119093_pir__S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013_ (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_ (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]

Seq. No.	129130
Contig ID	31969_1.R1010
5'-most EST	jC-alXLIB327436P2f01b1
Method	BLASTN
NCBI GI	g2252639
BLAST score	359
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	129131
Contig ID	31970_1.R1010
5'-most EST	jC-alXLIB327434P1c11b1
Method	BLASTN
NCBI GI	g4468801
BLAST score	225
E value	1.0e-123
Match length	483
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	129132
Contig ID	31972_1.R1010
5'-most EST	jC-alXLIB327434P1c10b1
Method	BLASTN
NCBI GI	g4587641
BLAST score	472
E value	0.0e+00
Match length	472
% identity	100

NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence
Seq. No.	129133
Contig ID	31981_2.R1010
5'-most EST	jC-alXLIB327436P4f01b1
Method	BLASTN
NCBI GI	g4757403
BLAST score	171
E value	4.0e-91
Match length	387
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence
Seq. No.	129134
Contig ID	31984_1.R1010
5'-most EST	jC-alXLIB327436P3f01b1
Method	BLASTN
NCBI GI	g3128166
BLAST score	157
E value	8.0e-83
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	129135
Contig ID	31995_1.R1010
5'-most EST	jC-alXLIB327436P3d05b1
Method	BLASTN
NCBI GI	g4159706
BLAST score	431
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence
Seq. No.	129136
Contig ID	32006_1.R1010
5'-most EST	jC-alXLIB327436P2g01b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	573
E value	4.0e-59
Match length	123
% identity	29
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
Seq. No.	129137
Contig ID	32009_1.R1010
5'-most EST	jC-alXLIB327434P1b04b1
Method	BLASTX
NCBI GI	g4406759
BLAST score	179

E value 7.0e-13
Match length 103
% identity 38
NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 129138
Contig ID 32013_1.R1010
5'-most EST g493301
Method BLASTX
NCBI GI g4006910
BLAST score 253
E value 4.0e-21
Match length 224
% identity 34
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 129139
Contig ID 32022_1.R1010
5'-most EST jC-alXLIB327436P4g05b1
Method BLASTX
NCBI GI g2497034
BLAST score 153
E value 7.0e-10
Match length 86
% identity 41
NCBI Description HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III >gi_3881502_emb_CAA87421_ (Z47357) ZK1128.2 [Caenorhabditis elegans]

Seq. No. 129140
Contig ID 32028_1.R1010
5'-most EST jC-atXLIB327417P4c09b1

Seq. No. 129141
Contig ID 32030_1.R1010
5'-most EST jC-atXLIB327417P2f02b1
Method BLASTN
NCBI GI g4455290
BLAST score 116
E value 4.0e-58
Match length 310
% identity 84
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No. 129142
Contig ID 32030_2.R1010
5'-most EST jC-atXLIB327417P2f02a1
Method BLASTX
NCBI GI g4455301
BLAST score 981
E value 1.0e-106
Match length 202
% identity 97
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 129143

Contig ID	32035_1.R1010
5'-most EST	jC-alXLIB327436P3g12b1
Method	BLASTX
NCBI GI	g4337195
BLAST score	694
E value	3.0e-73
Match length	157
% identity	87
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	129144
Contig ID	32039_1.R1010
5'-most EST	jC-alXLIB327436P4g10b1
Method	BLASTX
NCBI GI	g4689479
BLAST score	744
E value	3.0e-79
Match length	145
% identity	100
NCBI Description	(AC007213) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129145
Contig ID	32042_1.R1010
5'-most EST	jC-alXLIB327436P4h02b1

Seq. No.	129146
Contig ID	32043_1.R1010
5'-most EST	jC-alXLIB327436P3h02b1
Method	BLASTX
NCBI GI	g4680212
BLAST score	230
E value	1.0e-18
Match length	128
% identity	45
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	129147
Contig ID	32047_1.R1010
5'-most EST	jC-alXLIB327436P2h12b1
Method	BLASTX
NCBI GI	g2618691
BLAST score	1231
E value	1.0e-141
Match length	276
% identity	96
NCBI Description	(AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	129148
Contig ID	32053_1.R1010
5'-most EST	jC-alXLIB327436P4h12b1
Method	BLASTX
NCBI GI	g3818624
BLAST score	584
E value	2.0e-60
Match length	105
% identity	100

NCBI Description	(AF095912) actin related protein 2; ARP2 [Arabidopsis thaliana]
Seq. No.	129149
Contig ID	32057_1.R1010
5'-most EST	jC-atXLIB327437P2a01a2
Method	BLASTN
NCBI GI	g3449334
BLAST score	124
E value	5.0e-63
Match length	531
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.	129150
Contig ID	32074_1.R1010
5'-most EST	LIB25-067-Q1-E1-D1
Method	BLASTX
NCBI GI	g4678303
BLAST score	850
E value	2.0e-91
Match length	173
% identity	95
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]
Seq. No.	129151
Contig ID	32075_1.R1010
5'-most EST	LIB3177-017-P1-K2-C5
Method	BLASTX
NCBI GI	g728867
BLAST score	521
E value	1.0e-52
Match length	198
% identity	51
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi_99694_pir__S21961 proline-rich protein APG - Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana]
Seq. No.	129152
Contig ID	32076_1.R1010
5'-most EST	g2581708
Method	BLASTN
NCBI GI	g3510343
BLAST score	211
E value	1.0e-115
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.	129153
Contig ID	32078_1.R1010
5'-most EST	LIB25-067-Q1-E1-D4
Seq. No.	129154

Contig ID	32093_1.R1010
5'-most EST	g2722885
Method	BLASTX
NCBI GI	g4567253
BLAST score	327
E value	3.0e-30
Match length	135
% identity	53
NCBI Description	(AC007070) putative serpin protein [Arabidopsis thaliana]

Seq. No.	129155
Contig ID	32097_1.R1010
5'-most EST	LIB25-067-Q1-E1-F2
Method	BLASTX
NCBI GI	g3860250
BLAST score	215
E value	3.0e-17
Match length	65
% identity	63
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	129156
Contig ID	32098_1.R1010
5'-most EST	g2413335

Seq. No.	129157
Contig ID	32104_1.R1010
5'-most EST	g2756967
Method	BLASTX
NCBI GI	g2827548
BLAST score	1058
E value	1.0e-115
Match length	205
% identity	100
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	129158
Contig ID	32106_1.R1010
5'-most EST	jC-atXP53C183O19T7091a1
Method	BLASTX
NCBI GI	g3386614
BLAST score	212
E value	8.0e-17
Match length	62
% identity	51
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	129159
Contig ID	32106_2.R1010
5'-most EST	jC-atXLIB327437P4b01b2
Method	BLASTX
NCBI GI	g3386614
BLAST score	402
E value	3.0e-39

Match length	72
% identity	51
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	129160
Contig ID	32107_1.R1010
5'-most EST	ARABLI-032-Q1-B1-D9

Seq. No.	129161
Contig ID	32109_1.R1010
5'-most EST	jC-atXLIB327437P3b02b3
Method	BLASTX
NCBI GI	g2244792
BLAST score	746
E value	2.0e-79
Match length	150
% identity	97
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	129162
Contig ID	32111_1.R1010
5'-most EST	jC-atX25067Q1E1G05b1

Seq. No.	129163
Contig ID	32116_1.R1010
5'-most EST	jC-atX25067Q1E1H12b1
Method	BLASTX
NCBI GI	g1083296
BLAST score	312
E value	1.0e-28
Match length	131
% identity	50
NCBI Description	DNA mismatch repair protein rep-3 - mouse

Seq. No.	129164
Contig ID	32141_1.R1010
5'-most EST	jC-atX25068Q1E1B02b1
Method	BLASTX
NCBI GI	g1703478
BLAST score	392
E value	7.0e-69
Match length	153
% identity	58
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]

Seq. No.	129165
Contig ID	32147_1.R1010
5'-most EST	LIB3176-028-P1-K1-G1

Seq. No.	129166
Contig ID	32160_1.R1010
5'-most EST	jC-atXLIB327437P4a02b2
Method	BLASTX
NCBI GI	g3402672
BLAST score	484

E value	6.0e-49
Match length	98
% identity	99
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]

Seq. No.	129167
Contig ID	32163_1.R1010
5'-most EST	jC-atXLIB327403P3b04b2
Method	BLASTN
NCBI GI	g4490291
BLAST score	482
E value	0.0e+00
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	129168
Contig ID	32167_1.R1010
5'-most EST	jC-atXP91C245P7T7b1
Method	BLASTX
NCBI GI	g3461820
BLAST score	219
E value	2.0e-31
Match length	121
% identity	60
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	129169
Contig ID	32167_2.R1010
5'-most EST	jC-atXLIB327437P2a11a2
Method	BLASTN
NCBI GI	g3241917
BLAST score	270
E value	1.0e-150
Match length	437
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	129170
Contig ID	32172_1.R1010
5'-most EST	g2393445

Seq. No.	129171
Contig ID	32176_1.R1010
5'-most EST	LIB25-068-Q1-E1-E5
Method	BLASTX
NCBI GI	g2827699
BLAST score	921
E value	1.0e-100
Match length	225
% identity	88
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	129172
Contig ID	32179_1.R1010

5'-most EST	jC-atXP50C179K1T7095d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129173
Contig ID	32183_1.R1010
5'-most EST	LIB3234-006-P1-K1-H8
Method	BLASTX
NCBI GI	g1076632
BLAST score	634
E value	2.0e-66
Match length	145
% identity	81
NCBI Description	protein kinase - common tobacco >gi_506534_emb_CAA50374_ (X71057) protein kinase [Nicotiana tabacum]

Seq. No.	129174
Contig ID	32185_1.R1010
5'-most EST	LIB25-068-Q1-E1-F5
Method	BLASTX
NCBI GI	g2982466
BLAST score	268
E value	2.0e-23
Match length	70
% identity	71
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	129175
Contig ID	32186_1.R1010
5'-most EST	LIB3176-030-P1-K1-H4
Method	BLASTX
NCBI GI	g2286153
BLAST score	535
E value	1.0e-54
Match length	147
% identity	80
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	129176
Contig ID	32187_1.R1010
5'-most EST	jC-atX25068Q1E1F07b1

Seq. No.	129177
Contig ID	32188_1.R1010
5'-most EST	jC-atXLIB327437P2b05a2
Method	BLASTX
NCBI GI	g2832638
BLAST score	178
E value	1.0e-12
Match length	90
% identity	39

NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	129178
Contig ID	32192_1.R1010
5'-most EST	jC-atXLIB327417P1e09b1
Method	BLASTN
NCBI GI	g3985932
BLAST score	93
E value	2.0e-44
Match length	125
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]
Seq. No.	129179
Contig ID	32199_1.R1010
5'-most EST	jC-atX25068Q1E1G08b1
Seq. No.	129180
Contig ID	32210_1.R1010
5'-most EST	jC-atXP69C218P8T7043d1
Method	BLASTN
NCBI GI	g3702315
BLAST score	394
E value	0.0e+00
Match length	1066
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	129181
Contig ID	32214_1.R1010
5'-most EST	jC-alXLIB327434P1a02b1
Method	BLASTX
NCBI GI	g3559816
BLAST score	495
E value	6.0e-50
Match length	158
% identity	59
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]
Seq. No.	129182
Contig ID	32221_1.R1010
5'-most EST	jC-alXLIB327436P3h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	129183
Contig ID	32223_1.R1010
5'-most EST	jC-atXLIB327427P2d04b1
Method	BLASTN

NCBI GI	g3150396
BLAST score	252
E value	1.0e-139
Match length	484
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129184
Contig ID	32237_1.R1010
5'-most EST	jC-atXLIB327437P2a02a2

Seq. No.	129185
Contig ID	32237_2.R1010
5'-most EST	LIB25-069-Q1-E1-C7
Method	BLASTX
NCBI GI	g1729938
BLAST score	290
E value	1.0e-25
Match length	99
% identity	53
NCBI Description	THIOREDOXIN-LIKE PROTEIN SLR0233 >gi_1001610_dbj_BAA10238_ (D64000) thioredoxin M [Synechocystis sp.]

Seq. No.	129186
Contig ID	32240_1.R1010
5'-most EST	jC-atXP5C89M3T7059a1
Method	BLASTN
NCBI GI	g3172156
BLAST score	273
E value	1.0e-152
Match length	582
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129187
Contig ID	32240_2.R1010
5'-most EST	jC-atXP83C241A15T7025d1
Method	BLASTN
NCBI GI	g3172156
BLAST score	274
E value	1.0e-152
Match length	461
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129188
Contig ID	32260_1.R1010
5'-most EST	jC-atXP122C117I21T7057a1
Method	BLASTN
NCBI GI	g2828278
BLAST score	572
E value	0.0e+00
Match length	649
% identity	99

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)
Seq. No.	129189
Contig ID	32261_1.R1010
5'-most EST	LIB35-040-Q1-E1-A11
Method	BLASTN
NCBI GI	g2832689
BLAST score	354
E value	0.0e+00
Match length	364
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)
Seq. No.	129190
Contig ID	32268_1.R1010
5'-most EST	g2414103
Method	BLASTX
NCBI GI	g2244812
BLAST score	521
E value	2.0e-56
Match length	134
% identity	85
NCBI Description	(Z97336) auxin-responsive protein IAA1 [Arabidopsis thaliana]
Seq. No.	129191
Contig ID	32277_1.R1010
5'-most EST	jC-atX25077Q1E1B06a1
Seq. No.	129192
Contig ID	32281_1.R1010
5'-most EST	jC-atXLIB327423P4c06b1
Method	BLASTX
NCBI GI	g4586054
BLAST score	696
E value	2.0e-73
Match length	189
% identity	75
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.	129193
Contig ID	32284_1.R1010
5'-most EST	jC-atX25069Q1E1H07b1
Method	BLASTX
NCBI GI	g4531442
BLAST score	453
E value	6.0e-45
Match length	138
% identity	71
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]
Seq. No.	129194
Contig ID	32284_2.R1010
5'-most EST	LIB3175-055-P1-K1-G6
Method	BLASTN

NCBI GI	g4531433
BLAST score	115
E value	8.0e-58
Match length	344
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	129195
Contig ID	32292_1.R1010
5'-most EST	jC-alXLIB327436P2h11b1
Method	BLASTN
NCBI GI	g4589419
BLAST score	360
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	129196
Contig ID	32295_1.R1010
5'-most EST	jC-alXLIB327434P1a05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129197
Contig ID	32296_1.R1010
5'-most EST	jC-alXLIB327436P4h05b1
Method	BLASTN
NCBI GI	g2564045
BLAST score	266
E value	1.0e-148
Match length	447
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	129198
Contig ID	32299_1.R1010
5'-most EST	jC-alXLIB327436P3h07b1
Method	BLASTX
NCBI GI	g3075390
BLAST score	757
E value	1.0e-80
Match length	147
% identity	100
NCBI Description	(AC004484) protein kinase ARSK1 [Arabidopsis thaliana]

Seq. No.	129199
Contig ID	32300_1.R1010

5'-most EST	jC-alXLIB327436P3h08b1
Method	BLASTX
NCBI GI	g2459417
BLAST score	443
E value	7.0e-44
Match length	96
% identity	86
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	129200
Contig ID	32314_1.R1010
5'-most EST	jC-atXLIB327428P4a08b2
Method	BLASTX
NCBI GI	g4803710
BLAST score	62
E value	3.0e-38
Match length	100
% identity	77
NCBI Description	(AJ012374) iron sulfur subunit of succinate dehydrogenase (truncated) and ribosomal protein S14 [Zea mays]

Seq. No.	129201
Contig ID	32314_2.R1010
5'-most EST	g2757268
Method	BLASTX
NCBI GI	g729335
BLAST score	230
E value	6.0e-19
Match length	84
% identity	61
NCBI Description	SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN PRECURSOR (IP) >gi_508849 (L27705) succinate dehydrogenase iron-protein subunit [Drosophila melanogaster]

Seq. No.	129202
Contig ID	32314_3.R1010
5'-most EST	g935676
Method	BLASTX
NCBI GI	g729335
BLAST score	232
E value	3.0e-19
Match length	86
% identity	59
NCBI Description	SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN PRECURSOR (IP) >gi_508849 (L27705) succinate dehydrogenase iron-protein subunit [Drosophila melanogaster]

Seq. No.	129203
Contig ID	32320_1.R1010
5'-most EST	jC-atXLIB327437P2a08a2
Method	BLASTX
NCBI GI	g4191783
BLAST score	210
E value	3.0e-16
Match length	90
% identity	51

NCBI Description	(AC005917) hypothetical protein [Arabidopsis thaliana]
Seq. No.	129204
Contig ID	32326_1.R1010
5'-most EST	LIB3177-070-P1-K1-C4
Seq. No.	129205
Contig ID	32334_1.R1010
5'-most EST	g3449848
Seq. No.	129206
Contig ID	32343_1.R1010
5'-most EST	LIB25-070-Q1-E1-G3
Method	BLASTX
NCBI GI	g2435511
BLAST score	536
E value	9.0e-55
Match length	134
% identity	81
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]
Seq. No.	129207
Contig ID	32348_1.R1010
5'-most EST	LIB3175-046-P1-K1-A12
Method	BLASTX
NCBI GI	g4335758
BLAST score	209
E value	2.0e-16
Match length	80
% identity	55
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.	129208
Contig ID	32367_1.R1010
5'-most EST	jC-atX25071Q1E1A08b1
Method	BLASTN
NCBI GI	g4092471
BLAST score	264
E value	1.0e-146
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, complete sequence
Seq. No.	129209
Contig ID	32368_1.R1010
5'-most EST	LIB25-071-Q1-E1-A9
Method	BLASTX
NCBI GI	g4580990
BLAST score	462
E value	3.0e-46
Match length	90
% identity	98
NCBI Description	(AF120335) putative transposase [Arabidopsis thaliana]
Seq. No.	129210

Contig ID	32376_1.R1010
5'-most EST	jC-atXP46C174G23T7072a1

Seq. No.	129211
Contig ID	32376_2.R1010
5'-most EST	jC-atXLIB327421P4d10b1
Method	BLASTX
NCBI GI	g4262147
BLAST score	181
E value	4.0e-13
Match length	89
% identity	44
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	129212
Contig ID	32376_3.R1010
5'-most EST	LIB25-071-Q1-E1-B7
Method	BLASTX
NCBI GI	g2352492
BLAST score	450
E value	7.0e-45
Match length	127
% identity	67
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	129213
Contig ID	32380_1.R1010
5'-most EST	jC-atX25071Q1E1C10b1
Method	BLASTX
NCBI GI	g4455192
BLAST score	291
E value	3.0e-26
Match length	111
% identity	51
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	129214
Contig ID	32381_1.R1010
5'-most EST	jC-atX25071Q1E1C11b1

Seq. No.	129215
Contig ID	32383_1.R1010
5'-most EST	jC-atX25071Q1E1C02b1
Method	BLASTN
NCBI GI	g2795802
BLAST score	380
E value	0.0e+00
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129216
Contig ID	32385_1.R1010

5'-most EST	jC-atXP97C251A6T7d1
Method	BLASTX
NCBI GI	g3738298
BLAST score	744
E value	5.0e-79
Match length	186
% identity	87
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	129217
Contig ID	32385_3.R1010
5'-most EST	LIB25-071-Q1-E1-C5
Method	BLASTX
NCBI GI	g3738298
BLAST score	389
E value	2.0e-37
Match length	138
% identity	66
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	129218
Contig ID	32399_1.R1010
5'-most EST	LIB25-071-Q1-E1-D7
Method	BLASTN
NCBI GI	g3420042
BLAST score	380
E value	0.0e+00
Match length	380
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129219
Contig ID	32400_1.R1010
5'-most EST	jC-atXLIB327420P4d06b1
Method	BLASTX
NCBI GI	g4678222
BLAST score	209
E value	4.0e-16
Match length	153
% identity	33
NCBI Description	(AC007135) unknown protein [Arabidopsis thaliana]

Seq. No.	129220
Contig ID	32401_1.R1010
5'-most EST	jC-atXLIB327440P2g09a1
Method	BLASTX
NCBI GI	g4678323
BLAST score	829
E value	5.0e-89
Match length	195
% identity	88
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	129221
Contig ID	32406_1.R1010
5'-most EST	LIB25-071-Q1-E1-E3
Method	BLASTN
NCBI GI	g4589419
BLAST score	324
E value	0.0e+00
Match length	556
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	129222
Contig ID	32411_1.R1010
5'-most EST	jC-atX25071Q1E1E08b1

Seq. No.	129223
Contig ID	32419_1.R1010
5'-most EST	jC-atX25071Q1E1F05b1
Method	BLASTX
NCBI GI	g2501496
BLAST score	262
E value	6.0e-23
Match length	112
% identity	49
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 7 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 7) >gi_542017_pir__S41953 UTP-glucose glucosyltransferase - cassava >gi_453253_emb_CAA54614_ (X77464) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	129224
Contig ID	32420_1.R1010
5'-most EST	jC-alXLIB327435P4e11b1
Method	BLASTX
NCBI GI	g3176676
BLAST score	796
E value	4.0e-85
Match length	156
% identity	100
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	129225
Contig ID	32420_2.R1010
5'-most EST	g2758760
Method	BLASTX
NCBI GI	g3176676
BLAST score	380
E value	2.0e-36
Match length	87
% identity	92
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	129226
Contig ID	32422_1.R1010
5'-most EST	jC-atX25071Q1E1F08b1

Seq. No.	129227
Contig ID	32444_1.R1010
5'-most EST	jC-atXLIB327403P3a08b2
Method	BLASTN
NCBI GI	g4589438
BLAST score	317
E value	1.0e-178
Match length	317
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	129228
Contig ID	32445_1.R1010
5'-most EST	LIB25-073-Q1-E1-A12
Method	BLASTX
NCBI GI	g3980403
BLAST score	580
E value	6.0e-60
Match length	113
% identity	100
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	129229
Contig ID	32447_1.R1010
5'-most EST	jC-atXLIB327431P4h08a1

Seq. No.	129230
Contig ID	32458_1.R1010
5'-most EST	LIB3176-086-P1-K1-H1
Method	BLASTX
NCBI GI	g4455366
BLAST score	222
E value	9.0e-18
Match length	137
% identity	43
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	129231
Contig ID	32465_1.R1010
5'-most EST	jC-alX24076Q1E1D05b1

Seq. No.	129232
Contig ID	32466_1.R1010
5'-most EST	LIB3177-092-P1-K1-F4
Method	BLASTX
NCBI GI	g3420008
BLAST score	240
E value	4.0e-20
Match length	123
% identity	38

NCBI Description	(AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No.	129233
Contig ID	32473_1.R1010
5'-most EST	jC-atX25073Q1E1C08b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	255
E value	1.0e-141
Match length	301
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129234
Contig ID	32478_1.R1010
5'-most EST	jC-atX25073Q1E1D02b1
Method	BLASTN
NCBI GI	g4415905
BLAST score	214
E value	1.0e-117
Match length	462
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129235
Contig ID	32479_1.R1010
5'-most EST	jC-atX25073Q1E1D04b1
Method	BLASTX
NCBI GI	g1814401
BLAST score	682
E value	7.0e-72
Match length	175
% identity	75
NCBI Description	(U84888) phosphoglucomutase [Mesembryanthemum crystallinum]

Seq. No.	129236
Contig ID	32489_1.R1010
5'-most EST	jC-atXP70C222E16T7d1
Method	BLASTX
NCBI GI	g729775
BLAST score	336
E value	4.0e-31
Match length	92
% identity	70
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR) >gi_100264_pir__S25481 heat shock transcription factor 8 - Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]

Seq. No.	129237
Contig ID	32490_1.R1010
5'-most EST	LIB25-073-Q1-E1-E4
Method	BLASTX
NCBI GI	g4587572

BLAST score	723
E value	7.0e-77
Match length	140
% identity	99
NCBI Description	(AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]

Seq. No.	129238
Contig ID	32491_1.R1010
5'-most EST	jC-atXLIB327403P3b09b2
Method	BLASTN
NCBI GI	g3128136
BLAST score	119
E value	4.0e-60
Match length	410
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	129239
Contig ID	32492_1.R1010
5'-most EST	jC-atXLIB327403P3b10b2
Method	BLASTX
NCBI GI	g3426041
BLAST score	260
E value	2.0e-69
Match length	129
% identity	98
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	129240
Contig ID	32494_1.R1010
5'-most EST	jC-atXLIB327403P3b12b2
Method	BLASTX
NCBI GI	g2462743
BLAST score	395
E value	6.0e-38
Match length	167
% identity	50
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	129241
Contig ID	32495_1.R1010
5'-most EST	LIB25-073-Q1-E1-F1
Method	BLASTX
NCBI GI	g728867
BLAST score	334
E value	3.0e-31
Match length	133
% identity	50
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi_99694_pir__S21961 proline-rich protein APG - Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana]

Seq. No.	129242
Contig ID	32514_1.R1010
5'-most EST	jC-atXLIB327426P2c06b1
Method	BLASTX
NCBI GI	g2500341
BLAST score	165
E value	4.0e-11
Match length	38
% identity	76
NCBI Description	50S RIBOSOMAL PROTEIN L36 >gi_1652406_dbj_BAA17328_ (D90905) 50S ribosomal protein L36 [Synechocystis sp.]

Seq. No.	129243
Contig ID	32517_1.R1010
5'-most EST	jC-atX25073Q1E1G08b1
Method	BLASTX
NCBI GI	g4580468
BLAST score	648
E value	4.0e-68
Match length	130
% identity	96
NCBI Description	(AC006081) putative protein kinase; similar to human PKX1 and Drosophila DC2 [Arabidopsis thaliana]

Seq. No.	129244
Contig ID	32518_1.R1010
5'-most EST	jC-atXP69C220B14T7080d1
Method	BLASTN
NCBI GI	g3449330
BLAST score	67
E value	7.0e-29
Match length	336
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	129245
Contig ID	32520_1.R1010
5'-most EST	jC-atX25073Q1E1H10b1
Method	BLASTX
NCBI GI	g4587994
BLAST score	507
E value	2.0e-51
Match length	134
% identity	78
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129246
Contig ID	32532_1.R1010
5'-most EST	jC-atXLIB327403P3a07b2
Method	BLASTX
NCBI GI	g2462753
BLAST score	883
E value	3.0e-95
Match length	214
% identity	77
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No.	129247
Contig ID	32538_1.R1010
5'-most EST	jC-atX25074Q1E1B03b1
Method	BLASTX
NCBI GI	g1076715
BLAST score	158
E value	1.0e-15
Match length	92
% identity	48
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	129248
Contig ID	32542_1.R1010
5'-most EST	jC-alX24075Q1E1C10b1
Method	BLASTN
NCBI GI	g2264318
BLAST score	501
E value	0.0e+00
Match length	520
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	129249
Contig ID	32543_1.R1010
5'-most EST	LIB25-074-Q1-E1-B9
Method	BLASTX
NCBI GI	g3355465
BLAST score	806
E value	2.0e-86
Match length	155
% identity	99
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	129250
Contig ID	32544_1.R1010
5'-most EST	g2748881
Method	BLASTN
NCBI GI	g2264306
BLAST score	286
E value	1.0e-160
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	129251
Contig ID	32544_2.R1010
5'-most EST	ARABL1-04-Q1-B1-E3
Method	BLASTX
NCBI GI	g2829927
BLAST score	181
E value	1.0e-12

Match length 117
% identity 37
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 129252
Contig ID 32555_1.R1010
5'-most EST jC-atXmonuni27Aa07b1
Method BLASTN
NCBI GI g4376087
BLAST score 189
E value 1.0e-102
Match length 438
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No. 129253
Contig ID 32557_1.R1010
5'-most EST LIB25-074-Q1-E1-D3

Seq. No. 129254
Contig ID 32564_1.R1010
5'-most EST LIB25-074-Q1-E1-E2
Method BLASTN
NCBI GI g3659491
BLAST score 575
E value 0.0e+00
Match length 611
% identity 98
NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 129255
Contig ID 32574_1.R1010
5'-most EST LIB3177-015-P1-K2-A4
Method BLASTX
NCBI GI g4115936
BLAST score 211
E value 9.0e-17
Match length 107
% identity 37
NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No. 129256
Contig ID 32578_1.R1010
5'-most EST LIB25-074-Q1-E1-F6

Seq. No. 129257
Contig ID 32579_1.R1010
5'-most EST LIB25-074-Q1-E1-F7
Method BLASTX
NCBI GI g3281850
BLAST score 633
E value 4.0e-66
Match length 125
% identity 99
NCBI Description (AL031004) monogalactosyldiacylglycerol synthase - like

protein [Arabidopsis thaliana]

Seq. No.	129258
Contig ID	32583_1.R1010
5'-most EST	jC-atXLIB327401P4c01b2
Method	BLASTX
NCBI GI	g3184281
BLAST score	257
E value	5.0e-22
Match length	70
% identity	70
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	129259
Contig ID	32606_1.R1010
5'-most EST	LIB25-075-Q1-E1-D1
Method	BLASTX
NCBI GI	g2832685
BLAST score	736
E value	5.0e-78
Match length	154
% identity	93
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	129260
Contig ID	32606_2.R1010
5'-most EST	g2580824
Method	BLASTX
NCBI GI	g2832679
BLAST score	169
E value	1.0e-11
Match length	32
% identity	100
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	129261
Contig ID	32614_2.R1010
5'-most EST	jC-atXLIB327405P3g12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	62
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129262
Contig ID	32614_3.R1010
5'-most EST	LIB3177-095-P1-K1-B11

Seq. No.	129263
Contig ID	32615_1.R1010
5'-most EST	LIB3175-004-P1-K1-A2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46

E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129264
Contig ID	32615_2.R1010
5'-most EST	g2763564

Seq. No.	129265
Contig ID	32616_1.R1010
5'-most EST	jC-atXLIB327431P3e11a1
Method	BLASTN
NCBI GI	g2828185
BLAST score	160
E value	2.0e-84
Match length	631
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	129266
Contig ID	32617_1.R1010
5'-most EST	LIB3175-016-P1-K1-A6
Method	BLASTN
NCBI GI	g2564044
BLAST score	272
E value	1.0e-151
Match length	478
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	129267
Contig ID	32628_1.R1010
5'-most EST	jC-atXLIB327418P4a03b1
Method	BLASTN
NCBI GI	g2351063
BLAST score	451
E value	0.0e+00
Match length	492
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	129268
Contig ID	32629_1.R1010
5'-most EST	jC-atXLIB327416P4e04b1
Method	BLASTN
NCBI GI	g4220637
BLAST score	202
E value	1.0e-109
Match length	587
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	129269
Contig ID	32631_1.R1010
5'-most EST	jC-atXLIB327416P3e01b1
Method	BLASTN
NCBI GI	g4510408
BLAST score	168
E value	2.0e-89
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1E2 genomic sequence, complete sequence

Seq. No.	129270
Contig ID	32632_1.R1010
5'-most EST	jC-atXLIB327416P3e02b1
Method	BLASTN
NCBI GI	g2618600
BLAST score	472
E value	0.0e+00
Match length	476
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	129271
Contig ID	32634_1.R1010
5'-most EST	jC-atXLIB327416P4e03b1
Method	BLASTX
NCBI GI	g4522012
BLAST score	498
E value	3.0e-50
Match length	134
% identity	69
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129272
Contig ID	32641_1.R1010
5'-most EST	jC-atXLIB327416P3e09b1
Method	BLASTX
NCBI GI	g3023522
BLAST score	303
E value	2.0e-27
Match length	131
% identity	49
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_2454309 (AF002705) beta prime COP [Rattus norvegicus]

Seq. No.	129273
Contig ID	32642_1.R1010
5'-most EST	jC-atXLIB327416P3e10b1

Seq. No.	129274
Contig ID	32652_1.R1010
5'-most EST	jC-atXLIB327416P2f02b1
Method	BLASTX
NCBI GI	g3334144

BLAST score	415
E value	1.0e-40
Match length	114
% identity	69
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	129275
Contig ID	32656_1.R1010
5'-most EST	jC-atXLIB327402P1a04b1
Method	BLASTX
NCBI GI	g3461828
BLAST score	169
E value	1.0e-32
Match length	124
% identity	56
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	129276
Contig ID	32660_1.R1010
5'-most EST	LIB3176-002-Q1-K1-F1
Method	BLASTX
NCBI GI	g1706130
BLAST score	954
E value	1.0e-103
Match length	213
% identity	85
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]

Seq. No.	129277
Contig ID	32662_1.R1010
5'-most EST	jC-atXLIB327416P1f07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	2.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129278
Contig ID	32663_1.R1010
5'-most EST	jC-atXLIB327416P2f08b1

Seq. No.	129279
Contig ID	32664_1.R1010
5'-most EST	jC-atXP29C140G11T7016d1

Seq. No.	129280
Contig ID	32684_1.R1010
5'-most EST	LIB35-027-Q1-E1-F4
Method	BLASTX
NCBI GI	g1346802

BLAST score	509
E value	1.0e-51
Match length	116
% identity	79
NCBI Description	PROFILIN 1 >gi_1076516_pir__S49351 profilin - kidney bean >gi_556836_emb_CAA57508_ (X81982) profilin [Phaseolus vulgaris]

Seq. No.	129281
Contig ID	32689_1.R1010
5'-most EST	jC-atXLIB327416P4f10b1
Method	BLASTX
NCBI GI	g4063749
BLAST score	154
E value	5.0e-10
Match length	59
% identity	25
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129282
Contig ID	32693_1.R1010
5'-most EST	jC-atXLIB327416P4f09b1
Method	BLASTX
NCBI GI	g3355626
BLAST score	605
E value	7.0e-63
Match length	137
% identity	82
NCBI Description	(Y09204) histidinol-phosphate aminotransferase [Nicotiana tabacum]

Seq. No.	129283
Contig ID	32700_1.R1010
5'-most EST	jC-atXP96C248K10T7b1
Method	BLASTX
NCBI GI	g2760606
BLAST score	583
E value	5.0e-60
Match length	156
% identity	68
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	129284
Contig ID	32700_2.R1010
5'-most EST	jC-atXLIB327416P4f12b1
Method	BLASTX
NCBI GI	g2760606
BLAST score	409
E value	9.0e-40
Match length	106
% identity	71
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione

	peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]
Seq. No.	129285
Contig ID	32705_1.R1010
5'-most EST	jC-atXLIB327416P3e03b1
Method	BLASTN
NCBI GI	g3702733
BLAST score	200
E value	1.0e-108
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJP23, complete sequence [Arabidopsis thaliana]
Seq. No.	129286
Contig ID	32709_1.R1010
5'-most EST	jC-atXLIB327416P4e02b1
Method	BLASTX
NCBI GI	g3135251
BLAST score	272
E value	8.0e-24
Match length	117
% identity	50
NCBI Description	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] >gi_3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]
Seq. No.	129287
Contig ID	32711_1.R1010
5'-most EST	jC-atXLIB327416P3e08b1
Method	BLASTX
NCBI GI	g2353183
BLAST score	222
E value	5.0e-18
Match length	139
% identity	39
NCBI Description	(AF015566) CtrA [Dictyostelium discoideum]
Seq. No.	129288
Contig ID	32715_1.R1010
5'-most EST	jC-atXLIB327416P4e12b1
Method	BLASTX
NCBI GI	g4490756
BLAST score	293
E value	3.0e-26
Match length	138
% identity	43
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]
Seq. No.	129289
Contig ID	32718_1.R1010
5'-most EST	jC-atX25077Q1E1B06b1

Seq. No.	129290
Contig ID	32719_1.R1010
5'-most EST	jC-atXLIB327416P4e10b1
Method	BLASTX
NCBI GI	g2342690
BLAST score	245
E value	2.0e-20
Match length	71
% identity	66
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246). [Arabidopsis thaliana]

Seq. No.	129291
Contig ID	32720_1.R1010
5'-most EST	jC-atXLIB327416P4e11b1
Method	BLASTN
NCBI GI	g2583106
BLAST score	245
E value	1.0e-135
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129292
Contig ID	32724_1.R1010
5'-most EST	jC-atXLIB327416P2e04b1
Method	BLASTX
NCBI GI	g2832623
BLAST score	341
E value	6.0e-32
Match length	87
% identity	74
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	129293
Contig ID	32725_1.R1010
5'-most EST	jC-atXLIB327416P1f05b1
Method	BLASTN
NCBI GI	g4757410
BLAST score	497
E value	0.0e+00
Match length	497
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	129294
Contig ID	32730_1.R1010
5'-most EST	jC-atXLIB327416P1f03b1
Method	BLASTX
NCBI GI	g1429367
BLAST score	252
E value	2.0e-21
Match length	80
% identity	61

NCBI Description	(X77635) tumorous imaginal discs [Drosophila virilis]

Seq. No.	129295
Contig ID	32733_1.R1010
5'-most EST	jC-atXLIB327416P2f06b1
Method	BLASTX
NCBI GI	g1730502
BLAST score	182
E value	3.0e-13
Match length	88
% identity	45
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	129296
Contig ID	32737_1.R1010
5'-most EST	jC-atXLIB327416P2f09b1
Method	BLASTX
NCBI GI	g4512655
BLAST score	402
E value	6.0e-39
Match length	108
% identity	69
NCBI Description	(AC007048) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	129297
Contig ID	32738_1.R1010
5'-most EST	jC-atXLIB327416P2f10b1
Method	BLASTX
NCBI GI	g4206196
BLAST score	639
E value	7.0e-67
Match length	139
% identity	88
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129298
Contig ID	32739_1.R1010
5'-most EST	jC-atXLIB327416P1f11b1
Method	BLASTN
NCBI GI	g3449322
BLAST score	173
E value	2.0e-92
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	129299
Contig ID	32740_1.R1010
5'-most EST	jC-atXLIB327416P2f07b1

Seq. No.	129300
Contig ID	32746_1.R1010
5'-most EST	jC-atXLIB327416P4f02b1

Method	BLASTX
NCBI GI	g3319354
BLAST score	532
E value	3.0e-54
Match length	103
% identity	100
NCBI Description	(AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No.	129301
Contig ID	32753_1.R1010
5'-most EST	LIB25-077-Q1-E1-F1
Method	BLASTX
NCBI GI	g1438881
BLAST score	279
E value	9.0e-25
Match length	79
% identity	63
NCBI Description	(U43839) GmCK2p [Glycine max]

Seq. No.	129302
Contig ID	32768_1.R1010
5'-most EST	jC-atXLIB327416P3f08b1
Method	BLASTX
NCBI GI	g4539370
BLAST score	54
E value	4.0e-45
Match length	119
% identity	80
NCBI Description	(AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	129303
Contig ID	32769_1.R1010
5'-most EST	jC-atXLIB327416P3f09b1
Method	BLASTX
NCBI GI	g2673914
BLAST score	974
E value	1.0e-115
Match length	217
% identity	96
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129304
Contig ID	32773_1.R1010
5'-most EST	jC-atXLIB327416P1g03b1
Method	BLASTN
NCBI GI	g4159700
BLAST score	453
E value	0.0e+00
Match length	469
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	129305
Contig ID	32777_1.R1010

5'-most EST	jC-atXLIB327416P1g01b1
Method	BLASTX
NCBI GI	g4760343
BLAST score	200
E value	2.0e-15
Match length	81
% identity	49
NCBI Description	(AL049769) putative SNRNP SM-like protein [Schizosaccharomyces pombe]

Seq. No.	129306
Contig ID	32785_1.R1010
5'-most EST	g2446213
Method	BLASTX
NCBI GI	g81600
BLAST score	309
E value	5.0e-28
Match length	75
% identity	81
NCBI Description	chaperonin 60 beta (clone bX) - Arabidopsis thaliana (fragment)

Seq. No.	129307
Contig ID	32785_2.R1010
5'-most EST	jC-atXLIB327416P2g09b1
Method	BLASTX
NCBI GI	g4204266
BLAST score	1079
E value	1.0e-118
Match length	242
% identity	91
NCBI Description	(AC005223) 52263 [Arabidopsis thaliana]

Seq. No.	129308
Contig ID	32806_1.R1010
5'-most EST	jC-atX24104Q1E2G08b1
Method	BLASTN
NCBI GI	g3241926
BLAST score	140
E value	1.0e-72
Match length	392
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	129309
Contig ID	32809_1.R1010
5'-most EST	jC-atXLIB327416P1h12b1

Seq. No.	129310
Contig ID	32816_1.R1010
5'-most EST	jC-atXLIB327416P3h06b1
Method	BLASTN
NCBI GI	g4691223
BLAST score	124
E value	4.0e-63
Match length	325

% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	129311
Contig ID	32830_1.R1010
5'-most EST	jC-atXLIB327417P1a04b1
Method	BLASTN
NCBI GI	g4079614
BLAST score	534
E value	0.0e+00
Match length	645
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129312
Contig ID	32832_3.R1010
5'-most EST	jC-atXLIB327417P1a01b1
Method	BLASTX
NCBI GI	g3047078
BLAST score	996
E value	1.0e-108
Match length	213
% identity	99
NCBI Description	(AF058914) similar to 11-S seed storage proteins (Pfam: Seedstore_11s.hmm, score: 19.95) [Arabidopsis thaliana]

Seq. No.	129313
Contig ID	32839_1.R1010
5'-most EST	g2758296
Method	BLASTN
NCBI GI	g2832611
BLAST score	199
E value	1.0e-108
Match length	407
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	129314
Contig ID	32840_1.R1010
5'-most EST	g2748598
Method	BLASTX
NCBI GI	g1363492
BLAST score	219
E value	1.0e-17
Match length	61
% identity	69
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.	129315
Contig ID	32843_1.R1010
5'-most EST	LIB35-011-Q1-E1-C3

Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129316
Contig ID	32844_1.R1010
5'-most EST	jC-atXLIB327417P4a10b1
Method	BLASTN
NCBI GI	g2494110
BLAST score	152
E value	8.0e-80
Match length	480
% identity	100
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	129317
Contig ID	32851_1.R1010
5'-most EST	ARABL1-035-Q1-B1-C2

Seq. No.	129318
Contig ID	32851_2.R1010
5'-most EST	jC-atXLIB327416P2d08b1

Seq. No.	129319
Contig ID	32857_1.R1010
5'-most EST	jC-atXLIB327416P4g05b1
Method	BLASTN
NCBI GI	g3341671
BLAST score	298
E value	1.0e-167
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129320
Contig ID	32862_1.R1010
5'-most EST	jC-atXLIB327416P3g04b1
Method	BLASTN
NCBI GI	g3869075
BLAST score	418
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	129321
Contig ID	32863_1.R1010
5'-most EST	jC-atXLIB327423P3e02b1
Method	BLASTX
NCBI GI	g2244868

BLAST score	307
E value	6.0e-28
Match length	132
% identity	50
NCBI Description	(Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	129322
Contig ID	32869_1.R1010
5'-most EST	jC-atX24104Q1E1G04b1
Method	BLASTN
NCBI GI	g2264309
BLAST score	304
E value	1.0e-170
Match length	435
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	129323
Contig ID	32872_1.R1010
5'-most EST	LIB25-079-Q1-E1-C9
Method	BLASTX
NCBI GI	g2499553
BLAST score	368
E value	3.0e-35
Match length	73
% identity	97
NCBI Description	CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_629524_pir__S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana >gi_442529_bbs_139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa] [Arabidopsis thaliana]

Seq. No.	129324
Contig ID	32874_1.R1010
5'-most EST	g2048427

Seq. No.	129325
Contig ID	32880_1.R1010
5'-most EST	jC-atX24107Q1E1D09b1
Method	BLASTN
NCBI GI	g3193282
BLAST score	505
E value	0.0e+00
Match length	505
% identity	100
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	129326
Contig ID	32882_1.R1010
5'-most EST	jC-atXLIB327416P2h10b1

Seq. No.	129327
Contig ID	32884_1.R1010
5'-most EST	g932127

Method	BLASTN
NCBI GI	g4454587
BLAST score	544
E value	0.0e+00
Match length	761
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	129328
Contig ID	32884_2.R1010
5'-most EST	g2393217
Method	BLASTN
NCBI GI	g2191181
BLAST score	412
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana BAC TM021B04

Seq. No.	129329
Contig ID	32886_1.R1010
5'-most EST	jC-atXLIB327416P4h07b1
Method	BLASTX
NCBI GI	g3426062
BLAST score	361
E value	3.0e-34
Match length	133
% identity	56
NCBI Description	(AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No.	129330
Contig ID	32903_1.R1010
5'-most EST	jC-atXLIB327417P1a10b1
Method	BLASTX
NCBI GI	g2288981
BLAST score	303
E value	4.0e-41
Match length	136
% identity	44
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	129331
Contig ID	32905_1.R1010
5'-most EST	LIB25-113-Q1-E1-E4
Method	BLASTN
NCBI GI	g3985955
BLAST score	316
E value	1.0e-178
Match length	316
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	129332

Contig ID 32914_1.R1010
5'-most EST jC-atXLIB327417P3a08b1
Method BLASTN
NCBI GI g2582640
BLAST score 64
E value 4.0e-27
Match length 75
% identity 97
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 129333
Contig ID 32915_1.R1010
5'-most EST jC-atXLIB327417P4a09b1

Seq. No. 129334
Contig ID 32927_1.R1010
5'-most EST jC-atXLIB327416P1g06b1
Method BLASTX
NCBI GI g2935342
BLAST score 692
E value 5.0e-73
Match length 163
% identity 87
NCBI Description (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No. 129335
Contig ID 32930_1.R1010
5'-most EST jC-atXLIB327416P4g02b1
Method BLASTX
NCBI GI g2316016
BLAST score 375
E value 6.0e-36
Match length 141
% identity 55
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 129336
Contig ID 32936_1.R1010
5'-most EST jC-atXLIB327426P2h10b1
Method BLASTN
NCBI GI g4544381
BLAST score 278
E value 1.0e-155
Match length 433
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No. 129337
Contig ID 32938_1.R1010
5'-most EST jC-atXLIB327416P3g09b1
Method BLASTN
NCBI GI g4567300
BLAST score 175
E value 1.0e-93

Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	129338
Contig ID	32957_1.R1010
5'-most EST	jC-atXLIB327416P2g04b1
Method	BLASTN
NCBI GI	g2827698
BLAST score	118
E value	2.0e-59
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)

Seq. No.	129339
Contig ID	32958_1.R1010
5'-most EST	LIB3176-020-P1-K1-A7
Method	BLASTX
NCBI GI	g3881780
BLAST score	170
E value	1.0e-11
Match length	116
% identity	35
NCBI Description	(Z48638) similar to lipid transfer protein [Caenorhabditis elegans]

Seq. No.	129340
Contig ID	32961_1.R1010
5'-most EST	jC-atXLIB327416P3h01b1
Method	BLASTX
NCBI GI	g1335862
BLAST score	794
E value	5.0e-85
Match length	161
% identity	96
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	129341
Contig ID	32964_1.R1010
5'-most EST	jC-atXP113C132P19T7002a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	6.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129342
Contig ID	32964_2.R1010
5'-most EST	jC-atXP96C249F11T7b1
Method	BLASTX
NCBI GI	g4574738
BLAST score	157

E value 1.0e-19
Match length 189
% identity 37
NCBI Description (AF134238) PL6 protein [Mus musculus]

Seq. No. 129343
Contig ID 32964_12.R1010
5'-most EST jC-atXP113C132J12T7017a1

Seq. No. 129344
Contig ID 32973_1.R1010
5'-most EST LIB3175-022-P1-K1-H4
Method BLASTX
NCBI GI g2213536
BLAST score 163
E value 6.0e-11
Match length 96
% identity 42
NCBI Description (X98738) DNA-binding protein PD1 [Pisum sativum]

Seq. No. 129345
Contig ID 32974_1.R1010
5'-most EST jC-atXLIB327416P3h11b1
Method BLASTN
NCBI GI g2815404
BLAST score 640
E value 0.0e+00
Match length 659
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No. 129346
Contig ID 32981_1.R1010
5'-most EST jC-atXLIB327416P3h09b1
Method BLASTN
NCBI GI g3449327
BLAST score 168
E value 2.0e-89
Match length 439
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 129347
Contig ID 32998_1.R1010
5'-most EST jC-atXLIB327417P4a03b1
Method BLASTN
NCBI GI g2582640
BLAST score 59
E value 3.0e-24
Match length 71
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 129348

Contig ID	33006_1.R1010
5'-most EST	LIB3168-064-P1-K1-D4
Method	BLASTN
NCBI GI	g3449322
BLAST score	159
E value	4.0e-84
Match length	348
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	129349
Contig ID	33009_1.R1010
5'-most EST	jC-atXLIB327412P1g08b1
Method	BLASTX
NCBI GI	g2911067
BLAST score	239
E value	1.0e-39
Match length	141
% identity	64
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	129350
Contig ID	33017_1.R1010
5'-most EST	jC-atXLIB327416P4g03b1
Method	BLASTX
NCBI GI	g2689030
BLAST score	142
E value	1.0e-08
Match length	145
% identity	30
NCBI Description	(AF034568) RNA guanylyltransferase [Mus musculus] >gi_2697127 (AF025653) mRNA capping enzyme [Mus musculus]

Seq. No.	129351
Contig ID	33018_1.R1010
5'-most EST	jC-atXLIB327416P3g03b1
Method	BLASTX
NCBI GI	g4507943
BLAST score	331
E value	9.0e-31
Match length	141
% identity	48
NCBI Description	exportin 1 (CRM1, yeast, homolog) >gi_2626840_dbj_BAA23415_ (D89729) CRM1 protein [Homo sapiens]

Seq. No.	129352
Contig ID	33020_1.R1010
5'-most EST	LIB25-081-Q1-E1-B6

Seq. No.	129353
Contig ID	33023_1.R1010
5'-most EST	LIB3175-035-P1-K1-H1
Method	BLASTX
NCBI GI	g2129568
BLAST score	857

E value	4.0e-92
Match length	176
% identity	93
NCBI Description	cytosolic cyclophilin ROC2 - Arabidopsis thaliana >gi_1305457 (U40400) cytosolic cyclophilin [Arabidopsis thaliana]

Seq. No.	129354
Contig ID	33025_1.R1010
5'-most EST	jC-atXLIB327416P4g09b1
Method	BLASTX
NCBI GI	g2623296
BLAST score	624
E value	9.0e-65
Match length	134
% identity	96
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129355
Contig ID	33044_1.R1010
5'-most EST	g2048455

Seq. No.	129356
Contig ID	33044_2.R1010
5'-most EST	g2047741

Seq. No.	129357
Contig ID	33044_3.R1010
5'-most EST	jC-atXLIB327416P4h03b1
Method	BLASTX
NCBI GI	g3080405
BLAST score	196
E value	9.0e-15
Match length	61
% identity	39
NCBI Description	(AL022603) Lsd1 like protein [Arabidopsis thaliana] >gi_4455269_emb_CAB36805.1_ (AL035527) Lsd1 like protein [Arabidopsis thaliana]

Seq. No.	129358
Contig ID	33049_1.R1010
5'-most EST	g3450289
Method	BLASTN
NCBI GI	g4589423
BLAST score	341
E value	0.0e+00
Match length	381
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence

Seq. No.	129359
Contig ID	33049_2.R1010
5'-most EST	LIB25-081-Q1-E1-E6
Method	BLASTN
NCBI GI	g4589423
BLAST score	283

E value	1.0e-158
Match length	414
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence

Seq. No.	129360
Contig ID	33059_1.R1010
5'-most EST	LIB25-081-Q1-E1-F5
Method	BLASTN
NCBI GI	g2642152
BLAST score	424
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129361
Contig ID	33060_1.R1010
5'-most EST	jC-atXLIB327416P4h08b1
Method	BLASTX
NCBI GI	g4678934
BLAST score	350
E value	6.0e-33
Match length	118
% identity	71
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	129362
Contig ID	33062_1.R1010
5'-most EST	jC-atXLIB327416P3h08b1
Method	BLASTX
NCBI GI	g3023742
BLAST score	563
E value	1.0e-57
Match length	139
% identity	84
NCBI Description	FERREDOXIN 2 PRECURSOR >gi_1931646 (U95973) ferredoxin precusor isolog [Arabidopsis thaliana]

Seq. No.	129363
Contig ID	33066_1.R1010
5'-most EST	LIB25-081-Q1-E1-G11
Method	BLASTX
NCBI GI	g3822036
BLAST score	326
E value	3.0e-30
Match length	146
% identity	46
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	129364
Contig ID	33074_1.R1010
5'-most EST	g2762686
Method	BLASTX
NCBI GI	g3219938

BLAST score	173
E value	5.0e-12
Match length	96
% identity	39
NCBI Description	HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I >gi_2058378_emb_CAB08174_ (Z94864) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	129365
Contig ID	33075_1.R1010
5'-most EST	LIB25-081-Q1-E1-G9

Seq. No.	129366
Contig ID	33076_1.R1010
5'-most EST	jC-atXLIB327417P3a02b1
Method	BLASTX
NCBI GI	g4510354
BLAST score	222
E value	1.0e-34
Match length	133
% identity	66
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	129367
Contig ID	33087_1.R1010
5'-most EST	LIB25-082-Q1-E1-A12

Seq. No.	129368
Contig ID	33090_1.R1010
5'-most EST	LIB25-082-Q1-E1-A4
Method	BLASTN
NCBI GI	g4263586
BLAST score	183
E value	2.0e-98
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F28K20 sequence, complete sequence

Seq. No.	129369
Contig ID	33093_1.R1010
5'-most EST	LIB25-082-Q1-E1-A8
Method	BLASTX
NCBI GI	g2558938
BLAST score	392
E value	1.0e-37
Match length	188
% identity	46
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	129370
Contig ID	33094_1.R1010
5'-most EST	jC-atXLIB327417P1b10b1
Method	BLASTX
NCBI GI	g2462822
BLAST score	230
E value	1.0e-18

Match length	172
% identity	35
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129371
Contig ID	33097_1.R1010
5'-most EST	LIB25-082-Q1-E1-B12
Method	BLASTX
NCBI GI	g4678346
BLAST score	178
E value	5.0e-13
Match length	62
% identity	56
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	129372
Contig ID	33098_1.R1010
5'-most EST	jC-alX25082Q1E1B03b1

Seq. No.	129373
Contig ID	33099_1.R1010
5'-most EST	jC-atXLIB327417P4b03b1
Method	BLASTN
NCBI GI	g2894591
BLAST score	430
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	129374
Contig ID	33101_1.R1010
5'-most EST	jC-atXLIB327417P2b10b1
Method	BLASTX
NCBI GI	g2464932
BLAST score	379
E value	2.0e-46
Match length	111
% identity	89
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	129375
Contig ID	33101_2.R1010
5'-most EST	g2580777
Method	BLASTX
NCBI GI	g4220457
BLAST score	512
E value	7.0e-52
Match length	171
% identity	24
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. EST gb_N96478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	129376

Contig ID	33101_3.R1010
5'-most EST	jC-atXP89C245C5T7055d1
Method	BLASTX
NCBI GI	g2464932
BLAST score	102
E value	1.0e-38
Match length	96
% identity	90
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	129377
Contig ID	33101_8.R1010
5'-most EST	jC-atXP89C245C5T7s1
Method	BLASTN
NCBI GI	g4006885
BLAST score	269
E value	1.0e-150
Match length	295
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	129378
Contig ID	33109_1.R1010
5'-most EST	jC-atXLIB327417P1c01a1
Method	BLASTX
NCBI GI	g3540206
BLAST score	191
E value	4.0e-14
Match length	72
% identity	62
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	129379
Contig ID	33109_2.R1010
5'-most EST	jC-atXLIB327417P1c01b1
Method	BLASTX
NCBI GI	g3540206
BLAST score	924
E value	1.0e-109
Match length	198
% identity	93
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	129380
Contig ID	33111_1.R1010
5'-most EST	g496807
Method	BLASTX
NCBI GI	g4309727
BLAST score	119
E value	7.0e-38
Match length	118
% identity	80
NCBI Description	(AC006439) putative mitochondrial 60S ribosomal protein L6 [Arabidopsis thaliana]

Seq. No. 129381

Contig ID	33114_1.R1010
5'-most EST	LIB3176-058-P1-K1-G1

Seq. No.	129382
Contig ID	33119_1.R1010
5'-most EST	jC-atXP22C114P10T7051a1
Method	BLASTX
NCBI GI	g4322346
BLAST score	207
E value	5.0e-16
Match length	81
% identity	42
NCBI Description	(AF081825) sodium-dependent high-affinity dicarboxylate transporter [Rattus norvegicus]

Seq. No.	129383
Contig ID	33125_1.R1010
5'-most EST	jC-alX25082Q1E1E10b1
Method	BLASTX
NCBI GI	g2289001
BLAST score	662
E value	1.0e-69
Match length	135
% identity	95
NCBI Description	(AC002335) small nuclear ribonucleoprotein isolog [Arabidopsis thaliana]

Seq. No.	129384
Contig ID	33137_1.R1010
5'-most EST	jC-atXP108C179I20T7030d1
Method	BLASTX
NCBI GI	g3980400
BLAST score	250
E value	3.0e-68
Match length	160
% identity	84
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	129385
Contig ID	33137_2.R1010
5'-most EST	jC-atXLIB327420P4g11b1
Method	BLASTX
NCBI GI	g3980400
BLAST score	802
E value	1.0e-102
Match length	198
% identity	97
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	129386
Contig ID	33138_1.R1010
5'-most EST	jC-atXP70C221E14T7068a1
Method	BLASTN
NCBI GI	g2564046
BLAST score	330

E value	0.0e+00
Match length	439
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	129387
Contig ID	33140_1.R1010
5'-most EST	jC-atXLIB327417P3c11b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	5.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129388
Contig ID	33153_1.R1010
5'-most EST	jC-atXLIB327417P1d09b1
Method	BLASTX
NCBI GI	g3935185
BLAST score	1008
E value	1.0e-110
Match length	214
% identity	92
NCBI Description	(AC004557) F17L21.28 [Arabidopsis thaliana]

Seq. No.	129389
Contig ID	33154_1.R1010
5'-most EST	jC-atXLIB327417P2d09b1
Method	BLASTN
NCBI GI	g2583106
BLAST score	552
E value	0.0e+00
Match length	848
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129390
Contig ID	33157_1.R1010
5'-most EST	jC-atXLIB327417P3c05b1
Method	BLASTX
NCBI GI	g2832625
BLAST score	407
E value	1.0e-39
Match length	74
% identity	100
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	129391
Contig ID	33157_2.R1010
5'-most EST	LIB3177-085-P1-K1-A2
Method	BLASTX
NCBI GI	g2832625
BLAST score	189

E value 4.0e-14
Match length 130
% identity 72
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 129392
Contig ID 33162_1.R1010
5'-most EST jC-alX25082Q1E1H12b1
Method BLASTX
NCBI GI g2808439
BLAST score 394
E value 3.0e-38
Match length 118
% identity 65
NCBI Description (X79694) bg5 [Arabidopsis thaliana]

Seq. No. 129393
Contig ID 33163_1.R1010
5'-most EST jC-atXLIB327417P1d06b1
Method BLASTX
NCBI GI g3168840
BLAST score 296
E value 1.0e-26
Match length 67
% identity 81
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 129394
Contig ID 33163_2.R1010
5'-most EST LIB3234-090-P1-K1-B2
Method BLASTX
NCBI GI g3168840
BLAST score 99
E value 1.0e-03
Match length 58
% identity 81
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 129395
Contig ID 33172_1.R1010
5'-most EST LIB25-083-Q1-E1-A2

Seq. No. 129396
Contig ID 33178_1.R1010
5'-most EST LIB25-083-Q1-E1-A9
Method BLASTX
NCBI GI g2105430
BLAST score 202
E value 1.0e-15
Match length 61
% identity 66
NCBI Description (U97079) U5-116kD [Mus musculus]

Seq. No. 129397
Contig ID 33184_1.R1010
5'-most EST jC-atXLIB327417P3b02b1

Seq. No.	129398
Contig ID	33187_1.R1010
5'-most EST	jC-atXLIB327417P2b11b1

Seq. No.	129399
Contig ID	33196_1.R1010
5'-most EST	jC-atXLIB327417P4b08b1
Method	BLASTN
NCBI GI	g3600045
BLAST score	201
E value	1.0e-109
Match length	329
% identity	100
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	129400
Contig ID	33206_1.R1010
5'-most EST	jC-atXLIB327417P2c05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129401
Contig ID	33209_1.R1010
5'-most EST	jC-atXLIB327417P1c06b1
Method	BLASTX
NCBI GI	g3287695
BLAST score	312
E value	3.0e-47
Match length	195
% identity	51
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	129402
Contig ID	33213_1.R1010
5'-most EST	jC-atXLIB327417P4c03b1
Method	BLASTX
NCBI GI	g3128203
BLAST score	762
E value	5.0e-81
Match length	170
% identity	88
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	129403
Contig ID	33213_2.R1010
5'-most EST	LIB35-034-Q1-E1-H5
Method	BLASTX
NCBI GI	g3128203
BLAST score	242

E value	3.0e-34
Match length	104
% identity	76
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	129404
Contig ID	33219_2.R1010
5'-most EST	LIB3177-020-P1-K2-B4
Method	BLASTX
NCBI GI	g3924615
BLAST score	269
E value	1.0e-23
Match length	149
% identity	36
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129405
Contig ID	33225_1.R1010
5'-most EST	jC-atXLIB327417P4c12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129406
Contig ID	33228_1.R1010
5'-most EST	jC-atXLIB327417P3c09b1
Method	BLASTN
NCBI GI	g4732167
BLAST score	215
E value	1.0e-117
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana BAC F28D6

Seq. No.	129407
Contig ID	33234_1.R1010
5'-most EST	jC-atXLIB327417P2d08b1
Method	BLASTN
NCBI GI	g1245938
BLAST score	23
E value	1.4e-02
Match length	35
% identity	61
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	129408
Contig ID	33234_2.R1010
5'-most EST	LIB3234-008-P1-K1-G9

Seq. No.	129409
Contig ID	33241_1.R1010

5'-most EST	LIB25-088-Q1-E1-F2
Method	BLASTX
NCBI GI	g3831468
BLAST score	700
E value	1.0e-128
Match length	286
% identity	81
NCBI Description	(AC005700) putative phosphocholine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	129410
Contig ID	33242_1.R1010
5'-most EST	jC-atXLIB327417P4d05b1
Method	BLASTX
NCBI GI	g4699942
BLAST score	173
E value	3.0e-12
Match length	37
% identity	92
NCBI Description	(AC007166) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	129411
Contig ID	33245_1.R1010
5'-most EST	jC-atXLIB327417P3d08b1
Method	BLASTX
NCBI GI	g480725
BLAST score	617
E value	5.0e-64
Match length	168
% identity	71
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	129412
Contig ID	33248_1.R1010
5'-most EST	ARABL1-026-Q1-B1-G12
Method	BLASTX
NCBI GI	g4586054
BLAST score	358
E value	4.0e-34
Match length	89
% identity	82
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	129413
Contig ID	33253_1.R1010
5'-most EST	jC-atXP100CE3F2T7b1
Method	BLASTN
NCBI GI	g4406776
BLAST score	386
E value	0.0e+00
Match length	573
% identity	100

NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129414
Contig ID	33253_2.R1010
5'-most EST	jC-atXLIB327431P1e03a1
Method	BLASTN
NCBI GI	g4406776
BLAST score	108
E value	1.0e-53
Match length	303
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129415
Contig ID	33277_1.R1010
5'-most EST	jC-atXLIB327417P1c04b1
Method	BLASTX
NCBI GI	g4678232
BLAST score	374
E value	1.0e-35
Match length	226
% identity	39
NCBI Description	(AC007265) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129416
Contig ID	33285_1.R1010
5'-most EST	LIB25-084-Q1-E1-E1
Method	BLASTX
NCBI GI	g3135268
BLAST score	715
E value	9.0e-76
Match length	157
% identity	35
NCBI Description	(AC003058) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	129417
Contig ID	33289_1.R1010
5'-most EST	jC-atXP86CG10A12T7d2
Method	BLASTN
NCBI GI	g1070003
BLAST score	40
E value	9.0e-13
Match length	40
% identity	100
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	129418
Contig ID	33289_2.R1010
5'-most EST	jC-atXLIB327417P1c12b1

Seq. No.	129419
Contig ID	33294_1.R1010

5'-most EST	jC-atXLIB327417P2c10b1
Seq. No.	129420
Contig ID	33298_1.R1010
5'-most EST	jC-atXLIB327417P4c08b1
Method	BLASTN
NCBI GI	g4455321
BLAST score	281
E value	1.0e-157
Match length	454
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)
Seq. No.	129421
Contig ID	33306_1.R1010
5'-most EST	jC-atXLIB327422P2g07a2
Method	BLASTX
NCBI GI	g2288887
BLAST score	473
E value	3.0e-47
Match length	147
% identity	68
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
Seq. No.	129422
Contig ID	33316_1.R1010
5'-most EST	LIB25-104-Q1-E1-E5
Seq. No.	129423
Contig ID	33318_1.R1010
5'-most EST	jC-atXLIB327426P2h11b1
Method	BLASTN
NCBI GI	g4165340
BLAST score	275
E value	1.0e-153
Match length	513
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	129424
Contig ID	33318_2.R1010
5'-most EST	jC-atXP123C117D3T7012d1
Method	BLASTX
NCBI GI	g2950478
BLAST score	170
E value	1.0e-11
Match length	144
% identity	27
NCBI Description	(AL022070) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	129425

Contig ID	33322_1.R1010
5'-most EST	jC-atXLIB327417P3d01b1
Method	BLASTN
NCBI GI	g4757407
BLAST score	403
E value	0.0e+00
Match length	447
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	129426
Contig ID	33323_1.R1010
5'-most EST	jC-atXLIB327417P4c02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129427
Contig ID	33326_1.R1010
5'-most EST	g458740

Seq. No.	129428
Contig ID	33329_1.R1010
5'-most EST	jC-atXLIB327417P3a10b1
Method	BLASTN
NCBI GI	g2749918
BLAST score	311
E value	1.0e-174
Match length	501
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129429
Contig ID	33330_1.R1010
5'-most EST	jC-atXLIB327417P4a12b1
Method	BLASTN
NCBI GI	g4580744
BLAST score	156
E value	3.0e-82
Match length	443
% identity	100
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	129430
Contig ID	33336_1.R1010
5'-most EST	jC-alX25085Q1E1A06b1
Method	BLASTN
NCBI GI	g1480029
BLAST score	94

E value	3.0e-45
Match length	282
% identity	88
NCBI Description	Brassica rapa mRNA, polyA_site

Seq. No.	129431
Contig ID	33349_1.R1010
5'-most EST	jC-atXLIB327417P4b06b1
Method	BLASTX
NCBI GI	g2435522
BLAST score	1029
E value	1.0e-112
Match length	353
% identity	63
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	129432
Contig ID	33349_3.R1010
5'-most EST	LIB3176-014-P1-K1-G5
Method	BLASTX
NCBI GI	g2435522
BLAST score	161
E value	7.0e-46
Match length	170
% identity	55
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	129433
Contig ID	33357_1.R1010
5'-most EST	jC-atXLIB327417P3b04b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	218
E value	1.0e-119
Match length	740
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	129434
Contig ID	33362_1.R1010
5'-most EST	jC-atXLIB327417P2c04b1

Seq. No.	129435
Contig ID	33365_1.R1010
5'-most EST	jC-atXLIB327417P1c03b1
Method	BLASTN
NCBI GI	g3549651
BLAST score	120
E value	2.0e-60
Match length	756
% identity	90
NCBI Description	Arabidopsis thaliana MAP3K epsilon gene

Seq. No. 129436

Contig ID	33375_1.R1010
5'-most EST	jC-atXLIB327417P2c09b1
Method	BLASTX
NCBI GI	g3894393
BLAST score	401
E value	1.0e-38
Match length	185
% identity	5
NCBI Description	(AF053998) Hcr2-5D [Lycopersicon esculentum]

Seq. No.	129437
Contig ID	33376_1.R1010
5'-most EST	LIB3168-086-P1-K1-E5
Method	BLASTX
NCBI GI	g3540185
BLAST score	248
E value	5.0e-21
Match length	78
% identity	56
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	129438
Contig ID	33379_1.R1010
5'-most EST	LIB25-085-Q1-E1-F10
Method	BLASTN
NCBI GI	g3128166
BLAST score	278
E value	1.0e-155
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129439
Contig ID	33385_1.R1010
5'-most EST	LIB3177-072-P1-K1-D3
Method	BLASTX
NCBI GI	g4587526
BLAST score	242
E value	2.0e-20
Match length	130
% identity	38
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come from this gene

Seq. No.	129440
Contig ID	33386_1.R1010
5'-most EST	jC-atXLIB327417P3c04b1
Method	BLASTN
NCBI GI	g4589435
BLAST score	193
E value	1.0e-104
Match length	327
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	129441
Contig ID	33401_1.R1010
5'-most EST	LIB25-085-Q1-E1-H2
Method	BLASTN
NCBI GI	g1707006
BLAST score	370
E value	0.0e+00
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129442
Contig ID	33414_1.R1010
5'-most EST	jC-atXLIB327417P2e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	9.0e-29
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129443
Contig ID	33415_1.R1010
5'-most EST	jC-atXLIB327417P1e06b1
Method	BLASTX
NCBI GI	g2102691
BLAST score	245
E value	3.0e-20
Match length	143
% identity	36
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	129444
Contig ID	33416_1.R1010
5'-most EST	jC-atXLIB327417P1e07b1
Method	BLASTX
NCBI GI	g2289011
BLAST score	710
E value	1.0e-107
Match length	236
% identity	42
NCBI Description	(AC002335) MYB transcription factor isolog [Arabidopsis thaliana]

Seq. No.	129445
Contig ID	33420_1.R1010
5'-most EST	jC-atXLIB327417P4e06b1
Method	BLASTN
NCBI GI	g3046856
BLAST score	388
E value	0.0e+00

Match length	601
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	129446
Contig ID	33421_1.R1010
5'-most EST	jC-atXLIB327417P4e07b1
Method	BLASTX
NCBI GI	g4006920
BLAST score	449
E value	4.0e-80
Match length	160
% identity	94
NCBI Description	(Z99708) actin interacting protein [Arabidopsis thaliana]

Seq. No.	129447
Contig ID	33426_1.R1010
5'-most EST	jC-atXLIB327417P2f03b1

Seq. No.	129448
Contig ID	33430_1.R1010
5'-most EST	LIB25-086-Q1-E1-C6

Seq. No.	129449
Contig ID	33444_1.R1010
5'-most EST	jC-atXLIB327417P1g01a1
Method	BLASTX
NCBI GI	g3063459
BLAST score	433
E value	1.0e-42
Match length	85
% identity	95
NCBI Description	(AC003981) F22O13.21 [Arabidopsis thaliana]

Seq. No.	129450
Contig ID	33449_1.R1010
5'-most EST	jC-atXLIB327417P1g12b1
Method	BLASTX
NCBI GI	g2979559
BLAST score	313
E value	3.0e-28
Match length	66
% identity	88
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	129451
Contig ID	33452_1.R1010
5'-most EST	jC-atXLIB327417P1g10b1
Method	BLASTX
NCBI GI	g4417304
BLAST score	194
E value	5.0e-20
Match length	94
% identity	60
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	129452
Contig ID	33455_1.R1010
5'-most EST	jC-atXLIB327417P3f11b1
Method	BLASTX
NCBI GI	g4337178
BLAST score	699
E value	2.0e-80
Match length	180
% identity	89
NCBI Description	(AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No.	129453
Contig ID	33463_1.R1010
5'-most EST	jC-atXLIB327417P4g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	8.0e-21
Match length	69
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129454
Contig ID	33468_1.R1010
5'-most EST	jC-atXLIB327417P3g06b1
Method	BLASTN
NCBI GI	g4376087
BLAST score	262
E value	1.0e-145
Match length	266
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	129455
Contig ID	33481_1.R1010
5'-most EST	jC-atXLIB327417P2e08b1
Method	BLASTX
NCBI GI	g3785983
BLAST score	314
E value	9.0e-50
Match length	146
% identity	73
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129456
Contig ID	33488_1.R1010
5'-most EST	jC-atXLIB327417P3e05b1
Method	BLASTX
NCBI GI	g2443329
BLAST score	318
E value	5.0e-57
Match length	231

% identity	64
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	129457
Contig ID	33490_1.R1010
5'-most EST	jC-atXLIB327427P1d04b1
Method	BLASTN
NCBI GI	g2584827
BLAST score	489
E value	0.0e+00
Match length	638
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129458
Contig ID	33493_1.R1010
5'-most EST	jC-atXLIB327423P1e08a1

Seq. No.	129459
Contig ID	33494_1.R1010
5'-most EST	LIB3176-024-P1-K1-C5
Method	BLASTX
NCBI GI	g2501457
BLAST score	312
E value	1.0e-28
Match length	127
% identity	46
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1) >gi_1302630 (U41636) DUB-1 [Mus musculus]

Seq. No.	129460
Contig ID	33504_1.R1010
5'-most EST	jC-atXLIB327417P3f01b1
Method	BLASTX
NCBI GI	g4322327
BLAST score	159
E value	1.0e-10
Match length	95
% identity	37
NCBI Description	(AF080545) peptide transporter [Nepenthes alata]

Seq. No.	129461
Contig ID	33505_1.R1010
5'-most EST	jC-atXLIB327414P3e08a1
Method	BLASTX
NCBI GI	g3738331
BLAST score	242
E value	3.0e-20
Match length	61
% identity	70
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	129462
Contig ID	33506_1.R1010

5'-most EST	jC-atXLIB327417P2f11a1
Seq. No.	129463
Contig ID	33515_1.R1010
5'-most EST	jC-atXLIB327417P3f12b1
Method	BLASTN
NCBI GI	g2760165
BLAST score	451
E value	0.0e+00
Match length	595
% identity	73
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.	129464
Contig ID	33537_1.R1010
5'-most EST	jC-atXLIB327417P2e01b1
Method	BLASTN
NCBI GI	g4580744
BLAST score	291
E value	1.0e-163
Match length	340
% identity	99
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence
Seq. No.	129465
Contig ID	33543_1.R1010
5'-most EST	jC-atXLIB327417P3d10b1
Method	BLASTX
NCBI GI	g1279640
BLAST score	595
E value	2.0e-61
Match length	161
% identity	69
NCBI Description	(X92204) NAM [Petunia x hybrida]
Seq. No.	129466
Contig ID	33545_1.R1010
5'-most EST	jC-atXP1C64D12T7s2
Method	BLASTN
NCBI GI	g3687221
BLAST score	180
E value	2.0e-96
Match length	484
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	129467
Contig ID	33546_1.R1010
5'-most EST	jC-atXLIB327430P4a09b1
Method	BLASTX
NCBI GI	g4581141
BLAST score	431
E value	4.0e-42
Match length	138

% identity	73
NCBI Description	(AC006919) unknown protein [Arabidopsis thaliana]

Seq. No.	129468
Contig ID	33548_1.R1010
5'-most EST	jC-atXP79C240A9T7b1
Method	BLASTN
NCBI GI	g3336893
BLAST score	38
E value	2.0e-11
Match length	62
% identity	90
NCBI Description	Lycopersicon peruvianum mRNA for Hsp20.2 protein

Seq. No.	129469
Contig ID	33551_1.R1010
5'-most EST	jC-atXLIB327417P4e02b1
Method	BLASTN
NCBI GI	g1871173
BLAST score	227
E value	1.0e-124
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	129470
Contig ID	33561_1.R1010
5'-most EST	jC-atXLIB327417P4e09b1
Method	BLASTX
NCBI GI	g4006866
BLAST score	53
E value	5.0e-75
Match length	153
% identity	84
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	129471
Contig ID	33566_1.R1010
5'-most EST	LIB25-088-Q1-E1-D10
Method	BLASTN
NCBI GI	g3449332
BLAST score	115
E value	8.0e-58
Match length	331
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSF19, complete sequence [Arabidopsis thaliana]

Seq. No.	129472
Contig ID	33567_1.R1010
5'-most EST	jC-atXLIB327417P1f08b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	254
E value	1.0e-140
Match length	602

% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	129473
Contig ID	33569_1.R1010
5'-most EST	jC-atXLIB327417P1f09b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	197
E value	1.0e-106
Match length	610
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129474
Contig ID	33574_1.R1010
5'-most EST	jC-atXLIB327417P2f06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	8.0e-22
Match length	78
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129475
Contig ID	33575_1.R1010
5'-most EST	jC-alX25089Q1E1D09b1
Method	BLASTX
NCBI GI	g3367520
BLAST score	295
E value	1.0e-26
Match length	104
% identity	58
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	129476
Contig ID	33583_1.R1010
5'-most EST	jC-atXLIB327417P3f03b1
Method	BLASTX
NCBI GI	g3790575
BLAST score	190
E value	3.0e-14
Match length	80
% identity	51
NCBI Description	(AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]

Seq. No.	129477
Contig ID	33584_1.R1010
5'-most EST	jC-atXLIB327417P2f04b1
Method	BLASTN

NCBI GI	g4469002
BLAST score	311
E value	1.0e-174
Match length	533
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	129478
Contig ID	33605_1.R1010
5'-most EST	jC-atXLIB327417P1h02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	1.0e-20
Match length	72
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129479
Contig ID	33612_1.R1010
5'-most EST	jC-atXLIB327417P1e01b1
Method	BLASTN
NCBI GI	g3789706
BLAST score	242
E value	1.0e-133
Match length	607
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129480
Contig ID	33612_2.R1010
5'-most EST	jC-atXLIB327417P1e01a1
Method	BLASTN
NCBI GI	g3789706
BLAST score	114
E value	6.0e-57
Match length	237
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129481
Contig ID	33612_3.R1010
5'-most EST	jC-atXP73CF2F7T7d2
Method	BLASTX
NCBI GI	g3850581
BLAST score	1209
E value	1.0e-133
Match length	237
% identity	99
NCBI Description	(AC005278) EST gb_N96383 comes from this gene. [Arabidopsis thaliana]

Seq. No.	129482

Contig ID	33621_1.R1010
5'-most EST	jC-atXLIB327417P2e10b1
Method	BLASTN
NCBI GI	g4713943
BLAST score	416
E value	0.0e+00
Match length	740
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	129483
Contig ID	33624_1.R1010
5'-most EST	jC-atXLIB327417P3e01b1
Method	BLASTN
NCBI GI	g2191181
BLAST score	254
E value	1.0e-140
Match length	1112
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM021B04

Seq. No.	129484
Contig ID	33625_1.R1010
5'-most EST	jC-atXLIB327417P1e04b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	477
E value	1.0e-47
Match length	194
% identity	55
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	129485
Contig ID	33629_1.R1010
5'-most EST	jC-atXP118C155L16T7072d2
Method	BLASTX
NCBI GI	g2244909
BLAST score	1080
E value	1.0e-118
Match length	211
% identity	100
NCBI Description	(Z97339) pyruvate,orthophosphate dikinase [Arabidopsis thaliana]

Seq. No.	129486
Contig ID	33629_2.R1010
5'-most EST	LIB25-089-Q1-E1-C11
Method	BLASTX
NCBI GI	g2244909
BLAST score	655
E value	1.0e-68
Match length	225
% identity	52
NCBI Description	(Z97339) pyruvate,orthophosphate dikinase [Arabidopsis thaliana]

Seq. No.	129487
Contig ID	33630_1.R1010
5'-most EST	jC-atXP83CG3G4T7079d1
Method	BLASTX
NCBI GI	g2244792
BLAST score	289
E value	9.0e-26
Match length	61
% identity	79
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	129488
Contig ID	33630_2.R1010
5'-most EST	LIB3176-084-P1-K1-C9
Method	BLASTX
NCBI GI	g2244792
BLAST score	240
E value	4.0e-20
Match length	106
% identity	52
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	129489
Contig ID	33631_1.R1010
5'-most EST	jC-atXLIB327417P3e12b1
Method	BLASTX
NCBI GI	g4587574
BLAST score	310
E value	5.0e-28
Match length	134
% identity	45
NCBI Description	(AC006550) Contains PF_00010 helix-loop-helix DNA-binding domain. ESTs gb_T45640 and gb_T22783 come from this gene. [Arabidopsis thaliana]

Seq. No.	129490
Contig ID	33632_1.R1010
5'-most EST	jC-atXLIB327417P3e07b1
Method	BLASTX
NCBI GI	g4063751
BLAST score	221
E value	1.0e-49
Match length	284
% identity	43
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	129491
Contig ID	33635_2.R1010
5'-most EST	LIB25-089-Q1-E1-D10
Method	BLASTN
NCBI GI	g4689466
BLAST score	276
E value	1.0e-154
Match length	460

% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	129492
Contig ID	33646_1.R1010
5'-most EST	jC-atXLIB327417P4f06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129493
Contig ID	33647_1.R1010
5'-most EST	jC-atXLIB327417P4f08b1
Method	BLASTN
NCBI GI	g4589415
BLAST score	193
E value	1.0e-104
Match length	344
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	129494
Contig ID	33649_1.R1010
5'-most EST	jC-atXLIB327417P4h04b1
Method	BLASTX
NCBI GI	g3861153
BLAST score	231
E value	7.0e-19
Match length	57
% identity	72
NCBI Description	(AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT) [Rickettsia prowazekii]

Seq. No.	129495
Contig ID	33660_1.R1010
5'-most EST	jC-atXP22C116L2T7061a1
Method	BLASTX
NCBI GI	g4454051
BLAST score	231
E value	9.0e-19
Match length	110
% identity	45
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	129496
Contig ID	33660_2.R1010
5'-most EST	jC-atXP22C116L2T7d2
Method	BLASTX
NCBI GI	g4454051

BLAST score	384
E value	9.0e-37
Match length	181
% identity	45
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	129497
Contig ID	33660_3.R1010
5'-most EST	jC-alX24071Q1E1H08a1

Seq. No.	129498
Contig ID	33661_1.R1010
5'-most EST	jC-atXLIB327417P4g05b1

Seq. No.	129499
Contig ID	33673_1.R1010
5'-most EST	g905902
Method	BLASTN
NCBI GI	g4757392
BLAST score	803
E value	0.0e+00
Match length	998
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	129500
Contig ID	33679_1.R1010
5'-most EST	jC-atXLIB327418P1a02b1
Method	BLASTN
NCBI GI	g4432829
BLAST score	373
E value	0.0e+00
Match length	448
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129501
Contig ID	33680_1.R1010
5'-most EST	jC-atXLIB327417P4h05b1
Method	BLASTX
NCBI GI	g2911075
BLAST score	256
E value	6.0e-22
Match length	87
% identity	63
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	129502
Contig ID	33691_1.R1010
5'-most EST	g2062959
Method	BLASTN
NCBI GI	g3399678
BLAST score	363
E value	0.0e+00

Match length	475
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129503
Contig ID	33691_2.R1010
5'-most EST	jC-atXLIB327418P2a03b2
Method	BLASTN
NCBI GI	g3399678
BLAST score	108
E value	1.0e-53
Match length	418
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129504
Contig ID	33692_1.R1010
5'-most EST	g2764346
Method	BLASTX
NCBI GI	g3193330
BLAST score	507
E value	7.0e-57
Match length	125
% identity	96
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	129505
Contig ID	33695_1.R1010
5'-most EST	LIB25-090-Q1-E1-B7
Method	BLASTN
NCBI GI	g3128141
BLAST score	528
E value	0.0e+00
Match length	599
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	129506
Contig ID	33700_1.R1010
5'-most EST	jC-atXLIB327418P2a11b2
Method	BLASTX
NCBI GI	g3702351
BLAST score	126
E value	1.0e-60
Match length	129
% identity	92
NCBI Description	(AC005397) putative desiccation protectant protein [Arabidopsis thaliana]

Seq. No.	129507
Contig ID	33714_1.R1010
5'-most EST	jC-atXLIB327418P4a11b1
Method	BLASTN

NCBI GI	g3046854
BLAST score	199
E value	1.0e-107
Match length	405
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	129508
Contig ID	33714_2.R1010
5'-most EST	jC-atXLIB327418P4a11a1
Method	BLASTN
NCBI GI	g3046854
BLAST score	257
E value	1.0e-142
Match length	535
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	129509
Contig ID	33719_1.R1010
5'-most EST	LIB25-090-Q1-E1-E10
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129510
Contig ID	33724_1.R1010
5'-most EST	jC-atXLIB327418P1b09a1
Method	BLASTN
NCBI GI	g4753195
BLAST score	68
E value	1.0e-29
Match length	134
% identity	98
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	129511
Contig ID	33727_1.R1010
5'-most EST	jC-atXLIB327418P1b07b1
Method	BLASTN
NCBI GI	g3985949
BLAST score	203
E value	1.0e-110
Match length	351
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	129512
Contig ID	33727_2.R1010

5'-most EST	g2763051
Method	BLASTN
NCBI GI	g3985949
BLAST score	265
E value	1.0e-147
Match length	363
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	129513
Contig ID	33733_1.R1010
5'-most EST	ARABL1-07-Q1-B1-E3

Seq. No.	129514
Contig ID	33734_1.R1010
5'-most EST	jC-atXLIB327418P4e06b1
Method	BLASTN
NCBI GI	g2264303
BLAST score	156
E value	3.0e-82
Match length	204
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	129515
Contig ID	33741_1.R1010
5'-most EST	jC-atXLIB327432P2f09a2
Method	BLASTN
NCBI GI	g3004543
BLAST score	225
E value	1.0e-123
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129516
Contig ID	33747_1.R1010
5'-most EST	jC-atXLIB327418P3b09b1
Method	BLASTN
NCBI GI	g2351061
BLAST score	197
E value	1.0e-106
Match length	525
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	129517
Contig ID	33750_1.R1010
5'-most EST	LIB25-090-Q1-E1-H1

Seq. No.	129518
Contig ID	33756_1.R1010
5'-most EST	jC-atXLIB327418P2c12b2

Method	BLASTX
NCBI GI	g2316022
BLAST score	616
E value	3.0e-64
Match length	130
% identity	91
NCBI Description	(U96399) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	129519
Contig ID	33757_1.R1010
5'-most EST	jC-atXP39C161C3T7d1
Method	BLASTN
NCBI GI	g4468801
BLAST score	401
E value	0.0e+00
Match length	772
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	129520
Contig ID	33759_1.R1010
5'-most EST	jC-atXLIB327418P1c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	5.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129521
Contig ID	33762_1.R1010
5'-most EST	jC-alX25091Q1E1A01b1

Seq. No.	129522
Contig ID	33766_1.R1010
5'-most EST	LIB25-091-Q1-E1-A3
Method	BLASTX
NCBI GI	g3941720
BLAST score	202
E value	1.0e-15
Match length	125
% identity	43
NCBI Description	(AF087021) tyrosyl-tRNA synthetase; tyrosine--tRNA ligase [Bos taurus]

Seq. No.	129523
Contig ID	33771_1.R1010
5'-most EST	jC-atXLIB327430P4a12b1
Method	BLASTN
NCBI GI	g4544381
BLAST score	464
E value	0.0e+00
Match length	495
% identity	100

NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	129524
Contig ID	33779_1.R1010
5'-most EST	jC-atXLIB327418P1a05b1
Method	BLASTN
NCBI GI	g4589950
BLAST score	187
E value	1.0e-100
Match length	427
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	129525
Contig ID	33785_1.R1010
5'-most EST	jC-atXLIB327418P2a10a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	282
E value	1.0e-157
Match length	282
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129526
Contig ID	33794_1.R1010
5'-most EST	jC-atXLIB327418P2a09b2
Method	BLASTN
NCBI GI	g3335356
BLAST score	272
E value	1.0e-151
Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129527
Contig ID	33803_1.R1010
5'-most EST	jC-atXLIB327418P3a07b1
Method	BLASTN
NCBI GI	g3059018
BLAST score	139
E value	8.0e-72
Match length	280
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	129528
Contig ID	33803_2.R1010
5'-most EST	jC-atXP117C143B11T7a1
Method	BLASTX
NCBI GI	g2982445
BLAST score	486

E value	1.0e-55
Match length	141
% identity	89
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	129529
Contig ID	33804_1.R1010
5'-most EST	jC-atXLIB327418P4a08b1
Method	BLASTX
NCBI GI	g4584525
BLAST score	408
E value	2.0e-39
Match length	178
% identity	59
NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	129530
Contig ID	33805_1.R1010
5'-most EST	jC-atXLIB327418P1b08b1
Method	BLASTN
NCBI GI	g4455321
BLAST score	417
E value	0.0e+00
Match length	532
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	129531
Contig ID	33811_1.R1010
5'-most EST	LIB25-091-Q1-E1-E5

Seq. No.	129532
Contig ID	33812_1.R1010
5'-most EST	jC-atXLIB327418P1b06b1
Method	BLASTX
NCBI GI	g3298534
BLAST score	586
E value	1.0e-60
Match length	135
% identity	85
NCBI Description	(AC004681) Myb-related protein [Arabidopsis thaliana] >gi_3831450 (AC005700) myb-related protein [Arabidopsis thaliana]

Seq. No.	129533
Contig ID	33815_1.R1010
5'-most EST	jC-alXLIB327436P1g04b1
Method	BLASTX
NCBI GI	g2342724
BLAST score	558
E value	2.0e-57
Match length	110
% identity	100
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	129534
Contig ID	33820_1.R1010
5'-most EST	LIB25-091-Q1-E1-F2
Method	BLASTX
NCBI GI	g4406810
BLAST score	147
E value	7.0e-09
Match length	37
% identity	78
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	129535
Contig ID	33820_3.R1010
5'-most EST	g2446043
Method	BLASTX
NCBI GI	g2961378
BLAST score	117
E value	2.0e-43
Match length	141
% identity	77
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	129536
Contig ID	33823_1.R1010
5'-most EST	LIB25-091-Q1-E1-F5
Method	BLASTN
NCBI GI	g3449322
BLAST score	356
E value	0.0e+00
Match length	468
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	129537
Contig ID	33825_1.R1010
5'-most EST	jC-atXP3C81F8T7036a1
Method	BLASTX
NCBI GI	g2384675
BLAST score	784
E value	1.0e-83
Match length	176
% identity	89
NCBI Description	(AF012659) putative potassium transporter AtKT4p [Arabidopsis thaliana]

Seq. No.	129538
Contig ID	33825_2.R1010
5'-most EST	jC-atXP94CH4F9T7b1
Method	BLASTX
NCBI GI	g2384675
BLAST score	501
E value	1.0e-50
Match length	111
% identity	87
NCBI Description	(AF012659) putative potassium transporter AtKT4p [Arabidopsis thaliana]

Seq. No.	129539
Contig ID	33832_1.R1010
5'-most EST	jC-atXLIB327418P1c01b1
Method	BLASTN
NCBI GI	g2828185
BLAST score	124
E value	6.0e-63
Match length	454
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	129540
Contig ID	33837_1.R1010
5'-most EST	jC-atXLIB327418P4b10b1

Seq. No.	129541
Contig ID	33842_1.R1010
5'-most EST	jC-atXLIB327418P2c11b2
Method	BLASTX
NCBI GI	g3075399
BLAST score	206
E value	3.0e-16
Match length	67
% identity	61
NCBI Description	(AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No.	129542
Contig ID	33847_1.R1010
5'-most EST	jC-atXLIB327418P2c08b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	39
E value	2.0e-12
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	129543
Contig ID	33851_1.R1010
5'-most EST	jC-alX25092Q1E1A11b1
Method	BLASTX
NCBI GI	g1346760
BLAST score	332
E value	5.0e-31
Match length	66
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 6 >gi_829255_emb_CAA86339_ (Z46253) protein phosphatase type 1 [Arabidopsis thaliana] >gi_3153203 (U80921) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	129544
Contig ID	33863_1.R1010

5'-most EST	jC-atXLIB327417P4h11b1
Method	BLASTN
NCBI GI	g4678371
BLAST score	231
E value	1.0e-127
Match length	528
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	129545
Contig ID	33867_1.R1010
5'-most EST	jC-alX25092Q1E1B09b1
Method	BLASTN
NCBI GI	g4586024
BLAST score	230
E value	1.0e-126
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13C7 genomic sequence, complete sequence

Seq. No.	129546
Contig ID	33869_1.R1010
5'-most EST	jC-atXLIB327418P2a07b2
Method	BLASTN
NCBI GI	g2864607
BLAST score	281
E value	1.0e-157
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	129547
Contig ID	33872_1.R1010
5'-most EST	jC-atXLIB327418P2a08b2
Method	BLASTX
NCBI GI	g3785990
BLAST score	582
E value	3.0e-60
Match length	133
% identity	89
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129548
Contig ID	33874_1.R1010
5'-most EST	jC-atXLIB327418P2a05b2
Method	BLASTN
NCBI GI	g3132469
BLAST score	392
E value	0.0e+00
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129549
Contig ID	33875_1.R1010
5'-most EST	jC-atXLIB327418P1a06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	9.0e-22
Match length	63
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129550
Contig ID	33887_1.R1010
5'-most EST	jC-atXLIB327430P1b02b1
Method	BLASTX
NCBI GI	g3250679
BLAST score	282
E value	6.0e-25
Match length	51
% identity	100
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	129551
Contig ID	33892_1.R1010
5'-most EST	LIB25-092-Q1-E1-E10
Method	BLASTX
NCBI GI	g2569940
BLAST score	425
E value	5.0e-42
Match length	111
% identity	70
NCBI Description	(Y15194) GRS protein [Arabidopsis thaliana]

Seq. No.	129552
Contig ID	33899_1.R1010
5'-most EST	jC-atXLIB327418P3a12b1

Seq. No.	129553
Contig ID	33902_1.R1010
5'-most EST	g2764031

Seq. No.	129554
Contig ID	33909_1.R1010
5'-most EST	jC-atXLIB327418P2b10b2
Method	BLASTN
NCBI GI	g3668073
BLAST score	112
E value	6.0e-56
Match length	412
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129555

Contig ID	33934_1.R1010
5'-most EST	jC-atXLIB327418P1c06b1
Method	BLASTN
NCBI GI	g4680765
BLAST score	155
E value	1.0e-81
Match length	366
% identity	95
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	129556
Contig ID	33937_1.R1010
5'-most EST	jC-atXLIB327409P2h05a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	608
E value	0.0e+00
Match length	788
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	129557
Contig ID	33938_1.R1010
5'-most EST	jC-atXLIB327417P1h11b1
Method	BLASTN
NCBI GI	g4733957
BLAST score	675
E value	0.0e+00
Match length	698
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C18 genomic sequence, complete sequence

Seq. No.	129558
Contig ID	33939_1.R1010
5'-most EST	jC-atXLIB327417P2h11b1
Method	BLASTN
NCBI GI	g4220640
BLAST score	398
E value	0.0e+00
Match length	1126
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	129559
Contig ID	33944_1.R1010
5'-most EST	jC-alX25082Q1E1D04b1
Method	BLASTX
NCBI GI	g4835230
BLAST score	899
E value	1.0e-96
Match length	214
% identity	81
NCBI Description	(AL049862) putative LEA protein [Arabidopsis thaliana]

Seq. No.	129560
Contig ID	33952_1.R1010
5'-most EST	jC-atXLIB327438P1a11a1
Method	BLASTX
NCBI GI	g2791278
BLAST score	447
E value	4.0e-44
Match length	229
% identity	42
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No.	129561
Contig ID	33956_1.R1010
5'-most EST	jC-atXLIB327418P1a09b1
Method	BLASTX
NCBI GI	g2924773
BLAST score	600
E value	7.0e-65
Match length	144
% identity	93
NCBI Description	(AC002334) putative mitochondrial chaperonin HSP60 precursor [Arabidopsis thaliana]

Seq. No.	129562
Contig ID	33965_1.R1010
5'-most EST	LIB25-093-Q1-E1-D5
Method	BLASTX
NCBI GI	g4581139
BLAST score	343
E value	7.0e-33
Match length	64
% identity	98
NCBI Description	(AC006919) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	129563
Contig ID	33973_1.R1010
5'-most EST	jC-atXLIB327418P1b04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	64
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129564
Contig ID	33980_1.R1010
5'-most EST	jC-atXLIB327418P2b12b2
Method	BLASTX
NCBI GI	g2829925
BLAST score	402
E value	4.0e-39
Match length	117
% identity	76
NCBI Description	(AC002291) Similar to dnaj-like protein, gp_Y11969_2230757

[Arabidopsis thaliana]

Seq. No.	129565
Contig ID	33981_1.R1010
5'-most EST	jC-atXLIB327421P2b10b1
Method	BLASTX
NCBI GI	g4587530
BLAST score	362
E value	2.0e-34
Match length	114
% identity	61
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	129566
Contig ID	33985_1.R1010
5'-most EST	jC-atXLIB327418P1b11b1
Method	BLASTX
NCBI GI	g2289002
BLAST score	710
E value	2.0e-87
Match length	229
% identity	75
NCBI Description	(AC002335) unknown protein [Arabidopsis thaliana]

Seq. No.	129567
Contig ID	33991_1.R1010
5'-most EST	jC-atXLIB327418P4b08b1
Method	BLASTN
NCBI GI	g4220641
BLAST score	388
E value	0.0e+00
Match length	517
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	129568
Contig ID	33998_1.R1010
5'-most EST	jC-atXLIB327418P2c04b2
Method	BLASTX
NCBI GI	g2980767
BLAST score	582
E value	3.0e-60
Match length	143
% identity	85
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	129569
Contig ID	34000_1.R1010
5'-most EST	jC-atXLIB327418P4c08b1
Method	BLASTX
NCBI GI	g3738302
BLAST score	163
E value	7.0e-11
Match length	42

% identity	69
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	129570
Contig ID	34006_1.R1010
5'-most EST	jC-atXLIB327418P3c12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	2.0e-23
Match length	66
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129571
Contig ID	34009_1.R1010
5'-most EST	jC-atXLIB327418P4c09b1

Seq. No.	129572
Contig ID	34013_1.R1010
5'-most EST	jC-atXLIB327418P1d08b1
Method	BLASTN
NCBI GI	g2696018
BLAST score	120
E value	2.0e-60
Match length	301
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	129573
Contig ID	34015_1.R1010
5'-most EST	jC-atXLIB327418P1d10b1
Method	BLASTX
NCBI GI	g731775
BLAST score	157
E value	4.0e-12
Match length	79
% identity	52
NCBI Description	PUTATIVE MITOCHONDRIAL CARRIER YIL006W >gi_626359_pir__S48451 probable membrane protein YIL006w - yeast (Saccharomyces cerevisiae) >gi_558398_emb_CAA86245_ (Z38113) orf, len: 373aa, CAI: 0.10, similar to S36081 INTERNAL MEMBRANE PROTEIN - YEAST [Saccharomyces cerevisiae]

Seq. No.	129574
Contig ID	34015_2.R1010
5'-most EST	LIB3234-094-P1-K1-F12

Seq. No.	129575
Contig ID	34019_1.R1010
5'-most EST	jC-atXLIB327418P2d07b2
Method	BLASTX

NCBI GI	g2623311
BLAST score	581
E value	7.0e-60
Match length	161
% identity	73
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402720 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	129576
Contig ID	34034_1.R1010
5'-most EST	jC-atXLIB327418P2e05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	4.0e-17
Match length	55
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129577
Contig ID	34035_1.R1010
5'-most EST	g510769
Method	BLASTX
NCBI GI	g1532171
BLAST score	4273
E value	0.0e+00
Match length	821
% identity	100
NCBI Description	(U63815) AT.I.24-9 gene product [Arabidopsis thaliana]

Seq. No.	129578
Contig ID	34037_1.R1010
5'-most EST	jC-atXLIB327418P2e07b2
Method	BLASTN
NCBI GI	g2618600
BLAST score	192
E value	1.0e-104
Match length	196
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	129579
Contig ID	34038_1.R1010
5'-most EST	jC-atXLIB327418P1e02b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No. 129580

Contig ID	34042_1.R1010
5'-most EST	LIB3176-027-P1-K1-B11
Method	BLASTX
NCBI GI	g2275201
BLAST score	204
E value	4.0e-16
Match length	66
% identity	65
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	129581
Contig ID	34050_1.R1010
5'-most EST	g2445950
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	1.0e-14
Match length	51
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	129582
Contig ID	34050_3.R1010
5'-most EST	g958025

Seq. No.	129583
Contig ID	34053_1.R1010
5'-most EST	jC-atXLIB327418P4e04b1
Method	BLASTX
NCBI GI	g4587543
BLAST score	923
E value	1.0e-100
Match length	208
% identity	89
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. EST gb_AB015099 comes from this gene. [Arabidopsis thaliana]

Seq. No.	129584
Contig ID	34055_1.R1010
5'-most EST	jC-atXLIB327418P2f05b2
Method	BLASTN
NCBI GI	g2262097
BLAST score	294
E value	1.0e-164
Match length	314
% identity	99
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	129585
Contig ID	34059_2.R1010
5'-most EST	jC-atXLIB327418P1f01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	4.0e-28

Match length	65
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129586
Contig ID	34062_1.R1010
5'-most EST	jC-atXLIB327418P1f03b1
Method	BLASTN
NCBI GI	g3805839
BLAST score	121
E value	2.0e-61
Match length	372
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	129587
Contig ID	34069_1.R1010
5'-most EST	jC-atXLIB327418P4f04b1
Method	BLASTN
NCBI GI	g4049332
BLAST score	386
E value	0.0e+00
Match length	517
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	129588
Contig ID	34071_1.R1010
5'-most EST	jC-atXLIB327430P1b03b1
Method	BLASTX
NCBI GI	g4006909
BLAST score	320
E value	3.0e-29
Match length	85
% identity	75
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	129589
Contig ID	34071_2.R1010
5'-most EST	jC-atX25094Q1E1G07a2
Method	BLASTX
NCBI GI	g4006909
BLAST score	163
E value	5.0e-11
Match length	39
% identity	77
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	129590
Contig ID	34073_1.R1010
5'-most EST	ARABLI-025-Q1-B1-A1
Method	BLASTN
NCBI GI	g4538990
BLAST score	243

E value	1.0e-134
Match length	788
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	129591
Contig ID	34077_1.R1010
5'-most EST	jC-atXLIB327418P4f12b1
Method	BLASTX
NCBI GI	g3298542
BLAST score	655
E value	2.0e-68
Match length	189
% identity	64
NCBI Description	(AC004681) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	129592
Contig ID	34087_1.R1010
5'-most EST	jC-atXLIB327418P3c10b1
Method	BLASTN
NCBI GI	g2351073
BLAST score	168
E value	2.0e-89
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	129593
Contig ID	34089_1.R1010
5'-most EST	jC-atXLIB327418P4c12b1
Method	BLASTX
NCBI GI	g3426048
BLAST score	798
E value	3.0e-85
Match length	159
% identity	99
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	129594
Contig ID	34093_1.R1010
5'-most EST	jC-atXLIB327418P3c09b1
Method	BLASTN
NCBI GI	g2494106
BLAST score	205
E value	1.0e-111
Match length	205
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129595
Contig ID	34098_1.R1010
5'-most EST	jC-atXLIB327418P4f09b1

Method	BLASTX
NCBI GI	g2118017
BLAST score	486
E value	7.0e-49
Match length	147
% identity	59
NCBI Description	non-S-RNase (EC 3.1.-.-) - Japanese pear >gi_1526417_dbj_BAA08475_ (D49529) ribonuclease [Pyrus pyrifolia]

Seq. No.	129596
Contig ID	34099_1.R1010
5'-most EST	jC-atXLIB327418P1d05b1
Method	BLASTN
NCBI GI	g3128143
BLAST score	352
E value	0.0e+00
Match length	636
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	129597
Contig ID	34107_1.R1010
5'-most EST	LIB25-095-Q1-E1-C3

Seq. No.	129598
Contig ID	34118_1.R1010
5'-most EST	LIB3176-052-P1-K1-D4

Seq. No.	129599
Contig ID	34119_1.R1010
5'-most EST	jC-atXLIB327418P1e03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129600
Contig ID	34121_1.R1010
5'-most EST	LIB25-095-Q1-E1-E1
Method	BLASTX
NCBI GI	g4567286
BLAST score	192
E value	5.0e-15
Match length	54
% identity	72
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	129601
Contig ID	34126_1.R1010
5'-most EST	jC-atXLIB327418P1e12b1

Method	BLASTN
NCBI GI	g2160155
BLAST score	111
E value	4.0e-55
Match length	234
% identity	88
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	129602
Contig ID	34126_2.R1010
5'-most EST	jC-atX24110Q1E1D05b1
Method	BLASTX
NCBI GI	g2160189
BLAST score	842
E value	1.0e-90
Match length	181
% identity	91
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	129603
Contig ID	34127_1.R1010
5'-most EST	jC-atX25095Q1E1E08b1
Method	BLASTN
NCBI GI	g2651294
BLAST score	245
E value	1.0e-135
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129604
Contig ID	34137_1.R1010
5'-most EST	jC-atXP3C83H8T7d1
Method	BLASTX
NCBI GI	g3461848
BLAST score	908
E value	2.0e-98
Match length	180
% identity	99
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	129605
Contig ID	34141_1.R1010
5'-most EST	jC-atXLIB327418P4f03b1
Method	BLASTN
NCBI GI	g4220627
BLAST score	131
E value	3.0e-67
Match length	131
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	129606
Contig ID	34143_1.R1010
5'-most EST	jC-alXLIB327435P4g09b1
Method	BLASTX
NCBI GI	g1168750
BLAST score	268
E value	5.0e-23
Match length	159
% identity	36
NCBI Description	CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria gruberi]

Seq. No.	129607
Contig ID	34149_1.R1010
5'-most EST	g931143
Method	BLASTN
NCBI GI	g4249393
BLAST score	194
E value	1.0e-104
Match length	382
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129608
Contig ID	34152_1.R1010
5'-most EST	jC-atXLIB327418P3f11b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	180
E value	2.0e-96
Match length	552
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	129609
Contig ID	34153_1.R1010
5'-most EST	jC-atXLIB327421P2a02b1
Method	BLASTX
NCBI GI	g1297189
BLAST score	577
E value	1.0e-59
Match length	134
% identity	81
NCBI Description	(U53501) Theoretical protein with similarity to Swiss-Prot Accession Number P19456 plasma membrane ATPase 2 (proton pump) [Arabidopsis thaliana]

Seq. No.	129610
Contig ID	34162_1.R1010
5'-most EST	jC-atXLIB327418P4c04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	5.0e-23

Match length	61
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129611
Contig ID	34163_1.R1010
5'-most EST	jC-atXLIB327418P4c05b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129612
Contig ID	34166_2.R1010
5'-most EST	jC-atXLIB327418P4c07b1
Method	BLASTX
NCBI GI	g2914701
BLAST score	220
E value	2.0e-17
Match length	132
% identity	30
NCBI Description	(AC003974) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No.	129613
Contig ID	34166_4.R1010
5'-most EST	jC-atX25096Q1E1A04a1
Method	BLASTX
NCBI GI	g2914701
BLAST score	202
E value	1.0e-25
Match length	73
% identity	99
NCBI Description	(AC003974) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No.	129614
Contig ID	34169_1.R1010
5'-most EST	jC-atX25096Q1E1A07b1

Seq. No.	129615
Contig ID	34174_1.R1010
5'-most EST	jC-atXLIB327418P2d03b2

Seq. No.	129616
Contig ID	34210_1.R1010
5'-most EST	g2576780
Method	BLASTN
NCBI GI	g3449334
BLAST score	356
E value	0.0e+00
Match length	484
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	129617
Contig ID	34214_1.R1010
5'-most EST	jC-atX25096Q1E1F02b1
Method	BLASTN
NCBI GI	g3548797
BLAST score	313
E value	1.0e-176
Match length	313
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129618
Contig ID	34219_1.R1010
5'-most EST	jC-atXLIB327418P4e08b1
Method	BLASTX
NCBI GI	g4056505
BLAST score	159
E value	2.0e-20
Match length	148
% identity	59
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	129619
Contig ID	34225_1.R1010
5'-most EST	jC-atXLIB327418P1f12b1
Method	BLASTX
NCBI GI	g3377803
BLAST score	285
E value	1.0e-29
Match length	127
% identity	68
NCBI Description	(AF075597) Similar to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]

Seq. No.	129620
Contig ID	34228_1.R1010
5'-most EST	jC-atXLIB327418P1f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	2.0e-20
Match length	65
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129621
Contig ID	34229_2.R1010
5'-most EST	jC-atXLIB327418P1f09b1
Method	BLASTX
NCBI GI	g3123275
BLAST score	134
E value	1.0e-10
Match length	129
% identity	40

NCBI Description	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH) >gi_1146196 (L47648) phosphoglycerate dehydrogenase [Bacillus subtilis] >gi_2634742_emb_CAB14239_ (Z99116) phosphoglycerate dehydrogenase [Bacillus subtilis]
Seq. No.	129622
Contig ID	34245_1.R1010
5'-most EST	jC-atXLIB327418P3c07b1
Method	BLASTX
NCBI GI	g1652280
BLAST score	273
E value	5.0e-24
Match length	125
% identity	45
NCBI Description	(D90904) ribonuclease II [Synechocystis sp.]
Seq. No.	129623
Contig ID	34246_1.R1010
5'-most EST	jC-atXLIB327418P4d10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	2.0e-24
Match length	68
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	129624
Contig ID	34246_2.R1010
5'-most EST	jC-atXLIB327431P1d05a1
Method	BLASTN
NCBI GI	g531832
BLAST score	45
E value	6.0e-16
Match length	52
% identity	98
NCBI Description	Cloning vector pSport2, complete sequence
Seq. No.	129625
Contig ID	34250_1.R1010
5'-most EST	jC-atX24111Q1E1B07b1
Method	BLASTX
NCBI GI	g4775270
BLAST score	357
E value	5.0e-44
Match length	115
% identity	74
NCBI Description	(AJ131214) SF2/ASF-like splicing modulator Srp30 [Arabidopsis thaliana]
Seq. No.	129626
Contig ID	34261_1.R1010
5'-most EST	jC-atXLIB327418P4d01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50

E value	9.0e-19
Match length	54
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129627
Contig ID	34261_3.R1010
5'-most EST	jC-atXLI09Q1B1B10b1

Seq. No.	129628
Contig ID	34266_1.R1010
5'-most EST	jC-atXLIB327418P2d11b2
Method	BLASTN
NCBI GI	g2853071
BLAST score	115
E value	9.0e-58
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	129629
Contig ID	34275_2.R1010
5'-most EST	ARABLI-040-Q1-B1-E5

Seq. No.	129630
Contig ID	34283_1.R1010
5'-most EST	jC-atXLIB327418P1e11b1
Method	BLASTX
NCBI GI	g2252840
BLAST score	882
E value	4.0e-95
Match length	224
% identity	81
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	129631
Contig ID	34297_1.R1010
5'-most EST	LIB25-097-Q1-E1-G11
Method	BLASTX
NCBI GI	g3152559
BLAST score	367
E value	1.0e-34
Match length	128
% identity	68
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	129632
Contig ID	34297_2.R1010
5'-most EST	g2048696
Method	BLASTN
NCBI GI	g4757401
BLAST score	407

E value 0.0e+00
Match length 605
% identity 92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No. 129633
Contig ID 34299_1.R1010
5'-most EST jC-atXLIB327418P1f11b1
Method BLASTX
NCBI GI g4539422
BLAST score 873
E value 5.0e-94
Match length 155
% identity 100
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 129634
Contig ID 34306_1.R1010
5'-most EST jC-atXLIB327422P4d09a1
Method BLASTX
NCBI GI g1008904
BLAST score 273
E value 8.0e-24
Match length 140
% identity 43
NCBI Description (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]

Seq. No. 129635
Contig ID 34312_1.R1010
5'-most EST jC-atXLIB327418P1g05b1
Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 1.0e-26
Match length 78
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 129636
Contig ID 34319_1.R1010
5'-most EST jC-alXLIB327435P2f02a1

Seq. No. 129637
Contig ID 34322_1.R1010
5'-most EST jC-atXLIB327418P2g11a1
Method BLASTN
NCBI GI g3702723
BLAST score 259
E value 1.0e-143
Match length 259
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14B20, complete sequence [Arabidopsis thaliana]

Seq. No. 129638

Contig ID	34329_1.R1010
5'-most EST	jC-atXLIB327418P2g08b2
Method	BLASTX
NCBI GI	g4249382
BLAST score	421
E value	2.0e-41
Match length	132
% identity	60
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	129639
Contig ID	34331_1.R1010
5'-most EST	jC-atXLIB327438P1e06a1
Method	BLASTX
NCBI GI	g3152581
BLAST score	681
E value	2.0e-77
Match length	162
% identity	87
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	129640
Contig ID	34332_1.R1010
5'-most EST	jC-atXLIB327418P4g03b1
Method	BLASTX
NCBI GI	g2244855
BLAST score	409
E value	1.0e-39
Match length	100
% identity	81
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129641
Contig ID	34332_2.R1010
5'-most EST	LIB3168-053-P1-K1-D3

Seq. No.	129642
Contig ID	34334_1.R1010
5'-most EST	jC-atXLIB327418P4g05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	6.0e-23
Match length	73
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129643
Contig ID	34335_1.R1010
5'-most EST	jC-atXLIB327418P4g06b1
Method	BLASTN
NCBI GI	g4589412

BLAST score	161
E value	4.0e-85
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	129644
Contig ID	34341_1.R1010
5'-most EST	jC-atXLIB327418P4g02b1
Method	BLASTN
NCBI GI	g2656028
BLAST score	298
E value	1.0e-167
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	129645
Contig ID	34343_1.R1010
5'-most EST	jC-atXLIB327418P3g09b1
Method	BLASTN
NCBI GI	g4220638
BLAST score	204
E value	1.0e-111
Match length	367
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	129646
Contig ID	34350_1.R1010
5'-most EST	LIB25-098-Q1-E1-D6
Method	BLASTN
NCBI GI	g4454447
BLAST score	37
E value	3.0e-11
Match length	85
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129647
Contig ID	34355_1.R1010
5'-most EST	jC-atXLIB327418P2h03b2
Method	BLASTN
NCBI GI	g3449316
BLAST score	345
E value	0.0e+00
Match length	606
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	129648
Contig ID	34361_2.R1010

5'-most EST	LIB25-098-Q1-E1-E6
Method	BLASTN
NCBI GI	g2351065
BLAST score	71
E value	1.0e-31
Match length	119
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	129649
Contig ID	34372_1.R1010
5'-most EST	jC-atXLIB327418P1h06b1
Method	BLASTX
NCBI GI	g3135254
BLAST score	244
E value	3.0e-20
Match length	126
% identity	44
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129650
Contig ID	34372_2.R1010
5'-most EST	LIB3175-006-P1-K1-C9
Method	BLASTX
NCBI GI	g3135254
BLAST score	160
E value	9.0e-11
Match length	136
% identity	37
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129651
Contig ID	34376_1.R1010
5'-most EST	jC-atXLIB327418P4g12b1
Method	BLASTX
NCBI GI	g419789
BLAST score	436
E value	7.0e-43
Match length	116
% identity	66
NCBI Description	hypothetical protein - potato

Seq. No.	129652
Contig ID	34378_1.R1010
5'-most EST	jC-atXLIB327430P1b04b1
Method	BLASTX
NCBI GI	g4587577
BLAST score	199
E value	6.0e-15
Match length	61
% identity	59
NCBI Description	(AC006550) F10O3.17 [Arabidopsis thaliana]

Seq. No.	129653
Contig ID	34379_2.R1010
5'-most EST	jC-atXLIB327418P4h02b1

Method	BLASTN
NCBI GI	g4567259
BLAST score	123
E value	3.0e-62
Match length	308
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	129654
Contig ID	34379_3.R1010
5'-most EST	g1947043
Method	BLASTX
NCBI GI	g4567283
BLAST score	907
E value	4.0e-98
Match length	202
% identity	91
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	129655
Contig ID	34379_4.R1010
5'-most EST	g315638
Method	BLASTX
NCBI GI	g4567283
BLAST score	742
E value	6.0e-79
Match length	152
% identity	98
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	129656
Contig ID	34391_2.R1010
5'-most EST	LIB35-032-Q1-E1-G3
Method	BLASTX
NCBI GI	g1706958
BLAST score	246
E value	6.0e-21
Match length	137
% identity	37
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	129657
Contig ID	34393_1.R1010
5'-most EST	LIB25-098-Q1-E1-H8
Method	BLASTN
NCBI GI	g4757394
BLAST score	190
E value	1.0e-102
Match length	361
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19O4, complete sequence

Seq. No.	129658
Contig ID	34394_1.R1010
5'-most EST	jC-atXLIB327418P4h05b1

Method	BLASTX
NCBI GI	g2982942
BLAST score	163
E value	1.0e-21
Match length	153
% identity	33
NCBI Description	(AE000679) GMP synthase [Aquifex aeolicus]

Seq. No.	129659
Contig ID	34397_1.R1010
5'-most EST	LIB25-099-Q1-E1-A2

Seq. No.	129660
Contig ID	34401_1.R1010
5'-most EST	jC-atXLIB327418P2g03b2
Method	BLASTX
NCBI GI	g3130051
BLAST score	439
E value	2.0e-74
Match length	264
% identity	55
NCBI Description	(AL023518) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	129661
Contig ID	34402_2.R1010
5'-most EST	LIB25-099-Q1-E1-A8
Method	BLASTN
NCBI GI	g2264307
BLAST score	339
E value	0.0e+00
Match length	423
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	129662
Contig ID	34404_1.R1010
5'-most EST	jC-atXLIB327418P2g10b2
Method	BLASTN
NCBI GI	g531832
BLAST score	35
E value	5.0e-10
Match length	62
% identity	90
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	129663
Contig ID	34409_1.R1010
5'-most EST	jC-atXLIB327418P2g12b2
Method	BLASTX
NCBI GI	g3608134
BLAST score	665
E value	6.0e-70
Match length	146
% identity	88
NCBI Description	(AC005314) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	129664
Contig ID	34415_1.R1010
5'-most EST	jC-atXLIB327418P4g04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129665
Contig ID	34418_1.R1010
5'-most EST	jC-atXmonuni26Dc07b1
Method	BLASTN
NCBI GI	g4432847
BLAST score	356
E value	0.0e+00
Match length	473
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129666
Contig ID	34421_1.R1010
5'-most EST	jC-atXLIB327419P4g01b1
Method	BLASTN
NCBI GI	g2924729
BLAST score	203
E value	1.0e-110
Match length	536
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	129667
Contig ID	34424_1.R1010
5'-most EST	LIB25-099-Q1-E1-C9
Method	BLASTX
NCBI GI	g4689376
BLAST score	232
E value	3.0e-19
Match length	131
% identity	33
NCBI Description	(AF138872) zinc finger protein 3 [Arabidopsis thaliana]

Seq. No.	129668
Contig ID	34444_1.R1010
5'-most EST	g1053684
Method	BLASTX
NCBI GI	g4580390
BLAST score	912
E value	1.0e-98
Match length	211
% identity	87

NCBI Description	(AC007171) putative disease resistance response protein [Arabidopsis thaliana]
Seq. No.	129669
Contig ID	34466_1.R1010
5'-most EST	jC-atXLIB327418P2h10b2
Method	BLASTX
NCBI GI	g3786409
BLAST score	173
E value	8.0e-12
Match length	157
% identity	29
NCBI Description	(AF098499) contains similarity to Saccharomyces cerevisiae MAF1 protein (GB:U19492) [Caenorhabditis elegans]
Seq. No.	129670
Contig ID	34473_1.R1010
5'-most EST	LIB3176-026-P1-K1-H10
Method	BLASTX
NCBI GI	g169459
BLAST score	237
E value	1.0e-19
Match length	95
% identity	52
NCBI Description	(M18538) pop3 peptide [Populus balsamifera subsp. trichocarpa X Populus deltoides]
Seq. No.	129671
Contig ID	34476_1.R1010
5'-most EST	LIB25-099-Q1-E1-H5
Seq. No.	129672
Contig ID	34477_1.R1010
5'-most EST	LIB35-023-Q1-E1-E5
Method	BLASTN
NCBI GI	g4757414
BLAST score	300
E value	1.0e-168
Match length	584
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence
Seq. No.	129673
Contig ID	34477_2.R1010
5'-most EST	LIB3176-029-P1-K1-B1
Method	BLASTN
NCBI GI	g4757414
BLAST score	160
E value	2.0e-84
Match length	292
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence
Seq. No.	129674
Contig ID	34481_1.R1010

5'-most EST	jC-atX25100Q1E1A01b1
Method	BLASTX
NCBI GI	g4455357
BLAST score	248
E value	9.0e-26
Match length	152
% identity	49
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	129675
Contig ID	34496_1.R1010
5'-most EST	jC-atXLIB327420P1a11b1
Method	BLASTX
NCBI GI	g4056493
BLAST score	358
E value	2.0e-49
Match length	237
% identity	46
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	129676
Contig ID	34501_1.R1010
5'-most EST	jC-atX25100Q1E1C01b1
Method	BLASTN
NCBI GI	g2924652
BLAST score	347
E value	0.0e+00
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	129677
Contig ID	34502_1.R1010
5'-most EST	jC-atXLIB327420P4a08b1
Method	BLASTX
NCBI GI	g4455199
BLAST score	527
E value	1.0e-53
Match length	112
% identity	99
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	129678
Contig ID	34504_1.R1010
5'-most EST	jC-atXLIB327420P4a09b1
Method	BLASTN
NCBI GI	g4757407
BLAST score	106
E value	2.0e-52
Match length	444
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	129679
Contig ID	34507_1.R1010

5'-most EST	jC-atXLIB327420P4a11b1
Method	BLASTN
NCBI GI	g2815404
BLAST score	237
E value	1.0e-130
Match length	511
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	129680
Contig ID	34507_2.R1010
5'-most EST	g2062919
Method	BLASTN
NCBI GI	g2815404
BLAST score	246
E value	1.0e-136
Match length	489
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	129681
Contig ID	34509_1.R1010
5'-most EST	jC-atXP73CF3E1T7b1
Method	BLASTN
NCBI GI	g3282170
BLAST score	341
E value	0.0e+00
Match length	705
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129682
Contig ID	34515_1.R1010
5'-most EST	LIB25-100-Q1-E1-D3
Method	BLASTX
NCBI GI	g2245115
BLAST score	612
E value	6.0e-64
Match length	119
% identity	100
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	129683
Contig ID	34517_1.R1010
5'-most EST	jC-atXLIB327420P4b01b1
Method	BLASTX
NCBI GI	g4584255
BLAST score	240
E value	5.0e-20
Match length	94
% identity	43
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	129684

Contig ID	34520_1.R1010
5'-most EST	jC-atXLIB327420P3b07b1
Method	BLASTX
NCBI GI	g4580395
BLAST score	350
E value	5.0e-33
Match length	145
% identity	57
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	129685
Contig ID	34537_1.R1010
5'-most EST	LIB3176-067-P1-K1-D1
Method	BLASTX
NCBI GI	g2342687
BLAST score	233
E value	3.0e-19
Match length	88
% identity	51
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No.	129686
Contig ID	34538_1.R1010
5'-most EST	jC-atXLIB327420P4c10b1
Method	BLASTX
NCBI GI	g2190553
BLAST score	416
E value	1.0e-40
Match length	133
% identity	98
NCBI Description	(AC001229) Strong similarity to Arabidopsis zeta-crystallin-like protein (gb_Z49268). [Arabidopsis thaliana]

Seq. No.	129687
Contig ID	34539_1.R1010
5'-most EST	jC-atXLIB327420P3c11b1
Method	BLASTN
NCBI GI	g4757414
BLAST score	141
E value	3.0e-73
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	129688
Contig ID	34540_1.R1010
5'-most EST	LIB25-100-Q1-E1-G3

Seq. No.	129689
Contig ID	34546_1.R1010
5'-most EST	LIB25-100-Q1-E1-H3
Method	BLASTN

NCBI GI	g2264312
BLAST score	173
E value	1.0e-92
Match length	333
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	129690
Contig ID	34548_1.R1010
5'-most EST	jC-atXLIB327420P1d07b1
Method	BLASTX
NCBI GI	g2880047
BLAST score	908
E value	6.0e-98
Match length	276
% identity	54
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129691
Contig ID	34549_1.R1010
5'-most EST	jC-atXLIB327420P4c11b1
Method	BLASTX
NCBI GI	g4006879
BLAST score	415
E value	4.0e-61
Match length	120
% identity	98
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129692
Contig ID	34551_1.R1010
5'-most EST	g2756975
Method	BLASTN
NCBI GI	g3298532
BLAST score	143
E value	2.0e-74
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129693
Contig ID	34552_1.R1010
5'-most EST	LIB35-046-Q1-E1-E10

Seq. No.	129694
Contig ID	34563_1.R1010
5'-most EST	jC-atXLIB327420P1a08b1
Method	BLASTN
NCBI GI	g4263753
BLAST score	105
E value	1.0e-51
Match length	746
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	129695
Contig ID	34567_1.R1010
5'-most EST	jC-atXLIB327420P3a09b1

Seq. No.	129696
Contig ID	34575_1.R1010
5'-most EST	ARABL1-019-Q1-B1-H12
Method	BLASTN
NCBI GI	g2642152
BLAST score	390
E value	0.0e+00
Match length	435
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129697
Contig ID	34591_1.R1010
5'-most EST	jC-atXLIB327420P1c01b1
Method	BLASTN
NCBI GI	g3355463
BLAST score	192
E value	1.0e-103
Match length	647
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129698
Contig ID	34591_2.R1010
5'-most EST	jC-atXLIB327420P1c01a1
Method	BLASTN
NCBI GI	g3355463
BLAST score	236
E value	1.0e-130
Match length	547
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129699
Contig ID	34592_1.R1010
5'-most EST	LIB3176-092-P1-K1-E4
Method	BLASTX
NCBI GI	g3046696
BLAST score	429
E value	3.0e-42
Match length	79
% identity	100
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	129700
Contig ID	34594_1.R1010
5'-most EST	LIB25-101-Q1-E1-E8
Method	BLASTN
NCBI GI	g3046851

BLAST score	383
E value	0.0e+00
Match length	776
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	129701
Contig ID	34604_1.R1010
5'-most EST	LIB25-101-Q1-E1-F7

Seq. No.	129702
Contig ID	34609_1.R1010
5'-most EST	jC-atXLIB327420P4c12b1
Method	BLASTX
NCBI GI	g4415926
BLAST score	631
E value	4.0e-75
Match length	158
% identity	94
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	129703
Contig ID	34610_1.R1010
5'-most EST	g935965
Method	BLASTN
NCBI GI	g4589445
BLAST score	576
E value	0.0e+00
Match length	1096
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	129704
Contig ID	34612_1.R1010
5'-most EST	LIB25-101-Q1-E1-G5

Seq. No.	129705
Contig ID	34624_1.R1010
5'-most EST	LIB3175-035-P1-K1-D10
Method	BLASTX
NCBI GI	g1175395
BLAST score	184
E value	2.0e-13
Match length	124
% identity	34
NCBI Description	HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME I >gi_2130413_pir__S58099 hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe) >gi_914880_emb_CAA90460_ (Z50113) unknown [Schizosaccharomyces pombe]

Seq. No.	129706
Contig ID	34625_1.R1010
5'-most EST	jC-atX25102Q1E1A11b1
Method	BLASTX

NCBI GI g3386611
BLAST score 441
E value 3.0e-44
Match length 126
% identity 67
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 129707
Contig ID 34628_1.R1010
5'-most EST jC-atXLIB327408P3f08a1
Method BLASTX
NCBI GI g1877279
BLAST score 269
E value 3.0e-23
Match length 128
% identity 47
NCBI Description (Z92770) fadE2 [Mycobacterium tuberculosis]

Seq. No. 129708
Contig ID 34632_1.R1010
5'-most EST jC-atXLIB327421P2f04b1
Method BLASTN
NCBI GI g2582640
BLAST score 68
E value 1.0e-29
Match length 76
% identity 97
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 129709
Contig ID 34636_1.R1010
5'-most EST LIB25-102-Q1-E1-B2
Method BLASTX
NCBI GI g4406780
BLAST score 223
E value 2.0e-18
Match length 103
% identity 45
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 129710
Contig ID 34644_1.R1010
5'-most EST jC-atXLIB327420P3a04b1
Method BLASTX
NCBI GI g3776557
BLAST score 374
E value 9.0e-36
Match length 142
% identity 51
NCBI Description (AC005388) Contains similarity to gi_2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome gb_AL022020. [Arabidopsis thaliana]

Seq. No. 129711
Contig ID 34649_1.R1010

5'-most EST	jC-atX25102Q1E1C09b1
Method	BLASTX
NCBI GI	g1418990
BLAST score	217
E value	3.0e-17
Match length	99
% identity	42
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	129712
Contig ID	34658_1.R1010
5'-most EST	jC-atXLIB327420P3a12b1
Method	BLASTN
NCBI GI	g619750
BLAST score	400
E value	0.0e+00
Match length	433
% identity	89
NCBI Description	Arabidopsis thaliana phosphoribosylanthranilate isomerase (PAI1) gene, complete cds

Seq. No.	129713
Contig ID	34664_1.R1010
5'-most EST	jC-atXLIB327420P4b06b1
Method	BLASTX
NCBI GI	g2462749
BLAST score	904
E value	1.0e-97
Match length	236
% identity	75
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	129714
Contig ID	34667_1.R1010
5'-most EST	jC-atXP85C241G19T7b1
Method	BLASTN
NCBI GI	g4757392
BLAST score	44
E value	3.0e-15
Match length	72
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	129715
Contig ID	34668_1.R1010
5'-most EST	jC-atXLIB327420P3b02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	1.0e-28
Match length	73
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129716
Contig ID	34674_1.R1010
5'-most EST	LIB3175-030-P1-K1-D6
Method	BLASTX
NCBI GI	g2252841
BLAST score	63
E value	1.0e-141
Match length	329
% identity	76
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	129717
Contig ID	34679_1.R1010
5'-most EST	jC-atXLIB327420P1c03b1
Method	BLASTX
NCBI GI	g4008006
BLAST score	479
E value	7.0e-48
Match length	182
% identity	55
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	129718
Contig ID	34688_1.R1010
5'-most EST	LIB25-102-Q1-E1-G4

Seq. No.	129719
Contig ID	34690_1.R1010
5'-most EST	jC-atX24001Q1E1H06a1
Method	BLASTN
NCBI GI	g3510336
BLAST score	305
E value	1.0e-171
Match length	690
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	129720
Contig ID	34690_3.R1010
5'-most EST	jC-atX25102Q1E1G06b1
Method	BLASTN
NCBI GI	g3510336
BLAST score	288
E value	1.0e-161
Match length	350
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	129721
Contig ID	34696_1.R1010
5'-most EST	LIB25-102-Q1-E1-H3
Method	BLASTX
NCBI GI	g3885329
BLAST score	578

E value	5.0e-60
Match length	110
% identity	100
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	129722
Contig ID	34705_1.R1010
5'-most EST	jC-atXLIB327419P4h10b1
Method	BLASTN
NCBI GI	g4662628
BLAST score	325
E value	0.0e+00
Match length	537
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	129723
Contig ID	34706_1.R1010
5'-most EST	jC-atX25103Q1E1A04b1
Method	BLASTX
NCBI GI	g2829526
BLAST score	177
E value	1.0e-12
Match length	68
% identity	51
NCBI Description	GUANYLATE KINASE (GMP KINASE) >gi_1542897_emb_CAB02172_ (Z80108) gmk [Mycobacterium tuberculosis]

Seq. No.	129724
Contig ID	34710_1.R1010
5'-most EST	jC-atXLIB327420P1a04b1
Method	BLASTN
NCBI GI	g4159712
BLAST score	481
E value	0.0e+00
Match length	713
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	129725
Contig ID	34717_1.R1010
5'-most EST	jC-atXLIB327431P4e10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	129726
Contig ID	34720_1.R1010
5'-most EST	jC-atXLIB327420P4a04b1
Method	BLASTX
NCBI GI	g3510249

BLAST score	487
E value	5.0e-49
Match length	140
% identity	70
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	129727
Contig ID	34723_1.R1010
5'-most EST	jC-atXLIB327420P3a05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129728
Contig ID	34725_1.R1010
5'-most EST	LIB3176-030-P1-K1-D1
Method	BLASTN
NCBI GI	g4589443
BLAST score	197
E value	1.0e-107
Match length	448
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	129729
Contig ID	34727_1.R1010
5'-most EST	jC-atXLIB327420P4a01b1
Method	BLASTX
NCBI GI	g2924777
BLAST score	185
E value	1.0e-13
Match length	146
% identity	2
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	129730
Contig ID	34729_1.R1010
5'-most EST	LIB25-103-Q1-E1-D11
Method	BLASTN
NCBI GI	g2244991
BLAST score	325
E value	0.0e+00
Match length	387
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129731
Contig ID	34731_2.R1010
5'-most EST	jC-atX25103Q1E1C05b1

Seq. No.	129732
Contig ID	34733_1.R1010
5'-most EST	LIB25-103-Q1-E1-D4
Method	BLASTX
NCBI GI	g4490707
BLAST score	443
E value	3.0e-44
Match length	99
% identity	74
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	129733
Contig ID	34736_1.R1010
5'-most EST	jC-atXLIB327420P1b01b1

Seq. No.	129734
Contig ID	34737_1.R1010
5'-most EST	jC-atXLIB327420P1b02b1
Method	BLASTX
NCBI GI	g3193314
BLAST score	528
E value	2.0e-53
Match length	231
% identity	55
NCBI Description	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

Seq. No.	129735
Contig ID	34737_2.R1010
5'-most EST	jC-atXLIB327420P1b02a1
Method	BLASTX
NCBI GI	g3193314
BLAST score	304
E value	3.0e-27
Match length	161
% identity	48
NCBI Description	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

Seq. No.	129736
Contig ID	34738_1.R1010
5'-most EST	jC-atXLIB327420P3b01b1
Method	BLASTN
NCBI GI	g3985955
BLAST score	491
E value	0.0e+00
Match length	542
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	129737
Contig ID	34740_1.R1010
5'-most EST	jC-atXLIB327420P4b05b1
Method	BLASTX
NCBI GI	g114339

BLAST score 755
E value 2.0e-80
Match length 149
% identity 99
NCBI Description PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625 (J04737) ATPase [Arabidopsis thaliana]

Seq. No. 129738
Contig ID 34742_1.R1010
5'-most EST g493446
Method BLASTN
NCBI GI g166673
BLAST score 372
E value 0.0e+00
Match length 412
% identity 98
NCBI Description Arabidopsis thaliana carboxypeptidase Y-like protein gene, complete cds

Seq. No. 129739
Contig ID 34751_1.R1010
5'-most EST g2749689
Method BLASTN
NCBI GI g2244829
BLAST score 276
E value 1.0e-154
Match length 389
% identity 80
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 129740
Contig ID 34754_1.R1010
5'-most EST LIB25-103-Q1-E1-F3

Seq. No. 129741
Contig ID 34762_1.R1010
5'-most EST jC-atXLIB327420P3c04b1
Method BLASTN
NCBI GI g2582640
BLAST score 62
E value 4.0e-26
Match length 78
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 129742
Contig ID 34765_1.R1010
5'-most EST jC-atXLIB327420P3h08b1
Method BLASTX
NCBI GI g3776563
BLAST score 391
E value 9.0e-38
Match length 133

% identity	59
NCBI Description	(AC005388) Strong similarity to gb_L04680 5-epi-aristolochene synthase from Nicotiana tabacum and delta cadinene syntase gb_U88318 from Gosssypium hirsutum. [Arabidopsis thaliana]

Seq. No.	129743
Contig ID	34770_1.R1010
5'-most EST	LIB25-103-Q1-E1-H1
Method	BLASTN
NCBI GI	g2337888
BLAST score	340
E value	0.0e+00
Match length	364
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	129744
Contig ID	34771_1.R1010
5'-most EST	jC-atXLIB327420P1d05b1
Method	BLASTX
NCBI GI	g2651297
BLAST score	417
E value	3.0e-73
Match length	208
% identity	68
NCBI Description	(AC002336) putative expansin [Arabidopsis thaliana]

Seq. No.	129745
Contig ID	34782_1.R1010
5'-most EST	LIB25-104-Q1-E1-A11
Method	BLASTN
NCBI GI	g2564051
BLAST score	243
E value	1.0e-134
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	129746
Contig ID	34788_1.R1010
5'-most EST	jC-atXLIB327426P3d05b1
Method	BLASTX
NCBI GI	g4335763
BLAST score	408
E value	2.0e-39
Match length	155
% identity	50
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	129747
Contig ID	34789_1.R1010
5'-most EST	LIB25-104-Q1-E1-A8
Method	BLASTN
NCBI GI	g4539415

BLAST score	260
E value	1.0e-144
Match length	405
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	129748
Contig ID	34802_1.R1010
5'-most EST	LIB3177-093-P1-K1-A5
Method	BLASTN
NCBI GI	g3004543
BLAST score	55
E value	5.0e-22
Match length	280
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129749
Contig ID	34804_1.R1010
5'-most EST	LIB3234-079-P1-K1-D8

Seq. No.	129750
Contig ID	34816_1.R1010
5'-most EST	LIB25-104-Q1-E1-D12
Method	BLASTN
NCBI GI	g3176693
BLAST score	214
E value	1.0e-117
Match length	391
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129751
Contig ID	34834_1.R1010
5'-most EST	jC-alXLIB327435P4b04a1
Method	BLASTX
NCBI GI	g3063445
BLAST score	180
E value	7.0e-13
Match length	130
% identity	29
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	129752
Contig ID	34841_1.R1010
5'-most EST	LIB3176-021-P1-K1-D1
Method	BLASTX
NCBI GI	g2132842
BLAST score	235
E value	1.0e-19
Match length	106
% identity	42
NCBI Description	probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae) >gi_1419909_emb_CAA99087_ (Z74819) ORF YOL077c

[Saccharomyces cerevisiae]

Seq. No.	129753
Contig ID	34844_1.R1010
5'-most EST	LIB25-104-Q1-E1-F8
Method	BLASTX
NCBI GI	g2462826
BLAST score	619
E value	3.0e-64
Match length	140
% identity	89
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	129754
Contig ID	34856_1.R1010
5'-most EST	jC-atXLIB327417P4a07b1
Method	BLASTN
NCBI GI	g3426033
BLAST score	411
E value	0.0e+00
Match length	447
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129755
Contig ID	34863_1.R1010
5'-most EST	LIB35-042-Q1-E1-D6
Method	BLASTN
NCBI GI	g3869075
BLAST score	377
E value	0.0e+00
Match length	388
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	129756
Contig ID	34874_1.R1010
5'-most EST	LIB25-105-Q1-E1-A4
Method	BLASTN
NCBI GI	g2760173
BLAST score	359
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	129757
Contig ID	34877_1.R1010
5'-most EST	g2749537
Method	BLASTX
NCBI GI	g1620898
BLAST score	56
E value	1.0e-14
Match length	93

% identity	46
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	129758
Contig ID	34883_1.R1010
5'-most EST	jC-atXP111C124H12T7s1
Method	BLASTX
NCBI GI	g3258569
BLAST score	544
E value	8.0e-56
Match length	105
% identity	96
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	129759
Contig ID	34904_1.R1010
5'-most EST	g906262
Method	BLASTN
NCBI GI	g3128141
BLAST score	265
E value	1.0e-147
Match length	433
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	129760
Contig ID	34906_1.R1010
5'-most EST	jC-atXP3C84A10T7079a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	129761
Contig ID	34908_1.R1010
5'-most EST	g1328214
Method	BLASTN
NCBI GI	g3128143
BLAST score	329
E value	0.0e+00
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	129762
Contig ID	34954_1.R1010
5'-most EST	LIB3177-020-P1-K2-E8

Seq. No.	129763
Contig ID	34957_1.R1010

5'-most EST	jC-atXLIB327420P4d03b1
Method	BLASTX
NCBI GI	g2760326
BLAST score	584
E value	2.0e-60
Match length	137
% identity	82
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	129764
Contig ID	34958_1.R1010
5'-most EST	jC-atXLIB327420P4d04b1
Method	BLASTN
NCBI GI	g2245031
BLAST score	334
E value	0.0e+00
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129765
Contig ID	34960_1.R1010
5'-most EST	jC-atXLIB327420P3d05b1
Method	BLASTN
NCBI GI	g4092471
BLAST score	429
E value	0.0e+00
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	129766
Contig ID	34967_1.R1010
5'-most EST	jC-atXLIB327420P4d08b1

Seq. No.	129767
Contig ID	34968_1.R1010
5'-most EST	jC-atXLIB327420P3d08b1
Method	BLASTN
NCBI GI	g2995991
BLAST score	312
E value	1.0e-175
Match length	399
% identity	96
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	129768
Contig ID	34974_1.R1010
5'-most EST	jC-atXLIB327420P3d06b1
Method	BLASTN
NCBI GI	g3702724
BLAST score	361
E value	0.0e+00
Match length	361

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	129769
Contig ID	34983_1.R1010
5'-most EST	jC-atXP102CE4E6T7b1
Method	BLASTX
NCBI GI	g4056507
BLAST score	278
E value	3.0e-24
Match length	120
% identity	52
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	129770
Contig ID	34983_4.R1010
5'-most EST	g2764202
Method	BLASTN
NCBI GI	g3449320
BLAST score	248
E value	1.0e-137
Match length	300
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	129771
Contig ID	34988_1.R1010
5'-most EST	jC-atXLIB327420P1e05b1
Method	BLASTX
NCBI GI	g3461833
BLAST score	278
E value	2.0e-26
Match length	116
% identity	57
NCBI Description	(AC004138) putative expansin [Arabidopsis thaliana]

Seq. No.	129772
Contig ID	34989_1.R1010
5'-most EST	LIB25-106-Q1-E1-D10

Seq. No.	129773
Contig ID	34992_1.R1010
5'-most EST	LIB3177-078-P1-K1-E6
Method	BLASTX
NCBI GI	g1514639
BLAST score	726
E value	4.0e-77
Match length	150
% identity	93
NCBI Description	(X85181) alpha-glucan phosphorylase [Spinacia oleracea]

Seq. No.	129774
Contig ID	35001_1.R1010
5'-most EST	LIB3234-053-P1-K1-H4

Method	BLASTX
NCBI GI	g4704730
BLAST score	297
E value	9.0e-27
Match length	90
% identity	63
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	129775
Contig ID	35004_1.R1010
5'-most EST	jC-atXLIB327431P3e10a1
Method	BLASTN
NCBI GI	g4262221
BLAST score	169
E value	6.0e-90
Match length	484
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129776
Contig ID	35004_2.R1010
5'-most EST	LIB3175-021-P1-K1-F9
Method	BLASTN
NCBI GI	g4262221
BLAST score	312
E value	1.0e-175
Match length	328
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129777
Contig ID	35008_1.R1010
5'-most EST	jC-atXLIB327420P1e10b1
Method	BLASTX
NCBI GI	g3876338
BLAST score	384
E value	1.0e-36
Match length	231
% identity	37
NCBI Description	(Z79754) similar to DEAH-type helicase; cDNA EST EMBL:D37033 comes from this gene; cDNA EST EMBL:D34035 comes from this gene; cDNA EST yk421c9.3 comes from this gene; cDNA EST yk421c9.5 comes from this gene; cDNA EST yk277h10.3... >gi_3876497_emb_CAB05720_ (Z83224) similar to DEAH-type helicase; cDNA EST EMBL:D37033 comes from this gene; cDNA EST EMBL:D34035 comes from this gene; cDNA EST yk421c9.3 comes from this gene; cDNA EST yk421c9.5 comes from this gene; cDNA EST yk277h10.3

Seq. No.	129778
Contig ID	35014_1.R1010
5'-most EST	jC-atXLIB327420P3e04b1
Method	BLASTX
NCBI GI	g4335751
BLAST score	640

E value	2.0e-81
Match length	283
% identity	55
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	129779
Contig ID	35032_1.R1010
5'-most EST	LIB3176-073-P1-K1-E12
Method	BLASTN
NCBI GI	g2570223
BLAST score	272
E value	1.0e-151
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129780
Contig ID	35034_1.R1010
5'-most EST	LIB25-106-Q1-E1-H4
Method	BLASTN
NCBI GI	g2618683
BLAST score	190
E value	1.0e-103
Match length	190
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129781
Contig ID	35043_1.R1010
5'-most EST	LIB3176-093-P1-K1-H4
Method	BLASTN
NCBI GI	g2924257
BLAST score	97
E value	6.0e-47
Match length	392
% identity	86
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	129782
Contig ID	35045_1.R1010
5'-most EST	jC-atXLIB327420P4d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129783
Contig ID	35048_1.R1010
5'-most EST	jC-atXLIB327420P4d01b1
Method	BLASTX

NCBI GI	g4204273
BLAST score	440
E value	2.0e-43
Match length	111
% identity	88
NCBI Description	(AC005223) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	129784
Contig ID	35066_1.R1010
5'-most EST	jC-atXLIB327420P1e02a1
Method	BLASTX
NCBI GI	g4510419
BLAST score	449
E value	3.0e-44
Match length	83
% identity	100
NCBI Description	(AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	129785
Contig ID	35069_1.R1010
5'-most EST	LIB25-107-Q1-E1-C9
Method	BLASTX
NCBI GI	g2827714
BLAST score	630
E value	5.0e-66
Match length	121
% identity	98
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	129786
Contig ID	35071_1.R1010
5'-most EST	LIB25-107-Q1-E1-D10
Method	BLASTX
NCBI GI	g4490707
BLAST score	240
E value	4.0e-20
Match length	79
% identity	62
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	129787
Contig ID	35071_2.R1010
5'-most EST	jC-atXLIB327420P2e04a2

Seq. No.	129788
Contig ID	35074_1.R1010
5'-most EST	jC-atXLIB327420P1e07b1
Method	BLASTN
NCBI GI	g4768276
BLAST score	36
E value	2.0e-10
Match length	40
% identity	97
NCBI Description	Homo sapiens very long-chain acyl-CoA synthetase homolog 2 mRNA, complete cds

Seq. No.	129789
Contig ID	35083_1.R1010
5'-most EST	LIB3176-001-Q1-K1-A10
Method	BLASTX
NCBI GI	g4262242
BLAST score	766
E value	1.0e-81
Match length	151
% identity	99
NCBI Description	(AC006200) NADC homolog [Arabidopsis thaliana]

Seq. No.	129790
Contig ID	35084_1.R1010
5'-most EST	g2759515
Method	BLASTN
NCBI GI	g2244991
BLAST score	261
E value	1.0e-145
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129791
Contig ID	35088_1.R1010
5'-most EST	LIB3176-035-P1-K1-H5
Method	BLASTN
NCBI GI	g2264309
BLAST score	185
E value	2.0e-99
Match length	550
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	129792
Contig ID	35092_1.R1010
5'-most EST	jC-atXLIB327420P4e02b1
Method	BLASTN
NCBI GI	g2924729
BLAST score	297
E value	1.0e-166
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	129793
Contig ID	35093_1.R1010
5'-most EST	g502102
Method	BLASTX
NCBI GI	g2702376
BLAST score	263
E value	1.0e-22
Match length	100
% identity	49

NCBI Description	(AF038605) Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis elegans]

Seq. No.	129794
Contig ID	35099_1.R1010
5'-most EST	jC-atXLIB327409P3c02a1
Method	BLASTN
NCBI GI	g2842474
BLAST score	290
E value	1.0e-162
Match length	427
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	129795
Contig ID	35099_2.R1010
5'-most EST	jC-atXLIB327420P4e01b1
Method	BLASTX
NCBI GI	g4204297
BLAST score	288
E value	1.0e-33
Match length	182
% identity	54
NCBI Description	(AC003027) ADK1 [Arabidopsis thaliana]

Seq. No.	129796
Contig ID	35101_1.R1010
5'-most EST	LIB3168-075-P1-K1-E9

Seq. No.	129797
Contig ID	35101_2.R1010
5'-most EST	jC-atXLIB327420P3e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129798
Contig ID	35106_1.R1010
5'-most EST	jC-atXLIB327420P4e09b1
Method	BLASTX
NCBI GI	g3702328
BLAST score	332
E value	9.0e-31
Match length	62
% identity	98
NCBI Description	(AC005397) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No.	129799
Contig ID	35107_1.R1010
5'-most EST	jC-atX25107Q1E1H10b1
Method	BLASTX
NCBI GI	g4726118
BLAST score	640
E value	3.0e-67
Match length	127
% identity	96
NCBI Description	(AC006436) putative somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]

Seq. No.	129800
Contig ID	35120_1.R1010
5'-most EST	jC-atXLIB327420P1f08b1
Method	BLASTX
NCBI GI	g961450
BLAST score	293
E value	5.0e-26
Match length	147
% identity	43
NCBI Description	(D63879) KIAA0156 gene product is related to Xenopus nucleolin. [Homo sapiens]

Seq. No.	129801
Contig ID	35124_1.R1010
5'-most EST	LIB25-108-Q1-E1-A6
Method	BLASTX
NCBI GI	g2462734
BLAST score	475
E value	7.0e-48
Match length	113
% identity	87
NCBI Description	(AC002292) similar to "Mx" GTP-binding proteins [Arabidopsis thaliana]

Seq. No.	129802
Contig ID	35127_1.R1010
5'-most EST	LIB25-108-Q1-E1-A9
Method	BLASTN
NCBI GI	g2351065
BLAST score	81
E value	1.0e-37
Match length	290
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	129803
Contig ID	35130_1.R1010
5'-most EST	jC-atXLIB327420P4f01b1
Method	BLASTX
NCBI GI	g322598
BLAST score	356
E value	1.0e-33
Match length	141

% identity	54
NCBI Description	St12p protein - Arabidopsis thaliana

Seq. No.	129804
Contig ID	35132_1.R1010
5'-most EST	jC-atXLIB327420P4f02b1
Method	BLASTX
NCBI GI	g3043726
BLAST score	161
E value	8.0e-11
Match length	128
% identity	27
NCBI Description	(AB011173) KIAA0601 protein [Homo sapiens]

Seq. No.	129805
Contig ID	35133_1.R1010
5'-most EST	g2597796
Method	BLASTN
NCBI GI	g4263038
BLAST score	309
E value	1.0e-173
Match length	1052
% identity	98
NCBI Description	Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	129806
Contig ID	35133_2.R1010
5'-most EST	jC-atXLIB327420P3f02b1
Method	BLASTN
NCBI GI	g3236479
BLAST score	152
E value	8.0e-80
Match length	446
% identity	98
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	129807
Contig ID	35137_1.R1010
5'-most EST	jC-atXLIB327420P4f03b1
Method	BLASTX
NCBI GI	g2252828
BLAST score	563
E value	5.0e-58
Match length	128
% identity	90
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	129808
Contig ID	35142_1.R1010
5'-most EST	jC-atXLIB327420P3f07b1
Method	BLASTN
NCBI GI	g3492855
BLAST score	338
E value	0.0e+00
Match length	430

% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	129809
Contig ID	35156_1.R1010
5'-most EST	jC-atXLIB327420P1g04b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	612
E value	0.0e+00
Match length	874
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	129810
Contig ID	35158_1.R1010
5'-most EST	jC-atXLIB327420P1g05b1
Method	BLASTX
NCBI GI	g4580393
BLAST score	651
E value	9.0e-68
Match length	275
% identity	45
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129811
Contig ID	35160_1.R1010
5'-most EST	jC-atXLIB327420P1h01b1
Method	BLASTX
NCBI GI	g2960364
BLAST score	266
E value	5.0e-23
Match length	62
% identity	77
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	129812
Contig ID	35169_1.R1010
5'-most EST	jC-atXLIB327420P1g06b1
Method	BLASTN
NCBI GI	g3702734
BLAST score	41
E value	2.0e-13
Match length	125
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	129813
Contig ID	35172_1.R1010
5'-most EST	LIB25-108-Q1-E1-G1

Seq. No.	129814
Contig ID	35176_1.R1010

5'-most EST	jC-atXLIB327420P4g01b1
Method	BLASTX
NCBI GI	g3152572
BLAST score	529
E value	6.0e-54
Match length	138
% identity	74
NCBI Description	(AC002986) Contains homology to DNAJ heatshock protein gb_U32803 from Haemophilus influenzae. [Arabidopsis thaliana]

Seq. No.	129815
Contig ID	35178_1.R1010
5'-most EST	jC-atXLIB327421P3g01b1
Method	BLASTX
NCBI GI	g4490314
BLAST score	141
E value	6.0e-53
Match length	132
% identity	87
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	129816
Contig ID	35179_1.R1010
5'-most EST	jC-atXLIB327420P4g02b1
Method	BLASTX
NCBI GI	g4567275
BLAST score	638
E value	1.0e-66
Match length	127
% identity	51
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129817
Contig ID	35180_1.R1010
5'-most EST	jC-atXLIB327420P1g11b1
Method	BLASTX
NCBI GI	g4826399
BLAST score	930
E value	1.0e-100
Match length	217
% identity	84
NCBI Description	(AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]

Seq. No.	129818
Contig ID	35188_1.R1010
5'-most EST	jC-atXLIB327420P4g07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	1.0e-24
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 129819

Contig ID	35189_1.R1010
5'-most EST	jC-atXLIB327420P3g02b1
Method	BLASTX
NCBI GI	g3445207
BLAST score	535
E value	4.0e-65
Match length	162
% identity	76
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	129820
Contig ID	35191_1.R1010
5'-most EST	jC-atXLIB327420P1f07b1
Method	BLASTX
NCBI GI	g4522012
BLAST score	516
E value	4.0e-52
Match length	216
% identity	52
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129821
Contig ID	35195_1.R1010
5'-most EST	LIB25-109-Q1-E1-A2
Method	BLASTX
NCBI GI	g1742187
BLAST score	146
E value	3.0e-09
Match length	105
% identity	30
NCBI Description	(D90771) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_ (D90772) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1787591 (AE000231) orf, hypothetical protein [Escherichia coli]

Seq. No.	129822
Contig ID	35200_1.R1010
5'-most EST	jC-atXLIB327420P1f12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	6.0e-20
Match length	76
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129823
Contig ID	35221_1.R1010
5'-most EST	jC-atXLIB327420P4f11b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	265
E value	1.0e-147
Match length	450
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	129824
Contig ID	35222_1.R1010
5'-most EST	jC-atXLIB327420P4f12b1
Method	BLASTX
NCBI GI	g3980412
BLAST score	183
E value	2.0e-13
Match length	148
% identity	6
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	129825
Contig ID	35225_1.R1010
5'-most EST	g1053493
Method	BLASTX
NCBI GI	g1914683
BLAST score	416
E value	1.0e-40
Match length	117
% identity	75
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	129826
Contig ID	35225_2.R1010
5'-most EST	jC-atXLIB327420P3f08b1
Method	BLASTX
NCBI GI	g1914683
BLAST score	525
E value	3.0e-53
Match length	139
% identity	78
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	129827
Contig ID	35227_1.R1010
5'-most EST	LIB25-109-Q1-E1-E1
Method	BLASTN
NCBI GI	g3056579
BLAST score	338
E value	0.0e+00
Match length	346
% identity	99
NCBI Description	Arabidopsis thaliana BAC T1F9 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	129828
Contig ID	35228_1.R1010
5'-most EST	jC-atXLIB327420P1g03b1
Method	BLASTN
NCBI GI	g2160155
BLAST score	767
E value	0.0e+00
Match length	1339
% identity	99

NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	129829
Contig ID	35230_1.R1010
5'-most EST	jC-atXLIB327420P3f12b1
Method	BLASTX
NCBI GI	g913631
BLAST score	192
E value	8.0e-18
Match length	128
% identity	38
NCBI Description	class-3 aldehyde dehydrogenase, class-3 ALDH [Synechococcus, PCC7942, Peptide, 459 aa] >gi_2351120_dbj_BAA22052_ (D32049) Aldehyde dehydrogenase [Synechococcus PCC7942] >gi_1092933_prf__2102241A aldehyde dehydrogenase [Synechococcus sp.]
Seq. No.	129830
Contig ID	35230_2.R1010
5'-most EST	LIB3175-064-P1-K1-E11
Method	BLASTX
NCBI GI	g913631
BLAST score	156
E value	2.0e-10
Match length	88
% identity	39
NCBI Description	class-3 aldehyde dehydrogenase, class-3 ALDH [Synechococcus, PCC7942, Peptide, 459 aa] >gi_2351120_dbj_BAA22052_ (D32049) Aldehyde dehydrogenase [Synechococcus PCC7942] >gi_1092933_prf__2102241A aldehyde dehydrogenase [Synechococcus sp.]
Seq. No.	129831
Contig ID	35239_1.R1010
5'-most EST	jC-atXP17C110C22T7s3
Method	BLASTN
NCBI GI	g2244788
BLAST score	594
E value	0.0e+00
Match length	598
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	129832
Contig ID	35243_1.R1010
5'-most EST	g2763978
Method	BLASTN
NCBI GI	g2244991
BLAST score	432
E value	0.0e+00
Match length	500
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 129833
Contig ID 35246_1.R1010
5'-most EST LIB25-109-Q1-E1-G11

Seq. No. 129834
Contig ID 35247_1.R1010
5'-most EST LIB25-109-Q1-E1-G12
Method BLASTN
NCBI GI g3241924
BLAST score 219
E value 1.0e-120
Match length 351
% identity 94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No. 129835
Contig ID 35254_1.R1010
5'-most EST jC-atXLIB327420P4g04b1

Seq. No. 129836
Contig ID 35281_1.R1010
5'-most EST g2733744
Method BLASTN
NCBI GI g2924651
BLAST score 397
E value 0.0e+00
Match length 734
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 129837
Contig ID 35281_2.R1010
5'-most EST LIB3234-003-P1-K1-A2
Method BLASTN
NCBI GI g2924651
BLAST score 35
E value 5.0e-10
Match length 289
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 129838
Contig ID 35283_1.R1010
5'-most EST LIB3175-062-P1-K1-B2

Seq. No. 129839
Contig ID 35297_2.R1010
5'-most EST g2723156

Seq. No. 129840
Contig ID 35299_1.R1010
5'-most EST ARABL1-038-Q1-B1-H9
Method BLASTN
NCBI GI g3335356

BLAST score 421
E value 0.0e+00
Match length 474
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 129841
Contig ID 35300_1.R1010
5'-most EST g493443

Seq. No. 129842
Contig ID 35306_1.R1010
5'-most EST ARABLI-043-Q1-B1-E8
Method BLASTX
NCBI GI g1293686
BLAST score 93
E value 7.0e-03
Match length 152
% identity 6
NCBI Description (U53925) Mus musculus transcription factor C1 mRNA, complete cds. [Mus musculus]

Seq. No. 129843
Contig ID 35309_1.R1010
5'-most EST g3719096
Method BLASTX
NCBI GI g2392772
BLAST score 440
E value 1.0e-89
Match length 200
% identity 87
NCBI Description (AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No. 129844
Contig ID 35325_1.R1010
5'-most EST LIB3176-028-P1-K1-F1
Method BLASTX
NCBI GI g2459432
BLAST score 522
E value 3.0e-53
Match length 98
% identity 97
NCBI Description (AC002332) CONSTANS-like protein [Arabidopsis thaliana]

Seq. No. 129845
Contig ID 35328_1.R1010
5'-most EST LIB25-110-Q1-E1-H1

Seq. No. 129846
Contig ID 35340_1.R1010
5'-most EST LIB3168-004-P1-K1-D1
Method BLASTX
NCBI GI g2326363
BLAST score 935
E value 1.0e-101

Match length	199
% identity	92
NCBI Description	(AJ001037) DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No.	129847
Contig ID	35342_1.R1010
5'-most EST	g2047830
Method	BLASTX
NCBI GI	g3152585
BLAST score	302
E value	3.0e-27
Match length	107
% identity	63
NCBI Description	(AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis thaliana]

Seq. No.	129848
Contig ID	35349_1.R1010
5'-most EST	LIB25-111-Q1-E1-B5
Method	BLASTX
NCBI GI	g4115371
BLAST score	479
E value	6.0e-48
Match length	154
% identity	64
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	129849
Contig ID	35353_1.R1010
5'-most EST	g2759237
Method	BLASTX
NCBI GI	g3298536
BLAST score	673
E value	6.0e-71
Match length	151
% identity	89
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	129850
Contig ID	35356_1.R1010
5'-most EST	LIB25-111-Q1-E1-C2
Method	BLASTX
NCBI GI	g4734009
BLAST score	151
E value	2.0e-76
Match length	296
% identity	47
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129851
Contig ID	35376_1.R1010
5'-most EST	LIB3176-027-P1-K1-G11
Method	BLASTN
NCBI GI	g3449334
BLAST score	156

E value	2.0e-82
Match length	284
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	129852
Contig ID	35398_1.R1010
5'-most EST	g2393711
Method	BLASTN
NCBI GI	g4220468
BLAST score	477
E value	0.0e+00
Match length	498
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129853
Contig ID	35398_2.R1010
5'-most EST	jC-atXP8C92P6T7s1
Method	BLASTN
NCBI GI	g4220468
BLAST score	381
E value	0.0e+00
Match length	538
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129854
Contig ID	35405_1.R1010
5'-most EST	jC-atXP25C125F24T7d1
Method	BLASTN
NCBI GI	g3449321
BLAST score	84
E value	6.0e-39
Match length	377
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	129855
Contig ID	35406_1.R1010
5'-most EST	LIB35-028-Q1-E1-A3
Method	BLASTN
NCBI GI	g4757395
BLAST score	61
E value	1.0e-25
Match length	123
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	129856
Contig ID	35409_1.R1010
5'-most EST	g2062884

Method	BLASTX
NCBI GI	g2632106
BLAST score	235
E value	1.0e-19
Match length	68
% identity	72
NCBI Description	(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	129857
Contig ID	35413_1.R1010
5'-most EST	g2749518

Seq. No.	129858
Contig ID	35413_2.R1010
5'-most EST	jC-atXLIB327420P4g12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129859
Contig ID	35414_1.R1010
5'-most EST	jC-atXP94CH5H7T7066d1
Method	BLASTX
NCBI GI	g4567197
BLAST score	314
E value	1.0e-28
Match length	95
% identity	64
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	129860
Contig ID	35414_2.R1010
5'-most EST	jC-atXLIB327420P3g12b1
Method	BLASTX
NCBI GI	g4567197
BLAST score	325
E value	5.0e-30
Match length	68
% identity	79
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	129861
Contig ID	35423_1.R1010
5'-most EST	jC-atXLIB327420P1h08b1
Method	BLASTN
NCBI GI	g2564049
BLAST score	270
E value	1.0e-150
Match length	810
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	129862
Contig ID	35424_1.R1010
5'-most EST	jC-atXLIB327420P1h09b1
Method	BLASTX
NCBI GI	g4105697
BLAST score	706
E value	1.0e-97
Match length	227
% identity	76
NCBI Description	(AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	129863
Contig ID	35426_1.R1010
5'-most EST	LIB35-003-Q1-E1-A1

Seq. No.	129864
Contig ID	35428_1.R1010
5'-most EST	jC-atXLIB327420P3h12b1
Method	BLASTX
NCBI GI	g166341
BLAST score	465
E value	3.0e-46
Match length	184
% identity	47
NCBI Description	(M98267) alliinase [Allium cepa] >gi_1044969 (L48614) allinase [Allium cepa]

Seq. No.	129865
Contig ID	35433_1.R1010
5'-most EST	LIB35-055-Q1-E2-B4
Method	BLASTX
NCBI GI	g3980401
BLAST score	916
E value	5.0e-99
Match length	258
% identity	68
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	129866
Contig ID	35438_1.R1010
5'-most EST	jC-atXLIB327420P4h07b1
Method	BLASTX
NCBI GI	g3608153
BLAST score	770
E value	3.0e-82
Match length	148
% identity	100
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129867
Contig ID	35440_1.R1010
5'-most EST	jC-atXLIB327420P4h08b1
Method	BLASTX
NCBI GI	g4581116
BLAST score	813
E value	3.0e-87

Match length	153
% identity	97
NCBI Description	(AC005825) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	129868
Contig ID	35446_1.R1010
5'-most EST	jC-atXLIB327427P3a12b2
Method	BLASTX
NCBI GI	g1941990
BLAST score	213
E value	7.0e-17
Match length	66
% identity	55
NCBI Description	Human Rantes

Seq. No.	129869
Contig ID	35446_2.R1010
5'-most EST	LIB25-112-Q1-E1-D2
Method	BLASTX
NCBI GI	g2956783
BLAST score	168
E value	8.0e-12
Match length	50
% identity	54
NCBI Description	(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq. No.	129870
Contig ID	35452_1.R1010
5'-most EST	jC-atXLIB327421P1a07a1
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	3.0e-17
Match length	109
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	129871
Contig ID	35454_1.R1010
5'-most EST	jC-atX25112Q1E1E10b1
Method	BLASTX
NCBI GI	g3420982
BLAST score	254
E value	8.0e-22
Match length	123
% identity	40
NCBI Description	(Z97628) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans] >gi_3876969_emb_CAB03088_ (Z81080) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans]

Seq. No.	129872
Contig ID	35455_1.R1010
5'-most EST	jC-atXLIB327421P3a05b1

Method	BLASTX
NCBI GI	g4262235
BLAST score	367
E value	5.0e-35
Match length	99
% identity	75
NCBI Description	(AC006200) putative transcription factor [Arabidopsis thaliana]

Seq. No.	129873
Contig ID	35459_1.R1010
5'-most EST	jC-atXLIB327430P2b12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	4.0e-16
Match length	74
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129874
Contig ID	35469_1.R1010
5'-most EST	jC-atXLIB327421P1b03b1
Method	BLASTN
NCBI GI	g3643588
BLAST score	444
E value	0.0e+00
Match length	456
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129875
Contig ID	35474_1.R1010
5'-most EST	LIB25-112-Q1-E1-G1
Method	BLASTN
NCBI GI	g4757392
BLAST score	236
E value	1.0e-130
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	129876
Contig ID	35480_1.R1010
5'-most EST	jC-atXLIB327421P3b01b1
Method	BLASTX
NCBI GI	g3360289
BLAST score	791
E value	2.0e-84
Match length	249
% identity	60
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	129877
Contig ID	35482_1.R1010
5'-most EST	jC-atXLIB327421P2b09b1
Method	BLASTX
NCBI GI	g2997591
BLAST score	636
E value	2.0e-66
Match length	164
% identity	76
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	129878
Contig ID	35487_1.R1010
5'-most EST	jC-atXLIB327421P3b11b1
Method	BLASTX
NCBI GI	g3935154
BLAST score	743
E value	4.0e-79
Match length	143
% identity	100
NCBI Description	(AC005106) T25N20.18 [Arabidopsis thaliana]

Seq. No.	129879
Contig ID	35489_1.R1010
5'-most EST	jC-atXLIB327421P3b07b1
Method	BLASTX
NCBI GI	g2244956
BLAST score	154
E value	5.0e-10
Match length	136
% identity	29
NCBI Description	(Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	129880
Contig ID	35491_1.R1010
5'-most EST	jC-atXLIB327421P3b08b1
Method	BLASTX
NCBI GI	g3522935
BLAST score	610
E value	2.0e-63
Match length	140
% identity	89
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	129881
Contig ID	35495_1.R1010
5'-most EST	g937267
Method	BLASTX
NCBI GI	g3341672
BLAST score	414
E value	5.0e-56
Match length	147
% identity	79
NCBI Description	(AC003672) putative heme A:farnesyltransferase, 5' partial

[Arabidopsis thaliana]

Seq. No.	129882
Contig ID	35501_1.R1010
5'-most EST	LIB25-113-Q1-E1-B1

Seq. No.	129883
Contig ID	35503_1.R1010
5'-most EST	LIB25-113-Q1-E1-B11
Method	BLASTX
NCBI GI	g4585984
BLAST score	485
E value	4.0e-79
Match length	178
% identity	83
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	129884
Contig ID	35531_1.R1010
5'-most EST	jC-atXLIB327421P2a06b1
Method	BLASTN
NCBI GI	g4757407
BLAST score	240
E value	1.0e-132
Match length	462
% identity	75
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	129885
Contig ID	35539_1.R1010
5'-most EST	jC-atXLIB327421P3a03b1
Method	BLASTX
NCBI GI	g4678946
BLAST score	558
E value	2.0e-57
Match length	108
% identity	100
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	129886
Contig ID	35540_1.R1010
5'-most EST	jC-atXLIB327421P4a04b1
Method	BLASTX
NCBI GI	g4586061
BLAST score	666
E value	5.0e-70
Match length	142
% identity	90
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]

Seq. No.	129887
Contig ID	35543_1.R1010
5'-most EST	LIB25-113-Q1-E1-F10
Method	BLASTN
NCBI GI	g4454447
BLAST score	416

E value	0.0e+00
Match length	468
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129888
Contig ID	35544_1.R1010
5'-most EST	LIB25-113-Q1-E1-F11
Method	BLASTX
NCBI GI	g3152556
BLAST score	185
E value	2.0e-15
Match length	82
% identity	52
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. [Arabidopsis thaliana]

Seq. No.	129889
Contig ID	35546_1.R1010
5'-most EST	jC-atXLIB327421P2b02b1
Method	BLASTX
NCBI GI	g4586058
BLAST score	376
E value	5.0e-36
Match length	140
% identity	59
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	129890
Contig ID	35549_1.R1010
5'-most EST	jC-atXLIB327421P4a10b1
Method	BLASTX
NCBI GI	g3482974
BLAST score	463
E value	3.0e-46
Match length	147
% identity	65
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	129891
Contig ID	35558_3.R1010
5'-most EST	LIB25-113-Q1-E1-G4
Method	BLASTX
NCBI GI	g3150406
BLAST score	867
E value	2.0e-93
Match length	165
% identity	98
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	129892
Contig ID	35561_1.R1010
5'-most EST	jC-atXLIB327421P1b10b1

Method	BLASTN
NCBI GI	g4589424
BLAST score	93
E value	2.0e-44
Match length	175
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No.	129893
Contig ID	35566_1.R1010
5'-most EST	jC-alX25114Q1E1H10b1
Method	BLASTX
NCBI GI	g4538943
BLAST score	544
E value	3.0e-68
Match length	156
% identity	79
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	129894
Contig ID	35587_1.R1010
5'-most EST	jC-atXLIB327431P2h12b1
Method	BLASTX
NCBI GI	g1172556
BLAST score	401
E value	4.0e-40
Match length	202
% identity	46
NCBI Description	36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin II [Solanum tuberosum]

Seq. No.	129895
Contig ID	35602_1.R1010
5'-most EST	jC-atXLIB327420P3h01b1
Method	BLASTN
NCBI GI	g4580454
BLAST score	236
E value	1.0e-130
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	129896
Contig ID	35606_1.R1010
5'-most EST	jC-atXLIB327430P1b10b1
Method	BLASTN
NCBI GI	g4092472
BLAST score	384
E value	0.0e+00
Match length	536

% identity	47
NCBI Description	Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	129897
Contig ID	35609_1.R1010
5'-most EST	jC-atXLIB327421P4b07b1
Method	BLASTX
NCBI GI	g3122065
BLAST score	407
E value	4.0e-45
Match length	272
% identity	40
NCBI Description	PROBABLE PEROXISOMAL ENOYL-COA HYDRATASE >gi_2606086 (AF030343) ECH1p [Mus musculus]

Seq. No.	129898
Contig ID	35617_1.R1010
5'-most EST	jC-atXP34C153B20T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	46
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	129899
Contig ID	35617_2.R1010
5'-most EST	jC-atXP34C153B20T7d1
Method	BLASTN
NCBI GI	g4371278
BLAST score	35
E value	7.0e-10
Match length	79
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129900
Contig ID	35617_3.R1010
5'-most EST	jC-atXLIB327421P2a11b1

Seq. No.	129901
Contig ID	35617_4.R1010
5'-most EST	jC-atXLIB327407P1b07a2
Method	BLASTX
NCBI GI	g4584527
BLAST score	181
E value	4.0e-13
Match length	62
% identity	53
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	129902
Contig ID	35617_6.R1010
5'-most EST	g507078

Seq. No.	129903
Contig ID	35619_1.R1010
5'-most EST	jC-atX25108Q1E1H03b1
Method	BLASTN
NCBI GI	g3128142
BLAST score	46
E value	9.0e-17
Match length	178
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	129904
Contig ID	35625_1.R1010
5'-most EST	LIB25-114-Q1-E1-E9
Method	BLASTX
NCBI GI	g2832717
BLAST score	602
E value	1.0e-62
Match length	130
% identity	87
NCBI Description	(AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No.	129905
Contig ID	35629_1.R1010
5'-most EST	LIB25-114-Q1-E1-F5
Method	BLASTX
NCBI GI	g3135271
BLAST score	225
E value	2.0e-18
Match length	67
% identity	60
NCBI Description	(AC003058) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	129906
Contig ID	35631_1.R1010
5'-most EST	jC-atXLIB327421P3a07b1
Method	BLASTX
NCBI GI	g1176658
BLAST score	274
E value	4.0e-24
Match length	119
% identity	45
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	129907
Contig ID	35643_1.R1010
5'-most EST	jC-atXLIB327421P2b04b1
Method	BLASTX
NCBI GI	g3164132
BLAST score	373
E value	2.0e-41
Match length	135

% identity	67
NCBI Description	(D78601) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	129908
Contig ID	35651_1.R1010
5'-most EST	jC-atXLIB327430P4b02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	70
E value	7.0e-31
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129909
Contig ID	35678_1.R1010
5'-most EST	jC-atXLIB327420P4h03b1
Method	BLASTN
NCBI GI	g3108025
BLAST score	439
E value	0.0e+00
Match length	501
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	129910
Contig ID	35680_1.R1010
5'-most EST	jC-atXLIB327420P3h04b1
Method	BLASTX
NCBI GI	g4539008
BLAST score	661
E value	3.0e-69
Match length	173
% identity	82
NCBI Description	(AL049481) lipase-like protein [Arabidopsis thaliana]

Seq. No.	129911
Contig ID	35697_1.R1010
5'-most EST	jC-atXLIB327421P1a11b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	379
E value	0.0e+00
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	129912
Contig ID	35698_1.R1010
5'-most EST	jC-atXLIB327421P1a12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	70

E value	9.0e-31
Match length	78
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129913
Contig ID	35700_1.R1010
5'-most EST	jC-atXLIB327421P4a02b1
Method	BLASTX
NCBI GI	g3367528
BLAST score	454
E value	4.0e-45
Match length	111
% identity	83
NCBI Description	(AC004392) Strong similarity to gi_2160138 F19K23.6 gene product from A. thaliana BAC gb_AC000375. [Arabidopsis thaliana]

Seq. No.	129914
Contig ID	35705_1.R1010
5'-most EST	LIB3175-024-P1-K1-B2
Method	BLASTX
NCBI GI	g4512712
BLAST score	345
E value	3.0e-32
Match length	92
% identity	72
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	129915
Contig ID	35715_1.R1010
5'-most EST	jC-atXLIB327421P1b05b1
Method	BLASTX
NCBI GI	g3582436
BLAST score	459
E value	9.0e-46
Match length	153
% identity	58
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	129916
Contig ID	35716_1.R1010
5'-most EST	jC-atXLIB327421P1b06b1
Method	BLASTN
NCBI GI	g2244829
BLAST score	285
E value	1.0e-159
Match length	354
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	129917
Contig ID	35722_1.R1010
5'-most EST	jC-atXLIB327421P2b03b1
Method	BLASTX

NCBI GI	g4678924
BLAST score	403
E value	5.0e-39
Match length	174
% identity	49
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	129918
Contig ID	35730_1.R1010
5'-most EST	jC-atXLIB327421P3b06b1
Method	BLASTX
NCBI GI	g1086900
BLAST score	256
E value	5.0e-22
Match length	132
% identity	40
NCBI Description	(U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]

Seq. No.	129919
Contig ID	35735_1.R1010
5'-most EST	LIB25-115-Q1-E1-H9
Method	BLASTN
NCBI GI	g3201608
BLAST score	217
E value	1.0e-119
Match length	217
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129920
Contig ID	35742_1.R1010
5'-most EST	LIB25-116-Q1-E1-A6
Method	BLASTX
NCBI GI	g3335359
BLAST score	380
E value	1.0e-36
Match length	77
% identity	100
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	129921
Contig ID	35752_1.R1010
5'-most EST	jC-atXLIB327421P4c01b1
Method	BLASTX
NCBI GI	g3668074
BLAST score	511
E value	7.0e-52
Match length	96
% identity	100
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129922
Contig ID	35754_1.R1010
5'-most EST	jC-atXLIB327421P1c09b1

Method	BLASTX
NCBI GI	g2462822
BLAST score	580
E value	1.0e-59
Match length	121
% identity	35
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129923
Contig ID	35763_1.R1010
5'-most EST	jC-atXLIB327421P1c03b1
Method	BLASTX
NCBI GI	g4646219
BLAST score	787
E value	1.0e-156
Match length	322
% identity	84
NCBI Description	(AC007290) purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	129924
Contig ID	35764_1.R1010
5'-most EST	jC-atXLIB327421P3c03b1
Method	BLASTN
NCBI GI	g3128142
BLAST score	382
E value	0.0e+00
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	129925
Contig ID	35767_1.R1010
5'-most EST	jC-atXLIB327421P3c06b1
Method	BLASTN
NCBI GI	g4455348
BLAST score	467
E value	0.0e+00
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	129926
Contig ID	35782_1.R1010
5'-most EST	jC-atXLIB327421P1d04b1
Method	BLASTN
NCBI GI	g2696018
BLAST score	135
E value	1.0e-69
Match length	444
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 129927

Contig ID	35783_1.R1010
5'-most EST	jC-atXLIB327421P1d05b1
Method	BLASTX
NCBI GI	g2492613
BLAST score	446
E value	9.0e-44
Match length	329
% identity	33
NCBI Description	FLAVONOL SYNTHASE (FLS) >gi_1039357_emb_CAA63092_ (X92178) flavonol synthase [Solanum tuberosum]

Seq. No.	129928
Contig ID	35783_3.R1010
5'-most EST	jC-atXLIB327414P3e10a1
Method	BLASTX
NCBI GI	g4115913
BLAST score	245
E value	1.0e-20
Match length	129
% identity	36
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_ (AL049524) putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	129929
Contig ID	35790_1.R1010
5'-most EST	jC-atXLIB327421P2d08b1
Method	BLASTX
NCBI GI	g2244793
BLAST score	161
E value	7.0e-11
Match length	129
% identity	36
NCBI Description	(Z97336) TMV resistance protein homolog [Arabidopsis thaliana]

Seq. No.	129930
Contig ID	35793_1.R1010
5'-most EST	jC-atXLIB327421P1d10b1
Method	BLASTN
NCBI GI	g2618600
BLAST score	102
E value	7.0e-50
Match length	436
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	129931
Contig ID	35796_1.R1010
5'-most EST	jC-atXLIB327421P2d06b1
Method	BLASTN
NCBI GI	g2392762
BLAST score	645
E value	0.0e+00

Match length	670
% identity	99
NCBI Description	Arabidopsis thaliana BAC T32N15 from chromsome III near 54 cM, complete sequence

Seq. No.	129932
Contig ID	35797_1.R1010
5'-most EST	jC-atXLIB327421P1d07b1
Method	BLASTN
NCBI GI	g3869066
BLAST score	207
E value	1.0e-113
Match length	215
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	129933
Contig ID	35804_1.R1010
5'-most EST	LIB25-116-Q1-E1-G3
Method	BLASTX
NCBI GI	g2316022
BLAST score	323
E value	2.0e-74
Match length	181
% identity	86
NCBI Description	(U96399) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	129934
Contig ID	35806_1.R1010
5'-most EST	jC-atXLIB327421P3d02b1
Method	BLASTX
NCBI GI	g3157945
BLAST score	446
E value	3.0e-44
Match length	136
% identity	72
NCBI Description	(AC002131) Contains similarity to axi 1 gene gb_X80301 from Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No.	129935
Contig ID	35810_1.R1010
5'-most EST	jC-atXLIB327421P4d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129936
Contig ID	35810_2.R1010
5'-most EST	jC-atXLIB327423P4e06b1
Method	BLASTX
NCBI GI	g3297821

BLAST score 287
E value 1.0e-25
Match length 118
% identity 14
NCBI Description (AL031032) extensin-like protein [Arabidopsis thaliana]

Seq. No. 129937
Contig ID 35810_3.R1010
5'-most EST g2757667
Method BLASTX
NCBI GI g1076802
BLAST score 189
E value 3.0e-14
Match length 101
% identity 42
NCBI Description extensin-like protein - maize >gi_600118_emb_CAA84230_ (Z34465) extensin-like protein [Zea mays] >gi_1096557_prf__2111476A extensin-like domain [Zea mays]

Seq. No. 129938
Contig ID 35822_1.R1010
5'-most EST jC-atXLIB327421P2c05b1
Method BLASTX
NCBI GI g2832697
BLAST score 632
E value 7.0e-66
Match length 145
% identity 88
NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 129939
Contig ID 35830_1.R1010
5'-most EST jC-atXLIB327421P2c11b1
Method BLASTX
NCBI GI g465713
BLAST score 222
E value 6.0e-18
Match length 102
% identity 44
NCBI Description HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION >gi_539191_pir__S37926 hypothetical protein YKL099c - yeast (Saccharomyces cerevisiae) >gi_431217_emb_CAA50458_ (X71133) YKL449 [Saccharomyces cerevisiae] >gi_486165_emb_CAA81939_ (Z28099) ORF YKL099c [Saccharomyces cerevisiae]

Seq. No. 129940
Contig ID 35831_1.R1010
5'-most EST jC-atXLIB327439P2b06b2
Method BLASTN
NCBI GI g4006815
BLAST score 355
E value 0.0e+00
Match length 404
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129941
Contig ID	35834_1.R1010
5'-most EST	LIB35-051-Q1-E1-B9
Method	BLASTN
NCBI GI	g1742970
BLAST score	161
E value	2.0e-85
Match length	314
% identity	100
NCBI Description	A.thaliana genes encoding mitochondrial DNA-directed RNA polymerase, tRNA-Met initiator and ORF with unknown function

Seq. No.	129942
Contig ID	35844_1.R1010
5'-most EST	jC-atXLIB327421P4c04b1
Method	BLASTX
NCBI GI	g4581146
BLAST score	717
E value	8.0e-76
Match length	142
% identity	100
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	129943
Contig ID	35855_1.R1010
5'-most EST	g2759307

Seq. No.	129944
Contig ID	35862_1.R1010
5'-most EST	jC-atXLIB327421P1d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	129945
Contig ID	35864_1.R1010
5'-most EST	jC-atXLIB327421P2d09b1
Method	BLASTX
NCBI GI	g2245065
BLAST score	115
E value	2.0e-05
Match length	85
% identity	13
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129946
Contig ID	35864_2.R1010
5'-most EST	LIB3234-089-P1-K1-E2
Method	BLASTX

NCBI GI	g3668087
BLAST score	283
E value	2.0e-25
Match length	74
% identity	21
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	129947
Contig ID	35866_1.R1010
5'-most EST	jC-atXLIB327421P1d06b1
Method	BLASTX
NCBI GI	g4512627
BLAST score	590
E value	4.0e-61
Match length	148
% identity	82
NCBI Description	(AC004793) Similar to gb_Z29643 protein kinase C inhibitor (PKCI) from Zea mays and a member of HIT family PF_01230. [Arabidopsis thaliana]

Seq. No.	129948
Contig ID	35882_1.R1010
5'-most EST	jC-atXLIB327421P4d04b1
Method	BLASTX
NCBI GI	g480725
BLAST score	513
E value	4.0e-52
Match length	133
% identity	73
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	129949
Contig ID	35889_1.R1010
5'-most EST	LIB3234-077-P1-K1-A3
Method	BLASTX
NCBI GI	g3915961
BLAST score	969
E value	1.0e-105
Match length	224
% identity	86
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	129950
Contig ID	35945_1.R1010
5'-most EST	LIB3168-001-P1-K1-F2
Method	BLASTX
NCBI GI	g133406
BLAST score	164
E value	3.0e-11
Match length	34

% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_81501_pir__C23525 DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - spinach chloroplast >gi_12265_emb_CAA27214_ (X03496) pot. RNA polymerase alpha subunit (aa 1-335) [Spinacia oleracea]
Seq. No.	129951
Contig ID	35958_1.R1010
5'-most EST	LIB3168-070-P1-K1-A10
Method	BLASTX
NCBI GI	g3281855
BLAST score	510
E value	2.0e-53
Match length	138
% identity	79
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]
Seq. No.	129952
Contig ID	35961_1.R1010
5'-most EST	LIB3168-026-P1-K1-C8
Seq. No.	129953
Contig ID	36022_1.R1010
5'-most EST	LIB3168-002-P1-K1-E6
Method	BLASTN
NCBI GI	g3985950
BLAST score	571
E value	0.0e+00
Match length	611
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.	129954
Contig ID	36029_1.R1010
5'-most EST	LIB3234-058-P1-K1-D6
Method	BLASTN
NCBI GI	g3068702
BLAST score	95
E value	1.0e-45
Match length	95
% identity	100
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put
Seq. No.	129955
Contig ID	36038_1.R1010
5'-most EST	LIB3168-060-P1-K1-C11
Method	BLASTN
NCBI GI	g343498
BLAST score	229
E value	1.0e-126
Match length	405
% identity	93

NCBI Description	Tobacco chloroplast Arg-tRNA and Asn-tRNA 4.5S and 5S rRNA genes
Seq. No.	129956
Contig ID	36039_1.R1010
5'-most EST	g493467
Seq. No.	129957
Contig ID	36059_1.R1010
5'-most EST	LIB3168-003-P1-K1-A2
Seq. No.	129958
Contig ID	36069_1.R1010
5'-most EST	LIB3168-003-P1-K1-C7
Method	BLASTX
NCBI GI	g4455200
BLAST score	393
E value	3.0e-38
Match length	87
% identity	95
NCBI Description	(AL035440) putative CDP-diacylglycerol synthetase [Arabidopsis thaliana]
Seq. No.	129959
Contig ID	36084_1.R1010
5'-most EST	LIB3168-004-P1-K1-A7
Method	BLASTN
NCBI GI	g2828181
BLAST score	269
E value	1.0e-150
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE8, complete sequence [Arabidopsis thaliana]
Seq. No.	129960
Contig ID	36099_1.R1010
5'-most EST	jC-atXP37C157P4T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	8.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	129961
Contig ID	36099_2.R1010
5'-most EST	jC-alXLIB327436P2e07a1
Seq. No.	129962
Contig ID	36124_1.R1010
5'-most EST	LIB3234-011-P1-K1-D8
Method	BLASTX
NCBI GI	g114661
BLAST score	769
E value	6.0e-82

Match length 167
% identity 88
NCBI Description ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) >gi_67924_pir__LWNT6 H+-transporting ATP synthase (EC 3.6.1.34) chain a - common tobacco chloroplast >gi_11813_emb_CAA77344_ (Z00044) ATPase sunthase IV subunit [Nicotiana tabacum] >gi_225273_prf__1211235H ATPase a [Nicotiana tabacum]

Seq. No. 129963
Contig ID 36128_1.R1010
5'-most EST LIB3168-004-P1-K1-F6

Seq. No. 129964
Contig ID 36130_1.R1010
5'-most EST jC-atXP71C222M6T7044d1
Method BLASTX
NCBI GI g1321818
BLAST score 234
E value 3.0e-19
Match length 200
% identity 34
NCBI Description (X95455) RING zinc finger protein [Gallus gallus] >gi_1589724_prf__2211437A RING finger protein [Gallus gallus]

Seq. No. 129965
Contig ID 36163_1.R1010
5'-most EST jC-atXLIB327431P4d08a1
Method BLASTX
NCBI GI g4455358
BLAST score 871
E value 1.0e-93
Match length 218
% identity 83
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 129966
Contig ID 36163_3.R1010
5'-most EST g2758011
Method BLASTN
NCBI GI g4455348
BLAST score 295
E value 1.0e-165
Match length 333
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No. 129967
Contig ID 36174_1.R1010
5'-most EST LIB3168-058-P1-K1-G6

Seq. No. 129968
Contig ID 36211_2.R1010
5'-most EST jC-atX22031Q1E1C01a2
Method BLASTX

NCBI GI	g4510377
BLAST score	143
E value	9.0e-16
Match length	102
% identity	57
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	129969
Contig ID	36234_1.R1010
5'-most EST	LIB3234-095-P1-K1-A5

Seq. No.	129970
Contig ID	36239_1.R1010
5'-most EST	LIB3175-034-P1-K1-H5
Method	BLASTN
NCBI GI	g4455262
BLAST score	101
E value	2.0e-49
Match length	405
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	129971
Contig ID	36240_1.R1010
5'-most EST	LIB3175-046-P1-K1-D5
Method	BLASTX
NCBI GI	g2887500
BLAST score	338
E value	1.0e-31
Match length	70
% identity	84
NCBI Description	(AC002339) putative AP2 domain-containing protein [Arabidopsis thaliana]

Seq. No.	129972
Contig ID	36243_1.R1010
5'-most EST	LIB3168-006-P1-K1-B7

Seq. No.	129973
Contig ID	36277_1.R1010
5'-most EST	LIB3168-076-P1-K1-B4
Method	BLASTX
NCBI GI	g3367515
BLAST score	1266
E value	1.0e-140
Match length	254
% identity	97
NCBI Description	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No.	129974
Contig ID	36311_1.R1010
5'-most EST	LIB3168-006-P1-K1-H8
Method	BLASTX
NCBI GI	g2827635

BLAST score	639
E value	8.0e-67
Match length	138
% identity	93
NCBI Description	(AL021636) predicted protein [Arabidopsis thaliana]

Seq. No.	129975
Contig ID	36326_1.R1010
5'-most EST	g2747678
Method	BLASTN
NCBI GI	g4589428
BLAST score	128
E value	2.0e-65
Match length	398
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	129976
Contig ID	36330_1.R1010
5'-most EST	LIB3168-007-P1-K1-B7
Method	BLASTN
NCBI GI	g3309276
BLAST score	203
E value	1.0e-110
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3 cM, complete sequence

Seq. No.	129977
Contig ID	36345_1.R1010
5'-most EST	LIB3168-007-P1-K1-D11
Method	BLASTX
NCBI GI	g3367534
BLAST score	726
E value	6.0e-77
Match length	164
% identity	91
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	129978
Contig ID	36346_1.R1010
5'-most EST	LIB3168-007-P1-K1-D12
Method	BLASTX
NCBI GI	g441457
BLAST score	561
E value	1.0e-69
Match length	148
% identity	84
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	129979
Contig ID	36433_1.R1010

5'-most EST	LIB3168-009-P1-K1-D2
Method	BLASTX
NCBI GI	g2982437
BLAST score	534
E value	1.0e-54
Match length	155
% identity	66
NCBI Description	(AL022224) terpene cyclase like protein [Arabidopsis thaliana]

Seq. No.	129980
Contig ID	36435_2.R1010
5'-most EST	jC-atXP104CE8A8T7b1

Seq. No.	129981
Contig ID	36435_3.R1010
5'-most EST	LIB3168-009-P1-K1-D5
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	1.0e-15
Match length	65
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	129982
Contig ID	36458_1.R1010
5'-most EST	LIB3168-009-P1-K1-F5

Seq. No.	129983
Contig ID	36461_1.R1010
5'-most EST	LIB3168-009-P1-K1-F8
Method	BLASTX
NCBI GI	g2894378
BLAST score	564
E value	4.0e-58
Match length	156
% identity	69
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	129984
Contig ID	36480_1.R1010
5'-most EST	LIB3168-009-P1-K1-H8
Method	BLASTX
NCBI GI	g128877
BLAST score	343
E value	3.0e-32
Match length	100
% identity	73
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4L, CHLOROPLAST >gi_66167_pir__DENTNL NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - common tobacco chloroplast >gi_1223668_emb_CAA77396_ (Z00044) NADH dehydrogenase ND4L subunit [Nicotiana tabacum] >gi_225256_prf__1211235CQ NADH dehydrogenase 4L-like ORF 101 [Nicotiana tabacum]

Seq. No.	129985

Contig ID	36515_1.R1010
5'-most EST	LIB3168-010-P1-K1-F6
Method	BLASTN
NCBI GI	g3789706
BLAST score	171
E value	3.0e-91
Match length	361
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	129986
Contig ID	36520_1.R1010
5'-most EST	LIB3175-042-P1-K1-H2
Method	BLASTX
NCBI GI	g2244799
BLAST score	170
E value	8.0e-43
Match length	151
% identity	71
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No.	129987
Contig ID	36522_1.R1010
5'-most EST	LIB3176-033-P1-K1-F3
Method	BLASTX
NCBI GI	g133438
BLAST score	1156
E value	1.0e-127
Match length	246
% identity	89
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA' CHAIN >gi_81504_pir__B29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - spinach chloroplast >gi_295120 (M55297) RNA polymerase [Spinacia oleracea]

Seq. No.	129988
Contig ID	36525_1.R1010
5'-most EST	jC-atXLIB327411P1e12b1
Method	BLASTX
NCBI GI	g4580519
BLAST score	428
E value	5.0e-42
Match length	170
% identity	54
NCBI Description	(AF036303) scarecrow-like 6 [Arabidopsis thaliana]

Seq. No.	129989
Contig ID	36529_1.R1010
5'-most EST	LIB3168-010-P1-K1-E4
Method	BLASTN
NCBI GI	g397397
BLAST score	293
E value	1.0e-163
Match length	345
% identity	97
NCBI Description	A.thaliana chloroplast trnL gene, intron

Seq. No.	129990
Contig ID	36534_1.R1010
5'-most EST	g957614
Method	BLASTX
NCBI GI	g3688188
BLAST score	439
E value	6.0e-57
Match length	123
% identity	99
NCBI Description	(AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis thaliana]

Seq. No.	129991
Contig ID	36537_1.R1010
5'-most EST	LIB3234-059-P1-K1-D12
Method	BLASTN
NCBI GI	g2828185
BLAST score	166
E value	4.0e-88
Match length	584
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	129992
Contig ID	36559_1.R1010
5'-most EST	LIB3234-076-P1-K1-F5
Method	BLASTN
NCBI GI	g3860242
BLAST score	385
E value	0.0e+00
Match length	468
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence

Seq. No.	129993
Contig ID	36603_1.R1010
5'-most EST	LIB3234-010-P1-K1-C3
Method	BLASTX
NCBI GI	g82207
BLAST score	1373
E value	1.0e-152
Match length	283
% identity	94
NCBI Description	hypothetical protein 1708 - common tobacco chloroplast

Seq. No.	129994
Contig ID	36606_1.R1010
5'-most EST	LIB3234-070-P1-K1-G9
Method	BLASTX
NCBI GI	g3819164
BLAST score	643
E value	4.0e-75
Match length	162
% identity	86

NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No. 129995
Contig ID 36669_1.R1010
5'-most EST g937148

Seq. No. 129996
Contig ID 36676_1.R1010
5'-most EST jC-atXP27C131M21T7d2
Method BLASTN
NCBI GI g3702730
BLAST score 51
E value 1.0e-19
Match length 176
% identity 92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence [Arabidopsis thaliana]

Seq. No. 129997
Contig ID 36698_1.R1010
5'-most EST jC-atX25020Q1E1E05a2
Method BLASTN
NCBI GI g3873174
BLAST score 509
E value 0.0e+00
Match length 513
% identity 100
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No. 129998
Contig ID 36704_1.R1010
5'-most EST LIB3234-087-Q1-K1-H10
Method BLASTX
NCBI GI g2129767
BLAST score 2426
E value 0.0e+00
Match length 486
% identity 94
NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 129999
Contig ID 36717_1.R1010
5'-most EST g935122
Method BLASTX
NCBI GI g633890
BLAST score 539
E value 5.0e-55
Match length 128
% identity 80
NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No. 130000

Contig ID	36760_1.R1010
5'-most EST	LIB3168-013-P1-K1-C12
Method	BLASTX
NCBI GI	g1351837
BLAST score	1005
E value	1.0e-109
Match length	210
% identity	91
NCBI Description	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II beta-carboxyltransferase chain - rape chloroplast >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase carboxyltransferase (beta subunit) [Brassica napus] >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta [Brassica napus]

Seq. No.	130001
Contig ID	36799_1.R1010
5'-most EST	g2756683
Method	BLASTN
NCBI GI	g4757392
BLAST score	329
E value	0.0e+00
Match length	454
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	130002
Contig ID	36862_1.R1010
5'-most EST	jC-atXLIB327408P2f04a1
Method	BLASTN
NCBI GI	g3985931
BLAST score	556
E value	0.0e+00
Match length	560
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	130003
Contig ID	36866_1.R1010
5'-most EST	LIB3168-037-P1-K1-E3
Method	BLASTX
NCBI GI	g4006897
BLAST score	101
E value	1.0e-105
Match length	215
% identity	92
NCBI Description	(Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No.	130004
Contig ID	36870_1.R1010
5'-most EST	LIB3168-014-P1-K1-E6

Seq. No.	130005
Contig ID	36891_1.R1010

5'-most EST	LIB3176-008-P1-K3-B9
Seq. No.	130006
Contig ID	36908_1.R1010
5'-most EST	LIB3168-015-P1-K1-A11
Method	BLASTX
NCBI GI	g2832644
BLAST score	530
E value	8.0e-54
Match length	102
% identity	100
NCBI Description	(AL021710) teosinte branched1 - like protein [Arabidopsis thaliana]
Seq. No.	130007
Contig ID	36924_1.R1010
5'-most EST	jC-atXP78C229K3T7b1
Method	BLASTX
NCBI GI	g2443876
BLAST score	292
E value	1.0e-31
Match length	278
% identity	40
NCBI Description	(AC002294) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	130008
Contig ID	36932_1.R1010
5'-most EST	jC-alXLIB327435P3h05a1
Method	BLASTN
NCBI GI	g3548797
BLAST score	212
E value	1.0e-115
Match length	525
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130009
Contig ID	36943_1.R1010
5'-most EST	LIB3234-096-P1-K1-B3
Method	BLASTX
NCBI GI	g3335169
BLAST score	1058
E value	1.0e-116
Match length	237
% identity	80
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.	130010
Contig ID	36955_1.R1010
5'-most EST	g935581
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	4.0e-15

Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	130011
Contig ID	36955_2.R1010
5'-most EST	LIB3168-015-P1-K1-F10

Seq. No.	130012
Contig ID	36955_3.R1010
5'-most EST	jC-atXLIB327438P3d12a2

Seq. No.	130013
Contig ID	36982_1.R1010
5'-most EST	LIB3177-096-P1-K1-E2
Method	BLASTX
NCBI GI	g4006915
BLAST score	287
E value	2.0e-25
Match length	182
% identity	40
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130014
Contig ID	36993_1.R1010
5'-most EST	LIB3234-076-P1-K1-G2
Method	BLASTN
NCBI GI	g4468103
BLAST score	355
E value	0.0e+00
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	130015
Contig ID	36994_1.R1010
5'-most EST	LIB3176-041-P1-K1-F1
Method	BLASTX
NCBI GI	g4753882
BLAST score	350
E value	6.0e-33
Match length	130
% identity	54
NCBI Description	(AL049754) putative aspartate aminotransferase [Streptomyces coelicolor]

Seq. No.	130016
Contig ID	37003_1.R1010
5'-most EST	LIB3168-016-P1-K1-C11
Method	BLASTN
NCBI GI	g3298532
BLAST score	391
E value	0.0e+00
Match length	415
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130017
Contig ID	37030_1.R1010
5'-most EST	LIB3234-091-P1-K1-H3
Method	BLASTN
NCBI GI	g3540210
BLAST score	367
E value	0.0e+00
Match length	465
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130018
Contig ID	37119_1.R1010
5'-most EST	LIB3177-066-P1-K1-D9
Method	BLASTX
NCBI GI	g4510373
BLAST score	337
E value	2.0e-31
Match length	126
% identity	58
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	130019
Contig ID	37134_1.R1010
5'-most EST	LIB3168-017-P1-K1-H1
Method	BLASTN
NCBI GI	g4585890
BLAST score	401
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	130020
Contig ID	37145_1.R1010
5'-most EST	LIB3168-086-P1-K1-F10
Method	BLASTX
NCBI GI	g3063693
BLAST score	437
E value	4.0e-43
Match length	79
% identity	100
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	130021
Contig ID	37173_1.R1010
5'-most EST	g1217124

Seq. No.	130022
Contig ID	37183_1.R1010
5'-most EST	LIB3168-018-P1-K1-D5

Seq. No. 130023
Contig ID 37227_1.R1010
5'-most EST LIB3168-018-P1-K1-H5

Seq. No. 130024
Contig ID 37234_1.R1010
5'-most EST jC-atXP110CG7D9T7029a1
Method BLASTX
NCBI GI g114532
BLAST score 716
E value 2.0e-75
Match length 159
% identity 92
NCBI Description ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum] >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit [Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum]

Seq. No. 130025
Contig ID 37234_2.R1010
5'-most EST LIB3234-090-P1-K1-D6
Method BLASTX
NCBI GI g897638
BLAST score 272
E value 1.0e-23
Match length 56
% identity 91
NCBI Description (M10124) unknown protein [Nicotiana tabacum] >gi_224349_prf__1102209C ORF 3 [Nicotiana sp.]

Seq. No. 130026
Contig ID 37238_1.R1010
5'-most EST LIB3234-054-P1-K1-H4
Method BLASTX
NCBI GI g683553
BLAST score 146
E value 4.0e-09
Match length 117
% identity 30
NCBI Description (Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No. 130027
Contig ID 37278_1.R1010
5'-most EST LIB3168-019-P1-K1-G1
Method BLASTN
NCBI GI g4691223
BLAST score 384
E value 0.0e+00
Match length 440
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	130028
Contig ID	37281_1.R1010
5'-most EST	LIB3168-019-P1-K1-G2
Method	BLASTX
NCBI GI	g2947062
BLAST score	264
E value	1.0e-22
Match length	199
% identity	39
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	130029
Contig ID	37302_1.R1010
5'-most EST	jC-atXLIB327417P4a03a1

Seq. No.	130030
Contig ID	37302_2.R1010
5'-most EST	LIB3234-094-P1-K1-G9

Seq. No.	130031
Contig ID	37308_1.R1010
5'-most EST	g757607
Method	BLASTX
NCBI GI	g4678333
BLAST score	496
E value	3.0e-50
Match length	129
% identity	76
NCBI Description	(AL049658) H+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	130032
Contig ID	37319_1.R1010
5'-most EST	LIB3168-020-P1-K1-C4
Method	BLASTN
NCBI GI	g4159702
BLAST score	305
E value	1.0e-171
Match length	546
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence

Seq. No.	130033
Contig ID	37329_1.R1010
5'-most EST	LIB3234-009-P1-K1-C6
Method	BLASTX
NCBI GI	g2062167
BLAST score	293
E value	2.0e-26
Match length	74
% identity	73
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	130034

Contig ID	37340_1.R1010
5'-most EST	LIB3168-020-P1-K1-E4
Method	BLASTX
NCBI GI	g1708025
BLAST score	579
E value	5.0e-60
Match length	136
% identity	85
NCBI Description	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] >gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate dehydrogenase (NAD+) [Cuphea lanceolata]

Seq. No.	130035
Contig ID	37351_1.R1010
5'-most EST	LIB35-044-Q1-E1-G6
Method	BLASTN
NCBI GI	g4388714
BLAST score	154
E value	4.0e-81
Match length	437
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130036
Contig ID	37364_1.R1010
5'-most EST	LIB3168-020-P1-K1-H1
Method	BLASTN
NCBI GI	g4757401
BLAST score	212
E value	1.0e-115
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	130037
Contig ID	37412_1.R1010
5'-most EST	LIB3168-022-P1-K1-H8
Method	BLASTX
NCBI GI	g799177
BLAST score	167
E value	2.0e-11
Match length	184
% identity	30
NCBI Description	(U22055) 100 kDa coactivator [Homo sapiens]

Seq. No.	130038
Contig ID	37414_1.R1010
5'-most EST	LIB3234-089-P1-K1-H12
Method	BLASTX
NCBI GI	g4249382
BLAST score	498
E value	2.0e-50
Match length	120
% identity	77
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	130039
Contig ID	37420_1.R1010
5'-most EST	LIB3234-070-P1-K1-E10
Method	BLASTX
NCBI GI	g4505695
BLAST score	353
E value	2.0e-33
Match length	143
% identity	49
NCBI Description	3-phosphoinositide dependent protein kinase-1 >gi_2407613 (AF017995) 3-phosphoinositide dependent protein kinase-1 [Homo sapiens] >gi_2505936_emb_CAA75341_ (Y15056) PkB kinase [Homo sapiens]

Seq. No.	130040
Contig ID	37421_1.R1010
5'-most EST	LIB3177-093-P1-K1-B8

Seq. No.	130041
Contig ID	37442_1.R1010
5'-most EST	LIB3176-008-P1-K4-B5
Method	BLASTN
NCBI GI	g4220637
BLAST score	73
E value	1.0e-32
Match length	367
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	130042
Contig ID	37453_1.R1010
5'-most EST	LIB3168-021-P1-K1-G9
Method	BLASTX
NCBI GI	g4115935
BLAST score	406
E value	1.0e-39
Match length	80
% identity	99
NCBI Description	(AF118223) contains similarity to Helicobacter pylori peptide methionine sulfoxide reductase (msrA) (GB:AE000542) [Arabidopsis thaliana]

Seq. No.	130043
Contig ID	37459_1.R1010
5'-most EST	g3719191
Method	BLASTX
NCBI GI	g2132930
BLAST score	477
E value	9.0e-48
Match length	177
% identity	51
NCBI Description	probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) >gi_1420591_emb_CAA99484_ (Z75170) ORF YOR262w

[Saccharomyces cerevisiae]

Seq. No.	130044
Contig ID	37465_1.R1010
5'-most EST	LIB3168-022-P1-K1-A10
Method	BLASTX
NCBI GI	g4567311
BLAST score	265
E value	4.0e-23
Match length	66
% identity	73
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	130045
Contig ID	37470_1.R1010
5'-most EST	LIB3168-022-P1-K1-A5

Seq. No.	130046
Contig ID	37490_1.R1010
5'-most EST	LIB3168-022-P1-K1-C3

Seq. No.	130047
Contig ID	37496_1.R1010
5'-most EST	LIB3168-022-P1-K1-D10
Method	BLASTN
NCBI GI	g3885325
BLAST score	335
E value	0.0e+00
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130048
Contig ID	37514_1.R1010
5'-most EST	LIB3168-022-P1-K1-E7

Seq. No.	130049
Contig ID	37517_1.R1010
5'-most EST	LIB3168-054-P1-K1-E11
Method	BLASTX
NCBI GI	g3335372
BLAST score	162
E value	5.0e-11
Match length	75
% identity	40
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	130050
Contig ID	37540_1.R1010
5'-most EST	LIB3234-079-P1-K1-A5
Method	BLASTX
NCBI GI	g3395432
BLAST score	314
E value	1.0e-28
Match length	98
% identity	58

NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	130051
Contig ID	37542_1.R1010
5'-most EST	LIB3176-034-P1-K1-H5
Method	BLASTN
NCBI GI	g2947056
BLAST score	272
E value	1.0e-151
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130052
Contig ID	37556_1.R1010
5'-most EST	LIB3168-023-P1-K1-A7

Seq. No.	130053
Contig ID	37633_1.R1010
5'-most EST	LIB3168-024-P1-K1-A11
Method	BLASTN
NCBI GI	g4512656
BLAST score	406
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	130054
Contig ID	37640_1.R1010
5'-most EST	LIB3168-024-P1-K1-A7
Method	BLASTX
NCBI GI	g2769642
BLAST score	554
E value	4.0e-57
Match length	131
% identity	77
NCBI Description	(Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon esculentum]

Seq. No.	130055
Contig ID	37643_1.R1010
5'-most EST	LIB3168-024-P1-K1-B1
Method	BLASTX
NCBI GI	g4589972
BLAST score	245
E value	8.0e-21
Match length	95
% identity	69
NCBI Description	(AC007195) putative indole-3 acetic acid induced protein (ARG7) [Arabidopsis thaliana]

Seq. No.	130056
Contig ID	37649_1.R1010
5'-most EST	LIB3168-024-P1-K1-B4

Method	BLASTX
NCBI GI	g3150407
BLAST score	511
E value	5.0e-52
Match length	97
% identity	100
NCBI Description	(AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130057
Contig ID	37652_1.R1010
5'-most EST	LIB3234-080-P1-K1-D9

Seq. No.	130058
Contig ID	37655_1.R1010
5'-most EST	LIB3234-079-P1-K1-B6
Method	BLASTX
NCBI GI	g2499298
BLAST score	321
E value	4.0e-30
Match length	65
% identity	100
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST >gi_1619279_emb_CAA67670_ (X99278) ndhG [Arabidopsis thaliana]

Seq. No.	130059
Contig ID	37656_1.R1010
5'-most EST	LIB3168-024-P1-K1-C10

Seq. No.	130060
Contig ID	37660_1.R1010
5'-most EST	LIB3176-071-P1-K1-G12
Method	BLASTN
NCBI GI	g2924257
BLAST score	65
E value	8.0e-28
Match length	93
% identity	92
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	130061
Contig ID	37663_1.R1010
5'-most EST	g2764185

Seq. No.	130062
Contig ID	37664_1.R1010
5'-most EST	LIB3168-024-P1-K1-C7

Seq. No.	130063
Contig ID	37675_1.R1010
5'-most EST	LIB3168-024-P1-K1-D7
Method	BLASTX
NCBI GI	g3142300
BLAST score	716
E value	1.0e-75
Match length	233
% identity	57

NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	130064
Contig ID	37706_1.R1010
5'-most EST	LIB3168-024-P1-K1-G6
Method	BLASTX
NCBI GI	g3096920
BLAST score	644
E value	1.0e-67
Match length	126
% identity	100
NCBI Description	(AL023094) putative ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	130065
Contig ID	37724_1.R1010
5'-most EST	LIB3168-025-P1-K1-A12
Method	BLASTX
NCBI GI	g4587529
BLAST score	46
E value	2.0e-32
Match length	97
% identity	76
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. EST gb_H76902 comes from this gene

Seq. No.	130066
Contig ID	37731_1.R1010
5'-most EST	LIB3168-025-P1-K1-B1
Method	BLASTX
NCBI GI	g3915866
BLAST score	187
E value	6.0e-14
Match length	60
% identity	77
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	130067
Contig ID	37855_1.R1010
5'-most EST	LIB3168-026-P1-K1-E12
Method	BLASTX
NCBI GI	g2829898
BLAST score	584
E value	4.0e-60
Match length	159
% identity	70
NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	130068
Contig ID	37860_1.R1010
5'-most EST	jC-alXLIB327436P1f07b1

Method	BLASTN
NCBI GI	g4589437
BLAST score	471
E value	0.0e+00
Match length	538
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	130069
Contig ID	37866_1.R1010
5'-most EST	LIB3168-026-P1-K1-F11
Method	BLASTN
NCBI GI	g4544365
BLAST score	333
E value	0.0e+00
Match length	395
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F26H6 genomic sequence, complete sequence

Seq. No.	130070
Contig ID	37870_1.R1010
5'-most EST	LIB3168-026-P1-K1-F4

Seq. No.	130071
Contig ID	37887_1.R1010
5'-most EST	LIB3234-047-P1-K1-A6
Method	BLASTX
NCBI GI	g3687228
BLAST score	509
E value	1.0e-100
Match length	192
% identity	98
NCBI Description	(AC005169) putative malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	130072
Contig ID	37940_1.R1010
5'-most EST	LIB3234-077-P1-K1-G9
Method	BLASTX
NCBI GI	g2970654
BLAST score	343
E value	1.0e-31
Match length	213
% identity	44
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	130073
Contig ID	37940_2.R1010
5'-most EST	LIB3168-027-P1-K1-D8
Method	BLASTX
NCBI GI	g2970654
BLAST score	689
E value	3.0e-72
Match length	227

% identity	63
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	130074
Contig ID	37954_1.R1010
5'-most EST	LIB3168-030-P1-K1-B3
Method	BLASTX
NCBI GI	g3355477
BLAST score	771
E value	2.0e-82
Match length	173
% identity	47
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	130075
Contig ID	37976_1.R1010
5'-most EST	jC-atXP43C169G18T7086d1
Method	BLASTX
NCBI GI	g3776579
BLAST score	626
E value	8.0e-65
Match length	150
% identity	77
NCBI Description	(AC005388) Strong similarity to F22O13.22 gi_3063460 myosin homolog from A. thaliana BAC gb_AC003981. [Arabidopsis thaliana]

Seq. No.	130076
Contig ID	37976_3.R1010
5'-most EST	LIB3168-027-P1-K1-H2
Method	BLASTX
NCBI GI	g2444180
BLAST score	1043
E value	1.0e-114
Match length	255
% identity	82
NCBI Description	(U94785) unconventional myosin [Helianthus annuus]

Seq. No.	130077
Contig ID	37978_1.R1010
5'-most EST	g3719204
Method	BLASTX
NCBI GI	g4502897
BLAST score	511
E value	1.0e-51
Match length	168
% identity	57
NCBI Description	cleft lip and palate associated transmembrane protein 1 >gi_4039014 (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]

Seq. No.	130078
Contig ID	37978_2.R1010
5'-most EST	g2048384

Method	BLASTX
NCBI GI	g4502897
BLAST score	151
E value	4.0e-30
Match length	98
% identity	67
NCBI Description	cleft lip and palate associated transmembrane protein 1 >gi_4039014 (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]

Seq. No.	130079
Contig ID	37981_1.R1010
5'-most EST	LIB3168-028-P1-K1-A1
Method	BLASTN
NCBI GI	g2656026
BLAST score	289
E value	1.0e-161
Match length	359
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	130080
Contig ID	37987_1.R1010
5'-most EST	LIB3168-028-P1-K1-A4
Method	BLASTN
NCBI GI	g4757403
BLAST score	252
E value	1.0e-139
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	130081
Contig ID	37989_1.R1010
5'-most EST	LIB3234-071-P1-K1-B1
Method	BLASTN
NCBI GI	g4314374
BLAST score	323
E value	0.0e+00
Match length	335
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130082
Contig ID	38002_1.R1010
5'-most EST	LIB3168-028-P1-K1-C10

Seq. No.	130083
Contig ID	38031_1.R1010
5'-most EST	LIB3168-064-P1-K1-E9
Method	BLASTN
NCBI GI	g166609
BLAST score	140

E value	1.0e-72
Match length	341
% identity	85
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	130084
Contig ID	38040_1.R1010
5'-most EST	LIB3234-060-P1-K1-G1
Method	BLASTX
NCBI GI	g2702272
BLAST score	1252
E value	1.0e-138
Match length	328
% identity	56
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130085
Contig ID	38041_1.R1010
5'-most EST	LIB3176-023-P1-K1-B10

Seq. No.	130086
Contig ID	38074_1.R1010
5'-most EST	LIB3176-057-P1-K1-H3
Method	BLASTX
NCBI GI	g4454013
BLAST score	743
E value	4.0e-79
Match length	145
% identity	100
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	130087
Contig ID	38083_1.R1010
5'-most EST	jC-atXLIB327438P4c09a2
Method	BLASTX
NCBI GI	g2739046
BLAST score	377
E value	3.0e-36
Match length	123
% identity	54
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	130088
Contig ID	38084_1.R1010
5'-most EST	LIB3168-029-P1-K1-C5

Seq. No.	130089
Contig ID	38091_1.R1010
5'-most EST	jC-atXP115C250A12T7082d1
Method	BLASTX
NCBI GI	g1009234
BLAST score	646
E value	1.0e-79
Match length	215
% identity	70

NCBI Description	(L38829) SUP2 gene product [Nicotiana tabacum]

Seq. No.	130090
Contig ID	38091_2.R1010
5'-most EST	LIB3177-046-P1-K2-B9
Method	BLASTX
NCBI GI	g1009234
BLAST score	869
E value	9.0e-94
Match length	195
% identity	82
NCBI Description	(L38829) SUP2 gene product [Nicotiana tabacum]

Seq. No.	130091
Contig ID	38096_1.R1010
5'-most EST	LIB3168-029-P1-K1-D6
Method	BLASTN
NCBI GI	g3985932
BLAST score	247
E value	1.0e-137
Match length	251
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	130092
Contig ID	38121_1.R1010
5'-most EST	LIB3168-029-P1-K1-F9
Method	BLASTX
NCBI GI	g4678952
BLAST score	623
E value	5.0e-65
Match length	116
% identity	100
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	130093
Contig ID	38125_1.R1010
5'-most EST	LIB3168-029-P1-K1-G2
Method	BLASTX
NCBI GI	g131143
BLAST score	1822
E value	0.0e+00
Match length	401
% identity	86
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi_72670_pir__A1NTP7 photosystem I P700 apoprotein A1 - common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044) PSI P700 apoprotein A1 [Nicotiana tabacum] >gi_225198_prf__1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum]

Seq. No.	130094
Contig ID	38131_1.R1010
5'-most EST	LIB3234-025-P1-K1-H10
Method	BLASTX
NCBI GI	g2262113

BLAST score	658
E value	4.0e-69
Match length	165
% identity	78
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	130095
Contig ID	38138_2.R1010
5'-most EST	LIB3176-113-P2-K1-D7

Seq. No.	130096
Contig ID	38140_1.R1010
5'-most EST	LIB3176-097-P1-K1-G10
Method	BLASTN
NCBI GI	g2213606
BLAST score	513
E value	0.0e+00
Match length	569
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	130097
Contig ID	38163_1.R1010
5'-most EST	LIB3175-040-P1-K1-E7
Method	BLASTX
NCBI GI	g3413886
BLAST score	160
E value	1.0e-10
Match length	86
% identity	35
NCBI Description	(AB007931) KIAA0462 protein [Homo sapiens]

Seq. No.	130098
Contig ID	38176_1.R1010
5'-most EST	LIB3168-030-P1-K1-D11
Method	BLASTX
NCBI GI	g4191794
BLAST score	393
E value	3.0e-38
Match length	71
% identity	99
NCBI Description	(AC005917) putative zinc finger-like protein [Arabidopsis thaliana]

Seq. No.	130099
Contig ID	38177_1.R1010
5'-most EST	LIB3168-030-P1-K1-D12
Method	BLASTN
NCBI GI	g2262135
BLAST score	414
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	130100
Contig ID	38178_1.R1010
5'-most EST	LIB3168-030-P1-K1-D2

Seq. No.	130101
Contig ID	38200_1.R1010
5'-most EST	LIB3177-025-P1-K2-G3
Method	BLASTX
NCBI GI	g2739366
BLAST score	411
E value	6.0e-40
Match length	179
% identity	48
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	130102
Contig ID	38207_1.R1010
5'-most EST	LIB3168-076-P1-K1-D2

Seq. No.	130103
Contig ID	38346_1.R1010
5'-most EST	g473310
Method	BLASTN
NCBI GI	g4757407
BLAST score	360
E value	0.0e+00
Match length	412
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	130104
Contig ID	38367_1.R1010
5'-most EST	LIB3168-032-P1-K1-G3
Method	BLASTX
NCBI GI	g2245130
BLAST score	254
E value	7.0e-22
Match length	140
% identity	44
NCBI Description	(Z97344) GLABRA2 homolog [Arabidopsis thaliana]

Seq. No.	130105
Contig ID	38379_1.R1010
5'-most EST	LIB3168-032-P1-K1-H9
Method	BLASTX
NCBI GI	g3128168
BLAST score	644
E value	2.0e-67
Match length	157
% identity	70
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	130106
Contig ID	38412_1.R1010
5'-most EST	g2446176

Seq. No.	130107
Contig ID	38414_1.R1010
5'-most EST	jC-atXP73CF3D3T7b1
Method	BLASTN
NCBI GI	g4589450
BLAST score	231
E value	1.0e-127
Match length	548
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T31K7, complete sequence

Seq. No.	130108
Contig ID	38414_2.R1010
5'-most EST	jC-atXP73CF3D3T7d2
Method	BLASTN
NCBI GI	g4589450
BLAST score	447
E value	0.0e+00
Match length	566
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T31K7, complete sequence

Seq. No.	130109
Contig ID	38414_3.R1010
5'-most EST	jC-atXP76C227H19T7d1
Method	BLASTN
NCBI GI	g4589450
BLAST score	701
E value	0.0e+00
Match length	1116
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T31K7, complete sequence

Seq. No.	130110
Contig ID	38469_1.R1010
5'-most EST	LIB3168-034-P1-K1-A5
Method	BLASTX
NCBI GI	g4006915
BLAST score	164
E value	3.0e-11
Match length	107
% identity	40
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130111
Contig ID	38479_1.R1010
5'-most EST	LIB3168-034-P1-K1-B4
Method	BLASTX
NCBI GI	g3540180
BLAST score	699
E value	5.0e-74
Match length	135
% identity	99

NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.	130112
Contig ID	38494_1.R1010
5'-most EST	jC-atXP118C145M5T7005d2
Method	BLASTX
NCBI GI	g4115388
BLAST score	697
E value	2.0e-73
Match length	241
% identity	63
NCBI Description	(AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]
Seq. No.	130113
Contig ID	38494_2.R1010
5'-most EST	LIB3168-034-P1-K1-D1
Method	BLASTX
NCBI GI	g4115388
BLAST score	679
E value	2.0e-71
Match length	149
% identity	85
NCBI Description	(AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]
Seq. No.	130114
Contig ID	38496_1.R1010
5'-most EST	LIB3168-034-P1-K1-D11
Seq. No.	130115
Contig ID	38502_1.R1010
5'-most EST	LIB3234-082-Q1-K1-A9
Seq. No.	130116
Contig ID	38518_1.R1010
5'-most EST	LIB3234-004-P1-K1-B1
Method	BLASTN
NCBI GI	g3522932
BLAST score	228
E value	1.0e-125
Match length	1013
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130117
Contig ID	38545_1.R1010
5'-most EST	LIB3234-083-Q1-K1-G11
Method	BLASTN
NCBI GI	g3461810
BLAST score	178
E value	2.0e-95
Match length	304
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130118
Contig ID	38546_1.R1010
5'-most EST	LIB3168-035-P1-K1-A2
Method	BLASTX
NCBI GI	g4522003
BLAST score	374
E value	4.0e-46
Match length	127
% identity	82
NCBI Description	(AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No.	130119
Contig ID	38551_1.R1010
5'-most EST	LIB3168-035-P1-K1-B1
Method	BLASTX
NCBI GI	g3153205
BLAST score	371
E value	1.0e-35
Match length	74
% identity	99
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	130120
Contig ID	38575_1.R1010
5'-most EST	LIB3168-035-P1-K1-D12
Method	BLASTN
NCBI GI	g2244788
BLAST score	196
E value	1.0e-106
Match length	377
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130121
Contig ID	38578_1.R1010
5'-most EST	jC-atXLIB327405P3g11a1
Method	BLASTX
NCBI GI	g2673918
BLAST score	254
E value	1.0e-21
Match length	87
% identity	57
NCBI Description	(AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No.	130122
Contig ID	38604_1.R1010
5'-most EST	LIB3168-035-P1-K1-G3
Method	BLASTX
NCBI GI	g4056489
BLAST score	460
E value	5.0e-46
Match length	111
% identity	75
NCBI Description	(AC005896) putative white protein [Arabidopsis thaliana]

Seq. No.	130123
Contig ID	38609_1.R1010
5'-most EST	LIB3234-079-P1-K1-D7
Method	BLASTN
NCBI GI	g2924257
BLAST score	52
E value	5.0e-20
Match length	330
% identity	87
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	130124
Contig ID	38638_1.R1010
5'-most EST	g1158998
Method	BLASTX
NCBI GI	g3341679
BLAST score	611
E value	2.0e-63
Match length	175
% identity	64
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	130125
Contig ID	38640_1.R1010
5'-most EST	LIB3168-036-P1-K1-C12
Method	BLASTX
NCBI GI	g3738288
BLAST score	411
E value	5.0e-70
Match length	145
% identity	97
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	130126
Contig ID	38643_1.R1010
5'-most EST	LIB3168-084-P1-K1-B7
Method	BLASTX
NCBI GI	g2708747
BLAST score	481
E value	1.0e-48
Match length	97
% identity	96
NCBI Description	(AC003952) putative glycine-rich, zinc-finger DNA-binding protein [Arabidopsis thaliana]

Seq. No.	130127
Contig ID	38647_1.R1010
5'-most EST	g511083
Method	BLASTN
NCBI GI	g4572664
BLAST score	143
E value	2.0e-74
Match length	450
% identity	92

NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence
Seq. No.	130128
Contig ID	38669_1.R1010
5'-most EST	LIB3175-079-P1-K1-H6
Method	BLASTX
NCBI GI	g3914541
BLAST score	608
E value	4.0e-63
Match length	134
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi_1928872 (U91966) ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Arabidopsis thaliana]
Seq. No.	130129
Contig ID	38699_1.R1010
5'-most EST	LIB3168-037-P1-K1-A11
Seq. No.	130130
Contig ID	38737_1.R1010
5'-most EST	LIB3168-037-P1-K1-D7
Method	BLASTN
NCBI GI	g4519193
BLAST score	450
E value	0.0e+00
Match length	458
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence
Seq. No.	130131
Contig ID	38738_1.R1010
5'-most EST	LIB3168-037-P1-K1-D8
Method	BLASTN
NCBI GI	g3395421
BLAST score	409
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130132
Contig ID	38741_1.R1010
5'-most EST	LIB3234-018-P1-K1-E10
Method	BLASTX
NCBI GI	g3928086
BLAST score	699
E value	1.0e-73
Match length	143
% identity	95
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]
Seq. No.	130133

Contig ID	38746_1.R1010
5'-most EST	LIB3168-037-P1-K1-E6
Method	BLASTN
NCBI GI	g4467131
BLAST score	520
E value	0.0e+00
Match length	583
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	130134
Contig ID	38747_1.R1010
5'-most EST	LIB3234-088-Q1-K1-E2
Method	BLASTN
NCBI GI	g4263753
BLAST score	453
E value	0.0e+00
Match length	533
% identity	96
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	130135
Contig ID	38790_1.R1010
5'-most EST	LIB3176-071-P1-K1-A8
Method	BLASTN
NCBI GI	g2494106
BLAST score	149
E value	4.0e-78
Match length	421
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130136
Contig ID	38795_1.R1010
5'-most EST	LIB3168-040-P1-K1-B4

Seq. No.	130137
Contig ID	38796_1.R1010
5'-most EST	LIB3175-017-P1-K1-F5

Seq. No.	130138
Contig ID	38814_1.R1010
5'-most EST	LIB3176-032-P1-K1-F11

Seq. No.	130139
Contig ID	38823_1.R1010
5'-most EST	LIB3168-040-P1-K1-E5

Seq. No.	130140
Contig ID	38825_1.R1010
5'-most EST	LIB3168-040-P1-K1-E8
Method	BLASTN
NCBI GI	g2853071
BLAST score	389

E value	0.0e+00
Match length	440
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	130141
Contig ID	38840_1.R1010
5'-most EST	LIB3168-040-P1-K1-G2

Seq. No.	130142
Contig ID	38845_1.R1010
5'-most EST	LIB3234-038-P1-K1-B3
Method	BLASTN
NCBI GI	g3402745
BLAST score	198
E value	1.0e-107
Match length	431
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	130143
Contig ID	38854_1.R1010
5'-most EST	jC-atXP92C246M21T7089d1
Method	BLASTX
NCBI GI	g4512685
BLAST score	98
E value	1.0e-28
Match length	102
% identity	60
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130144
Contig ID	38854_2.R1010
5'-most EST	LIB3234-082-Q1-K1-F11

Seq. No.	130145
Contig ID	38890_1.R1010
5'-most EST	LIB3168-041-P1-K1-D12
Method	BLASTX
NCBI GI	g1001311
BLAST score	155
E value	4.0e-10
Match length	81
% identity	48
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	130146
Contig ID	38907_1.R1010
5'-most EST	LIB3168-041-P1-K1-F10
Method	BLASTN
NCBI GI	g4432829
BLAST score	446
E value	0.0e+00

Match length	470
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130147
Contig ID	38912_1.R1010
5'-most EST	g906520

Seq. No.	130148
Contig ID	38925_1.R1010
5'-most EST	LIB3168-041-P1-K1-G7
Method	BLASTX
NCBI GI	g4056500
BLAST score	285
E value	2.0e-25
Match length	58
% identity	100
NCBI Description	(AC005896) putative acetyltransferase [Arabidopsis thaliana]

Seq. No.	130149
Contig ID	38932_1.R1010
5'-most EST	LIB3168-041-P1-K1-H5
Method	BLASTN
NCBI GI	g3869067
BLAST score	338
E value	0.0e+00
Match length	431
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	130150
Contig ID	38960_1.R1010
5'-most EST	ARABL1-01-Q1-E1-H6
Method	BLASTN
NCBI GI	g3298610
BLAST score	183
E value	2.0e-98
Match length	330
% identity	99
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	130151
Contig ID	38988_1.R1010
5'-most EST	LIB3175-030-P1-K1-C2
Method	BLASTX
NCBI GI	g2262112
BLAST score	665
E value	8.0e-70
Match length	126
% identity	99
NCBI Description	(AC002343) trehalase precusor isolog [Arabidopsis thaliana]

Seq. No.	130152
Contig ID	39032_1.R1010

5'-most EST	LIB3168-044-P1-K1-C1
Method	BLASTX
NCBI GI	g4755189
BLAST score	340
E value	6.0e-32
Match length	146
% identity	53
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	130153
Contig ID	39078_1.R1010
5'-most EST	jC-atXLIB327431P1f05a1
Method	BLASTX
NCBI GI	g1730622
BLAST score	192
E value	2.0e-14
Match length	87
% identity	46
NCBI Description	HYPOTHETICAL 56.1 KD PROTEIN F59A2.4 IN CHROMOSOME III

Seq. No.	130154
Contig ID	39083_1.R1010
5'-most EST	LIB3168-044-P1-K1-G4
Method	BLASTN
NCBI GI	g3449320
BLAST score	199
E value	1.0e-108
Match length	421
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	130155
Contig ID	39089_1.R1010
5'-most EST	LIB3168-044-P1-K1-H10
Method	BLASTX
NCBI GI	g1176671
BLAST score	325
E value	5.0e-30
Match length	123
% identity	49
NCBI Description	PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 >gi_3874174_emb_CAA86666_ (Z46676) C08B11.8 [Caenorhabditis elegans]

Seq. No.	130156
Contig ID	39165_1.R1010
5'-most EST	LIB3234-086-Q1-K1-B8

Seq. No.	130157
Contig ID	39166_1.R1010
5'-most EST	LIB3168-045-P1-K1-G2

Seq. No.	130158
Contig ID	39197_1.R1010
5'-most EST	LIB3168-046-P1-K1-B10

Seq. No.	130159
Contig ID	39225_1.R1010
5'-most EST	jC-atXLIB327414P4d06a2
Method	BLASTX
NCBI GI	g3395436
BLAST score	532
E value	2.0e-54
Match length	107
% identity	99
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	130160
Contig ID	39248_1.R1010
5'-most EST	LIB3168-046-P1-K1-F9
Method	BLASTN
NCBI GI	g2264314
BLAST score	223
E value	1.0e-122
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	130161
Contig ID	39255_1.R1010
5'-most EST	ARABL1-04-Q1-B1-F5
Method	BLASTX
NCBI GI	g3914467
BLAST score	831
E value	4.0e-89
Match length	199
% identity	82
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No.	130162
Contig ID	39265_1.R1010
5'-most EST	LIB3168-046-P1-K1-H3
Method	BLASTN
NCBI GI	g2864607
BLAST score	397
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	130163
Contig ID	39274_1.R1010
5'-most EST	jC-atXP111C126H21T7s1
Method	BLASTX
NCBI GI	g4581109
BLAST score	197
E value	4.0e-21
Match length	128
% identity	38

NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	130164
Contig ID	39277_1.R1010
5'-most EST	LIB3177-017-P1-K2-B4
Method	BLASTX
NCBI GI	g118053
BLAST score	80
E value	6.5e-01
Match length	274
% identity	85
NCBI Description	APOCYTOCHROME F PRECURSOR >gi_65614_pir__CFNT plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - common tobacco chloroplast >gi_11845_emb_CAA77365_ (Z00044) cytochrome f [Nicotiana tabacum] >gi_225213_prf__1211235AU cytochrome f [Nicotiana tabacum]

Seq. No.	130165
Contig ID	39277_2.R1010
5'-most EST	LIB3176-017-P1-K1-E3
Method	BLASTX
NCBI GI	g122781
BLAST score	491
E value	2.0e-49
Match length	101
% identity	89
NCBI Description	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) >gi_82210_pir__A05198 hypothetical protein 229 - common tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]

Seq. No.	130166
Contig ID	39281_1.R1010
5'-most EST	LIB3168-047-P1-K1-B1
Method	BLASTN
NCBI GI	g4455168
BLAST score	386
E value	0.0e+00
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	130167
Contig ID	39289_1.R1010
5'-most EST	LIB3176-063-P1-K1-G8
Method	BLASTN
NCBI GI	g2688838
BLAST score	142
E value	7.0e-74
Match length	282
% identity	88
NCBI Description	Thlaspi goesingense ATP phosphoribosyltransferase (THG1) mRNA, complete cds

Seq. No.	130168
Contig ID	39303_1.R1010
5'-most EST	g2748893
Method	BLASTX
NCBI GI	g2384669
BLAST score	244
E value	2.0e-20
Match length	75
% identity	61
NCBI Description	(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]

Seq. No.	130169
Contig ID	39303_2.R1010
5'-most EST	LIB3168-047-P1-K1-C9
Method	BLASTX
NCBI GI	g4454033
BLAST score	208
E value	3.0e-16
Match length	106
% identity	42
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	130170
Contig ID	39322_1.R1010
5'-most EST	LIB35-052-Q1-E1-E10
Method	BLASTX
NCBI GI	g3738324
BLAST score	179
E value	3.0e-46
Match length	116
% identity	78
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	130171
Contig ID	39331_1.R1010
5'-most EST	g2762746

Seq. No.	130172
Contig ID	39366_1.R1010
5'-most EST	LIB3234-080-P1-K1-G9

Seq. No.	130173
Contig ID	39376_1.R1010
5'-most EST	LIB3168-048-P1-K1-B8
Method	BLASTX
NCBI GI	g4406820
BLAST score	722
E value	1.0e-76
Match length	184
% identity	80
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis thaliana]

Seq. No.	130174
Contig ID	39386_1.R1010

5'-most EST	LIB3168-066-P1-K1-D3
Method	BLASTX
NCBI GI	g2924258
BLAST score	1001
E value	1.0e-109
Match length	290
% identity	70
NCBI Description	(Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No.	130175
Contig ID	39392_1.R1010
5'-most EST	LIB3168-048-P1-K1-D6
Method	BLASTX
NCBI GI	g4115377
BLAST score	94
E value	6.0e-68
Match length	201
% identity	63
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	130176
Contig ID	39396_1.R1010
5'-most EST	LIB3168-048-P1-K1-E1

Seq. No.	130177
Contig ID	39414_1.R1010
5'-most EST	LIB3176-117-P2-K1-H2
Method	BLASTX
NCBI GI	g3281868
BLAST score	733
E value	1.0e-77
Match length	140
% identity	99
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	130178
Contig ID	39425_1.R1010
5'-most EST	LIB3168-048-P1-K1-H11

Seq. No.	130179
Contig ID	39445_1.R1010
5'-most EST	LIB3168-050-P1-K1-B11
Method	BLASTN
NCBI GI	g2337888
BLAST score	464
E value	0.0e+00
Match length	597
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	130180
Contig ID	39445_2.R1010
5'-most EST	g3449572
Method	BLASTX
NCBI GI	g2132171
BLAST score	361

E value	4.0e-34
Match length	151
% identity	48
NCBI Description	hypothetical protein YPL063w - yeast (Saccharomyces cerevisiae) >gi_1079679 (U39205) similar to Caenorhabditis elegans CELF45E12_5 F45E12.1 gene product, encoded by GenBank Accession Number U29536 [Saccharomyces cerevisiae]

Seq. No.	130181
Contig ID	39460_1.R1010
5'-most EST	LIB3168-050-P1-K1-C6
Method	BLASTN
NCBI GI	g4406752
BLAST score	275
E value	1.0e-153
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130182
Contig ID	39513_1.R1010
5'-most EST	jC-atXP86CG9F3T7d2
Method	BLASTX
NCBI GI	g3033397
BLAST score	838
E value	5.0e-90
Match length	181
% identity	88
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	130183
Contig ID	39523_2.R1010
5'-most EST	jC-atXL104Q1B1B04b1
Method	BLASTX
NCBI GI	g4559388
BLAST score	284
E value	3.0e-25
Match length	76
% identity	59
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130184
Contig ID	39563_1.R1010
5'-most EST	LIB3234-087-Q1-K1-E8
Method	BLASTN
NCBI GI	g3004543
BLAST score	316
E value	1.0e-178
Match length	341
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130185
Contig ID	39572_1.R1010
5'-most EST	jC-atXP12C103A17T7044a1

Method	BLASTN
NCBI GI	g2262155
BLAST score	384
E value	0.0e+00
Match length	713
% identity	99
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	130186
Contig ID	39572_2.R1010
5'-most EST	LIB3168-051-P1-K1-F9
Method	BLASTN
NCBI GI	g2262155
BLAST score	429
E value	0.0e+00
Match length	583
% identity	99
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	130187
Contig ID	39582_1.R1010
5'-most EST	LIB3234-086-Q1-K1-G9
Method	BLASTN
NCBI GI	g3335356
BLAST score	148
E value	1.0e-77
Match length	343
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130188
Contig ID	39593_1.R1010
5'-most EST	ARABLI-046-Q1-B1-H12

Seq. No.	130189
Contig ID	39598_1.R1010
5'-most EST	LIB3168-052-P1-K1-A5
Method	BLASTX
NCBI GI	g2792155
BLAST score	202
E value	9.0e-16
Match length	76
% identity	46
NCBI Description	(AJ223291) chalcone reductase [Sesbania rostrata]

Seq. No.	130190
Contig ID	39603_1.R1010
5'-most EST	LIB3168-052-P1-K1-B1

Seq. No.	130191
Contig ID	39613_1.R1010
5'-most EST	LIB3168-052-P1-K1-C10
Method	BLASTN
NCBI GI	g3402695

BLAST score	210
E value	1.0e-114
Match length	363
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130192
Contig ID	39617_1.R1010
5'-most EST	LIB3234-089-P1-K1-H6
Method	BLASTX
NCBI GI	g66179
BLAST score	744
E value	5.0e-79
Match length	183
% identity	80
NCBI Description	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common tobacco chloroplast >gi_225255_prf__1211235CP NADH dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. No.	130193
Contig ID	39617_2.R1010
5'-most EST	LIB3168-090-P1-K1-E7
Method	BLASTX
NCBI GI	g66179
BLAST score	179
E value	6.0e-64
Match length	161
% identity	79
NCBI Description	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common tobacco chloroplast >gi_225255_prf__1211235CP NADH dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. No.	130194
Contig ID	39619_1.R1010
5'-most EST	LIB3168-052-P1-K1-C6
Method	BLASTX
NCBI GI	g4101589
BLAST score	372
E value	1.0e-35
Match length	120
% identity	55
NCBI Description	(AF005050) aspartyl aminopeptidase [Homo sapiens]

Seq. No.	130195
Contig ID	39625_1.R1010
5'-most EST	g905541
Method	BLASTX
NCBI GI	g4160402
BLAST score	259
E value	4.0e-22
Match length	117
% identity	53
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]

Seq. No. 130196

Contig ID	39633_1.R1010
5'-most EST	LIB3168-052-P1-K1-D9
Method	BLASTX
NCBI GI	g2851581
BLAST score	687
E value	2.0e-72
Match length	136
% identity	99
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_2196464_emb_CAA74024_ (Y13690) DNA-dependent RNA polymerase subunit beta [Arabidopsis thaliana]

Seq. No.	130197
Contig ID	39640_1.R1010
5'-most EST	LIB3168-052-P1-K1-E5
Method	BLASTN
NCBI GI	g4159707
BLAST score	555
E value	0.0e+00
Match length	699
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	130198
Contig ID	39670_1.R1010
5'-most EST	LIB3168-052-P1-K1-H5
Method	BLASTX
NCBI GI	g3695380
BLAST score	211
E value	8.0e-17
Match length	134
% identity	22
NCBI Description	(AF096370) partial CDS; contains similarity to Nicotiana tabacum membrane-associated salt-inducible protein (GB:U08285) [Arabidopsis thaliana]

Seq. No.	130199
Contig ID	39697_1.R1010
5'-most EST	LIB3168-053-P1-K1-C10
Method	BLASTN
NCBI GI	g3668073
BLAST score	520
E value	0.0e+00
Match length	548
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130200
Contig ID	39704_1.R1010
5'-most EST	g1159004

Seq. No.	130201
Contig ID	39719_1.R1010
5'-most EST	jC-atXP4C88D7T7d1
Method	BLASTX

NCBI GI	g2244953
BLAST score	710
E value	3.0e-78
Match length	160
% identity	89
NCBI Description	(Z97340) ATsEH homolog [Arabidopsis thaliana]

Seq. No.	130202
Contig ID	39723_1.R1010
5'-most EST	LIB3175-063-P1-K1-C6
Method	BLASTX
NCBI GI	g1480347
BLAST score	1240
E value	1.0e-152
Match length	368
% identity	71
NCBI Description	(X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]

Seq. No.	130203
Contig ID	39748_1.R1010
5'-most EST	LIB3168-053-P1-K1-H1
Method	BLASTN
NCBI GI	g3298610
BLAST score	411
E value	0.0e+00
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	130204
Contig ID	39749_1.R1010
5'-most EST	LIB3176-098-P1-K1-F11
Method	BLASTX
NCBI GI	g3341697
BLAST score	399
E value	1.0e-38
Match length	104
% identity	71
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130205
Contig ID	39757_1.R1010
5'-most EST	LIB3168-076-P1-K1-A5
Method	BLASTN
NCBI GI	g2351067
BLAST score	355
E value	0.0e+00
Match length	429
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	130206
Contig ID	39783_1.R1010
5'-most EST	LIB3168-054-P1-K1-C4
Method	BLASTN
NCBI GI	g4589408

BLAST score	412
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F14A1, complete sequence

Seq. No.	130207
Contig ID	39785_1.R1010
5'-most EST	LIB3168-054-P1-K1-C8

Seq. No.	130208
Contig ID	39802_1.R1010
5'-most EST	LIB3234-091-P1-K1-G9

Seq. No.	130209
Contig ID	39810_1.R1010
5'-most EST	LIB3168-054-P1-K1-F5
Method	BLASTN
NCBI GI	g3758832
BLAST score	42
E value	2.0e-14
Match length	70
% identity	90
NCBI Description	Medicago truncatula mRNA for MtN6 gene

Seq. No.	130210
Contig ID	39825_1.R1010
5'-most EST	LIB3168-058-P1-K1-D4
Method	BLASTX
NCBI GI	g3258637
BLAST score	305
E value	7.0e-28
Match length	109
% identity	60
NCBI Description	(AF041050) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No.	130211
Contig ID	39840_1.R1010
5'-most EST	LIB3234-012-P1-K1-A3
Method	BLASTX
NCBI GI	g2621324
BLAST score	146
E value	1.0e-19
Match length	153
% identity	40
NCBI Description	(AE000813) conserved protein [Methanobacterium thermoautotrophicum]

Seq. No.	130212
Contig ID	39847_1.R1010
5'-most EST	LIB3168-055-P1-K1-B1
Method	BLASTX
NCBI GI	g131276
BLAST score	189
E value	2.0e-80
Match length	173

% identity	88
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	130213
Contig ID	39889_1.R1010
5'-most EST	LIB3168-055-P1-K1-F10
Method	BLASTN
NCBI GI	g2264316
BLAST score	274
E value	1.0e-152
Match length	489
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	130214
Contig ID	39890_1.R1010
5'-most EST	LIB3168-055-P1-K1-F11
Method	BLASTX
NCBI GI	g4510348
BLAST score	193
E value	9.0e-15
Match length	57
% identity	61
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	130215
Contig ID	39940_1.R1010
5'-most EST	LIB3168-056-P1-K1-C8
Method	BLASTN
NCBI GI	g4406805
BLAST score	340
E value	0.0e+00
Match length	348
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130216
Contig ID	40017_1.R1010
5'-most EST	g936202
Method	BLASTN
NCBI GI	g4755185
BLAST score	277
E value	1.0e-154
Match length	336
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	130217
Contig ID	40018_1.R1010

5'-most EST	LIB3234-089-P1-K1-D5
Method	BLASTX
NCBI GI	g129868
BLAST score	370
E value	7.0e-36
Match length	80
% identity	90
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_100816_pir__S14962 plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K protein - wheat chloroplast >gi_12364_emb_CAA38552_ (X54751) subunit IV of cytochrome bf complex [Triticum aestivum]

Seq. No.	130218
Contig ID	40038_1.R1010
5'-most EST	LIB3234-089-P1-K1-E4
Method	BLASTN
NCBI GI	g3059018
BLAST score	273
E value	1.0e-152
Match length	336
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	130219
Contig ID	40068_1.R1010
5'-most EST	LIB3168-058-P1-K1-B2

Seq. No.	130220
Contig ID	40088_1.R1010
5'-most EST	LIB3176-096-P1-K1-A3
Method	BLASTN
NCBI GI	g2351062
BLAST score	771
E value	0.0e+00
Match length	1195
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	130221
Contig ID	40104_2.R1010
5'-most EST	jC-atXLIB327421P1e05b1
Method	BLASTX
NCBI GI	g3935169
BLAST score	341
E value	7.0e-32
Match length	68
% identity	99
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No.	130222
Contig ID	40104_3.R1010
5'-most EST	g2393611
Method	BLASTX
NCBI GI	g3935171

BLAST score	271
E value	9.0e-38
Match length	102
% identity	82
NCBI Description	(AC004557) F17L21.14 [Arabidopsis thaliana]

Seq. No.	130223
Contig ID	40131_1.R1010
5'-most EST	LIB3168-059-P1-K1-A4
Method	BLASTX
NCBI GI	g3915961
BLAST score	672
E value	7.0e-71
Match length	143
% identity	90
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	130224
Contig ID	40155_2.R1010
5'-most EST	LIB3175-064-P1-K1-G7
Method	BLASTN
NCBI GI	g2827538
BLAST score	449
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	130225
Contig ID	40168_1.R1010
5'-most EST	LIB3234-089-P1-K1-B11
Method	BLASTX
NCBI GI	g128838
BLAST score	126
E value	5.0e-64
Match length	151
% identity	77
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE 49 KD SUBUNIT, CHLOROPLAST (ORF 393) >gi_82215_pir__A05216 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 393 - common tobacco chloroplast >gi_1223674_emb_CAA77398_ (Z00044) NADH dehydrogenase 49kD subunit [Nicotiana tabacum] >gi_225262_prf__1211235CX ORF 393 [Nicotiana tabacum]

Seq. No.	130226
Contig ID	40198_1.R1010
5'-most EST	LIB3176-086-P1-K1-E2
Method	BLASTX
NCBI GI	g3510249
BLAST score	888
E value	1.0e-113
Match length	236
% identity	89

NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.	130227
Contig ID	40222_1.R1010
5'-most EST	LIB3234-091-P1-K1-H9
Method	BLASTN
NCBI GI	g4063756
BLAST score	245
E value	1.0e-135
Match length	274
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130228
Contig ID	40246_1.R1010
5'-most EST	g2749063
Method	BLASTX
NCBI GI	g1750376
BLAST score	238
E value	9.0e-20
Match length	47
% identity	98
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]
Seq. No.	130229
Contig ID	40246_2.R1010
5'-most EST	g2749052
Method	BLASTX
NCBI GI	g1750376
BLAST score	302
E value	3.0e-27
Match length	75
% identity	84
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]
Seq. No.	130230
Contig ID	40282_1.R1010
5'-most EST	LIB35-005-Q1-E1-E1
Seq. No.	130231
Contig ID	40284_1.R1010
5'-most EST	LIB3168-060-P1-K1-H12
Seq. No.	130232
Contig ID	40300_1.R1010
5'-most EST	LIB3168-061-P1-K1-B11
Method	BLASTX
NCBI GI	g3264778
BLAST score	77
E value	2.0e-33
Match length	92
% identity	83

NCBI Description	(AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]

Seq. No.	130233
Contig ID	40301_1.R1010
5'-most EST	LIB3168-062-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	171
E value	4.0e-12
Match length	53
% identity	64
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	130234
Contig ID	40309_1.R1010
5'-most EST	LIB3234-043-P1-K1-E10
Method	BLASTN
NCBI GI	g336274
BLAST score	173
E value	2.0e-92
Match length	356
% identity	90
NCBI Description	Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA, tRNA-Arg, and tRNA-Asn genes

Seq. No.	130235
Contig ID	40336_1.R1010
5'-most EST	LIB3234-090-P1-K1-H6
Method	BLASTX
NCBI GI	g2961373
BLAST score	284
E value	2.0e-25
Match length	102
% identity	56
NCBI Description	(AL022141) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	130236
Contig ID	40341_1.R1010
5'-most EST	LIB3168-062-P1-K1-F11
Method	BLASTX
NCBI GI	g112681
BLAST score	45
E value	2.0e-11
Match length	82
% identity	57
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	130237
Contig ID	40359_1.R1010

5'-most EST	LIB3168-062-P1-K1-C9
Method	BLASTN
NCBI GI	g2842474
BLAST score	80
E value	4.0e-37
Match length	181
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	130238
Contig ID	40365_1.R1010
5'-most EST	g2757972
Method	BLASTX
NCBI GI	g3738315
BLAST score	646
E value	1.0e-67
Match length	185
% identity	62
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	130239
Contig ID	40375_1.R1010
5'-most EST	LIB3234-083-Q1-K1-A5
Method	BLASTN
NCBI GI	g4314374
BLAST score	24
E value	2.0e-03
Match length	642
% identity	18
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130240
Contig ID	40377_1.R1010
5'-most EST	LIB3168-079-P1-K1-F4
Method	BLASTN
NCBI GI	g2842474
BLAST score	175
E value	1.0e-93
Match length	422
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	130241
Contig ID	40387_1.R1010
5'-most EST	LIB3168-091-P1-K1-D6
Method	BLASTX
NCBI GI	g112682
BLAST score	171
E value	3.0e-12
Match length	61
% identity	61
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	130242
Contig ID	40437_1.R1010
5'-most EST	LIB3168-064-P1-K1-D9
Method	BLASTN
NCBI GI	g4519195
BLAST score	72
E value	4.0e-32
Match length	138
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	130243
Contig ID	40447_1.R1010
5'-most EST	LIB3234-090-P1-K1-A4

Seq. No.	130244
Contig ID	40465_1.R1010
5'-most EST	LIB3168-064-P1-K1-G9
Method	BLASTN
NCBI GI	g166610
BLAST score	113
E value	1.0e-56
Match length	280
% identity	83
NCBI Description	A.thaliana at2S2 gene encoding albumin 2S subunit 2, complete cds

Seq. No.	130245
Contig ID	40471_1.R1010
5'-most EST	LIB3176-037-P1-K1-G4
Method	BLASTX
NCBI GI	g4220523
BLAST score	1148
E value	1.0e-126
Match length	261
% identity	79
NCBI Description	(AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No.	130246
Contig ID	40473_1.R1010
5'-most EST	g2593456
Method	BLASTN
NCBI GI	g2262097
BLAST score	357
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	130247
Contig ID	40479_1.R1010
5'-most EST	LIB3168-065-P1-K1-A2

Method	BLASTN
NCBI GI	g4757407
BLAST score	206
E value	1.0e-112
Match length	446
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	130248
Contig ID	40495_1.R1010
5'-most EST	LIB3234-096-P1-K1-G11
Method	BLASTN
NCBI GI	g2244747
BLAST score	227
E value	1.0e-125
Match length	239
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130249
Contig ID	40514_1.R1010
5'-most EST	LIB3177-052-P1-K1-H11
Method	BLASTX
NCBI GI	g4539452
BLAST score	784
E value	1.0e-83
Match length	258
% identity	56
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	130250
Contig ID	40514_2.R1010
5'-most EST	g1054261

Seq. No.	130251
Contig ID	40524_1.R1010
5'-most EST	jC-atXLIB327423P1d09b1
Method	BLASTX
NCBI GI	g4324409
BLAST score	229
E value	2.0e-18
Match length	211
% identity	30
NCBI Description	(AF104119) intracellular chloride ion channel protein p64H1 [Rattus norvegicus]

Seq. No.	130252
Contig ID	40524_2.R1010
5'-most EST	g1158610
Method	BLASTX
NCBI GI	g2429467
BLAST score	149
E value	5.0e-09
Match length	66

% identity	42
NCBI Description	(AF025462) contains similarity to glutathione S transferases [Caenorhabditis elegans]

Seq. No.	130253
Contig ID	40539_1.R1010
5'-most EST	LIB3168-065-P1-K1-F4
Method	BLASTX
NCBI GI	g2252832
BLAST score	79
E value	1.0e-10
Match length	108
% identity	45
NCBI Description	(AF013293) contains similarity to S. cerevisiae ADR1 gene (PID:g924931) [Arabidopsis thaliana]

Seq. No.	130254
Contig ID	40545_1.R1010
5'-most EST	g2749605

Seq. No.	130255
Contig ID	40545_2.R1010
5'-most EST	LIB3168-065-P1-K1-G11
Method	BLASTX
NCBI GI	g294845
BLAST score	536
E value	1.0e-58
Match length	240
% identity	50
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	130256
Contig ID	40547_1.R1010
5'-most EST	g2723218
Method	BLASTX
NCBI GI	g4454043
BLAST score	295
E value	3.0e-26
Match length	101
% identity	57
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	130257
Contig ID	40550_1.R1010
5'-most EST	LIB3176-042-P1-K1-G8
Method	BLASTX
NCBI GI	g2961377
BLAST score	636
E value	1.0e-66
Match length	124
% identity	24
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	130258
Contig ID	40605_1.R1010

5'-most EST	LIB3168-066-P1-K1-E3
Method	BLASTX
NCBI GI	g4454009
BLAST score	307
E value	7.0e-28
Match length	126
% identity	55
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	130259
Contig ID	40610_1.R1010
5'-most EST	jC-atXP8C92J13T7s1
Method	BLASTX
NCBI GI	g729486
BLAST score	175
E value	2.0e-12
Match length	102
% identity	41
NCBI Description	PRE-RRNA PROCESSING PROTEIN FHL1 >gi_626950_pir__S43738 transcription activator FHL1 - yeast (Saccharomyces cerevisiae) >gi_454255_emb_CAA82202_ (Z28348) Fhl1p [Saccharomyces cerevisiae] >gi_914975 (U32445) Pre-rRNA processing protein Fhl1 (Swiss Prot. accession number P39521) [Saccharomyces cerevisiae]

Seq. No.	130260
Contig ID	40612_1.R1010
5'-most EST	LIB3168-066-P1-K1-F1
Method	BLASTX
NCBI GI	g2851581
BLAST score	655
E value	7.0e-69
Match length	145
% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_2196464_emb_CAA74024_ (Y13690) DNA-dependent RNA polymerase subunit beta [Arabidopsis thaliana]

Seq. No.	130261
Contig ID	40639_1.R1010
5'-most EST	LIB3176-050-P1-K1-G6
Method	BLASTN
NCBI GI	g4691223
BLAST score	300
E value	1.0e-168
Match length	511
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	130262
Contig ID	40640_1.R1010
5'-most EST	LIB3168-066-P1-K1-H8
Method	BLASTX
NCBI GI	g4510348
BLAST score	632
E value	4.0e-66

Match length	126
% identity	96
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	130263
Contig ID	40670_1.R1010
5'-most EST	g623741
Method	BLASTX
NCBI GI	g1906830
BLAST score	964
E value	1.0e-105
Match length	196
% identity	95
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	130264
Contig ID	40695_1.R1010
5'-most EST	LIB3176-008-P1-K1-A2
Method	BLASTX
NCBI GI	g2864609
BLAST score	249
E value	4.0e-21
Match length	93
% identity	51
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	130265
Contig ID	40723_1.R1010
5'-most EST	g905878
Method	BLASTN
NCBI GI	g3510345
BLAST score	285
E value	1.0e-159
Match length	462
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	130266
Contig ID	40736_1.R1010
5'-most EST	LIB3176-074-P1-K1-F11
Method	BLASTN
NCBI GI	g2337888
BLAST score	573
E value	0.0e+00
Match length	744
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	130267
Contig ID	40768_1.R1010
5'-most EST	LIB3168-068-P1-K1-D6
Method	BLASTN
NCBI GI	g2182287

BLAST score	428
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	130268
Contig ID	40793_1.R1010
5'-most EST	jC-atXP115C248019T7d1
Method	BLASTX
NCBI GI	g3834314
BLAST score	773
E value	1.0e-82
Match length	160
% identity	93
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	130269
Contig ID	40831_1.R1010
5'-most EST	LIB3168-069-P1-K1-B5
Method	BLASTN
NCBI GI	g3894156
BLAST score	159
E value	5.0e-84
Match length	351
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130270
Contig ID	40859_1.R1010
5'-most EST	LIB3234-095-P1-K1-F5
Method	BLASTN
NCBI GI	g4512690
BLAST score	413
E value	0.0e+00
Match length	459
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	130271
Contig ID	40864_1.R1010
5'-most EST	LIB3168-069-P1-K1-E7

Seq. No.	130272
Contig ID	40866_1.R1010
5'-most EST	g905488
Method	BLASTN
NCBI GI	g2264309
BLAST score	234
E value	1.0e-129
Match length	423

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	130273
Contig ID	40880_1.R1010
5'-most EST	LIB3234-020-P1-K1-F12
Method	BLASTX
NCBI GI	g82223
BLAST score	55
E value	2.0e-10
Match length	60
% identity	72
NCBI Description	hypothetical protein 70B - common tobacco chloroplast >gi_11878_emb_CAA77391_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_1223681_emb_CAA77402_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225250_prf__1211235CJ ORF 70B [Nicotiana tabacum]

Seq. No.	130274
Contig ID	40956_1.R1010
5'-most EST	LIB3168-071-P1-K1-A11
Method	BLASTX
NCBI GI	g3023799
BLAST score	154
E value	3.0e-10
Match length	64
% identity	47
NCBI Description	DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_1118003 (U40768) dihydroneopterin aldolase [Staphylococcus haemolyticus] >gi_1586495_prf__2204217C dihydroneopterin aldolase [Staphylococcus haemolyticus]

Seq. No.	130275
Contig ID	40962_1.R1010
5'-most EST	LIB3234-050-P1-K1-H7
Method	BLASTN
NCBI GI	g4115930
BLAST score	361
E value	0.0e+00
Match length	453
% identity	94
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	130276
Contig ID	40977_1.R1010
5'-most EST	LIB3176-048-P1-K1-D2
Method	BLASTX
NCBI GI	g3757522
BLAST score	243
E value	2.0e-20
Match length	102
% identity	58
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	130277
Contig ID	40999_1.R1010

5'-most EST	LIB3234-059-P1-K1-G1
Seq. No.	130278
Contig ID	41004_1.R1010
5'-most EST	LIB3168-071-P1-K1-E6
Seq. No.	130279
Contig ID	41014_1.R1010
5'-most EST	LIB3234-093-P1-K1-F7
Seq. No.	130280
Contig ID	41026_1.R1010
5'-most EST	g2413114
Method	BLASTN
NCBI GI	g2264316
BLAST score	183
E value	4.0e-98
Match length	692
% identity	42
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.	130281
Contig ID	41027_1.R1010
5'-most EST	LIB3168-071-P1-K1-H1
Method	BLASTN
NCBI GI	g3449331
BLAST score	40
E value	5.0e-13
Match length	541
% identity	39
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.	130282
Contig ID	41066_1.R1010
5'-most EST	LIB3168-072-P1-K1-C4
Method	BLASTX
NCBI GI	g3935167
BLAST score	544
E value	1.0e-55
Match length	123
% identity	85
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.	130283
Contig ID	41069_1.R1010
5'-most EST	LIB3234-060-P1-K1-B4
Seq. No.	130284
Contig ID	41076_1.R1010
5'-most EST	jC-atXP29C137M11T7s1
Seq. No.	130285
Contig ID	41103_1.R1010
5'-most EST	LIB3168-072-P1-K1-F6

Seq. No.	130286
Contig ID	41112_1.R1010
5'-most EST	jC-atXP84CG5G12T7b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	130287
Contig ID	41125_1.R1010
5'-most EST	LIB3168-073-P1-K1-A1
Method	BLASTX
NCBI GI	g4115383
BLAST score	515
E value	2.0e-52
Match length	139
% identity	35
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	130288
Contig ID	41134_1.R1010
5'-most EST	LIB3168-073-P1-K1-A7
Method	BLASTX
NCBI GI	g398963
BLAST score	172
E value	3.0e-12
Match length	82
% identity	48
NCBI Description	4-COUMARATE--COA LIGASE 1 (4CL) >gi_100413_pir__A39827 4-coumarate--CoA ligase (EC 6.2.1.12) 1 - potato >gi_169574 (M62755) 4-coumarate--CoA ligase [Solanum tuberosum]

Seq. No.	130289
Contig ID	41148_1.R1010
5'-most EST	LIB3234-009-P1-K1-E11
Method	BLASTN
NCBI GI	g2191126
BLAST score	267
E value	1.0e-148
Match length	530
% identity	95
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	130290
Contig ID	41156_1.R1010
5'-most EST	jC-atXP9C94E18T7d1
Method	BLASTX
NCBI GI	g2252866
BLAST score	223
E value	4.0e-18
Match length	60
% identity	68

NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	130291
Contig ID	41169_1.R1010
5'-most EST	LIB3168-073-P1-K1-E3
Method	BLASTX
NCBI GI	g2129553
BLAST score	728
E value	1.0e-120
Match length	313
% identity	67
NCBI Description	calcium-dependent protein kinase 6 - Arabidopsis thaliana

Seq. No.	130292
Contig ID	41172_1.R1010
5'-most EST	LIB3168-077-P1-K1-E6
Method	BLASTN
NCBI GI	g2264321
BLAST score	328
E value	0.0e+00
Match length	472
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	130293
Contig ID	41215_1.R1010
5'-most EST	LIB3168-074-P1-K1-B11
Method	BLASTX
NCBI GI	g1113941
BLAST score	97
E value	2.0e-03
Match length	100
% identity	67
NCBI Description	(U40713) Pv42p [Phaseolus vulgaris]

Seq. No.	130294
Contig ID	41239_1.R1010
5'-most EST	LIB35-030-Q1-E1-E3
Method	BLASTN
NCBI GI	g3869069
BLAST score	444
E value	0.0e+00
Match length	472
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	130295
Contig ID	41245_1.R1010
5'-most EST	LIB3168-074-P1-K1-E11
Method	BLASTN
NCBI GI	g2088638
BLAST score	643
E value	0.0e+00
Match length	679

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130296
Contig ID	41275_1.R1010
5'-most EST	g937927
Method	BLASTX
NCBI GI	g3402678
BLAST score	469
E value	1.0e-136
Match length	295
% identity	86
NCBI Description	(AC004697) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	130297
Contig ID	41277_1.R1010
5'-most EST	LIB3168-074-P1-K1-H1

Seq. No.	130298
Contig ID	41300_1.R1010
5'-most EST	LIB3234-093-P1-K1-C5
Method	BLASTX
NCBI GI	g2828281
BLAST score	482
E value	2.0e-48
Match length	171
% identity	58
NCBI Description	(AL021687) hypothetical protein [Arabidopsis thaliana] >gi_2832635_emb_CAA16764_ (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130299
Contig ID	41305_1.R1010
5'-most EST	LIB3176-017-P1-K1-G10
Method	BLASTX
NCBI GI	g3894158
BLAST score	249
E value	5.0e-21
Match length	124
% identity	39
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	130300
Contig ID	41311_1.R1010
5'-most EST	LIB3168-075-P1-K1-C2
Method	BLASTX
NCBI GI	g133917
BLAST score	615
E value	2.0e-77
Match length	162
% identity	87
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 >gi_70856_pir__R3NT2 ribosomal protein S2 - common tobacco chloroplast >gi_11814_emb_CAA77345_ (Z00044) ribosomal protein S2 [Nicotiana tabacum] >gi_225274_prf__1211235J ribosomal

protein S2 [Nicotiana tabacum]

Seq. No.	130301
Contig ID	41328_1.R1010
5'-most EST	g2758604
Method	BLASTX
NCBI GI	g1903357
BLAST score	569
E value	2.0e-58
Match length	217
% identity	46
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	130302
Contig ID	41328_2.R1010
5'-most EST	LIB3168-075-P1-K1-D9
Method	BLASTX
NCBI GI	g1903357
BLAST score	300
E value	3.0e-27
Match length	95
% identity	60
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	130303
Contig ID	41365_1.R1010
5'-most EST	LIB3168-075-P1-K1-H5
Method	BLASTN
NCBI GI	g16559
BLAST score	170
E value	1.0e-90
Match length	232
% identity	95
NCBI Description	A.thaliana gene for tRNA-Ala (P-2-L)

Seq. No.	130304
Contig ID	41409_1.R1010
5'-most EST	LIB3234-093-P1-K1-A9
Method	BLASTN
NCBI GI	g2924257
BLAST score	216
E value	1.0e-118
Match length	304
% identity	46
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	130305
Contig ID	41425_1.R1010
5'-most EST	LIB3168-076-P1-K1-E6
Method	BLASTX
NCBI GI	g3176714
BLAST score	811
E value	8.0e-87
Match length	163
% identity	96

NCBI Description	(AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No.	130306
Contig ID	41430_1.R1010
5'-most EST	LIB3168-076-P1-K1-F2
Method	BLASTN
NCBI GI	g1707006
BLAST score	642
E value	0.0e+00
Match length	670
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130307
Contig ID	41452_1.R1010
5'-most EST	jC-atXP111C124I7T7d1

Seq. No.	130308
Contig ID	41467_1.R1010
5'-most EST	g3868957

Seq. No.	130309
Contig ID	41483_1.R1010
5'-most EST	LIB3175-068-P1-K1-F3
Method	BLASTX
NCBI GI	g2605769
BLAST score	251
E value	6.0e-21
Match length	100
% identity	60
NCBI Description	(AF027288) NADH dehydrogenase [Olea europaea]

Seq. No.	130310
Contig ID	41492_2.R1010
5'-most EST	g1053729
Method	BLASTX
NCBI GI	g2894561
BLAST score	243
E value	3.0e-20
Match length	134
% identity	39
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	130311
Contig ID	41599_1.R1010
5'-most EST	LIB3168-078-P1-K1-F6
Method	BLASTN
NCBI GI	g4191771
BLAST score	403
E value	0.0e+00
Match length	467
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130312
Contig ID	41655_1.R1010
5'-most EST	LIB3234-091-P1-K1-A6
Method	BLASTX
NCBI GI	g3935151
BLAST score	781
E value	2.0e-83
Match length	144
% identity	100
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	130313
Contig ID	41669_1.R1010
5'-most EST	LIB3176-011-P1-K1-F1
Method	BLASTN
NCBI GI	g4539378
BLAST score	234
E value	1.0e-128
Match length	725
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	130314
Contig ID	41670_1.R1010
5'-most EST	LIB3168-079-P1-K1-E8

Seq. No.	130315
Contig ID	41689_1.R1010
5'-most EST	LIB3168-079-P1-K1-H10
Method	BLASTX
NCBI GI	g2708741
BLAST score	932
E value	1.0e-101
Match length	181
% identity	99
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130316
Contig ID	41691_1.R1010
5'-most EST	g2763273
Method	BLASTX
NCBI GI	g2924784
BLAST score	263
E value	2.0e-27
Match length	109
% identity	37
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	130317
Contig ID	41704_1.R1010
5'-most EST	g757653

Seq. No.	130318
Contig ID	41720_1.R1010
5'-most EST	LIB3168-080-P1-K1-C12

Method	BLASTX
NCBI GI	g1170191
BLAST score	624
E value	4.0e-65
Match length	132
% identity	95
NCBI Description	HOMEOBOX PROTEIN HD1 >gi_1076449_pir__S47535 homeodomain-containing protein - rape >gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing protein [Brassica napus] >gi_1090522_prf__2019252A homeobox protein [Brassica napus]

Seq. No.	130319
Contig ID	41776_1.R1010
5'-most EST	LIB3234-100-P1-K1-F12
Method	BLASTX
NCBI GI	g2252634
BLAST score	198
E value	3.0e-15
Match length	59
% identity	64
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130320
Contig ID	41779_1.R1010
5'-most EST	jC-atXLIB327427P3a08b2
Method	BLASTN
NCBI GI	g1402874
BLAST score	87
E value	8.0e-41
Match length	119
% identity	94
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	130321
Contig ID	41813_1.R1010
5'-most EST	LIB3168-082-P1-K1-E3
Method	BLASTX
NCBI GI	g2501296
BLAST score	261
E value	1.0e-22
Match length	126
% identity	40
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]

Seq. No.	130322
Contig ID	41909_1.R1010
5'-most EST	g773477
Method	BLASTX
NCBI GI	g4336436
BLAST score	504
E value	1.0e-93
Match length	286
% identity	64
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	130323
Contig ID	41910_1.R1010
5'-most EST	LIB3168-083-P1-K1-G3
Method	BLASTX
NCBI GI	g2832777
BLAST score	322
E value	1.0e-29
Match length	131
% identity	44
NCBI Description	(AL021086) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /match=(desc:; /match=(desc:; EST embl_AA735498_AA735498 comes from the 5' UTR [Drosophila melanogaster]

Seq. No.	130324
Contig ID	41920_1.R1010
5'-most EST	LIB3168-083-P1-K1-H3
Method	BLASTN
NCBI GI	g4100059
BLAST score	347
E value	0.0e+00
Match length	400
% identity	49
NCBI Description	Arabidopsis thaliana AthlecRK4 pseudogene, complete sequence, receptor lectin kinase 3 (AthlecRK3) gene, complete cds, and AthlecRK2 pseudogene, complete sequence

Seq. No.	130325
Contig ID	41920_2.R1010
5'-most EST	jC-alXLIB327436P4b12a1
Method	BLASTN
NCBI GI	g4100059
BLAST score	202
E value	1.0e-109
Match length	214
% identity	50
NCBI Description	Arabidopsis thaliana AthlecRK4 pseudogene, complete sequence, receptor lectin kinase 3 (AthlecRK3) gene, complete cds, and AthlecRK2 pseudogene, complete sequence

Seq. No.	130326
Contig ID	41926_1.R1010
5'-most EST	LIB3234-100-P1-K1-A6
Method	BLASTX
NCBI GI	g2244897
BLAST score	751
E value	7.0e-80
Match length	147
% identity	99
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130327
Contig ID	41941_1.R1010
5'-most EST	LIB3168-084-P1-K1-B3

Seq. No.	130328
Contig ID	41970_1.R1010

5'-most EST	g2722506
Method	BLASTX
NCBI GI	g4455227
BLAST score	680
E value	2.0e-71
Match length	134
% identity	99
NCBI Description	(AL035440) SNF8 like protein [Arabidopsis thaliana]

Seq. No.	130329
Contig ID	41972_1.R1010
5'-most EST	LIB3176-028-P1-K1-F10
Method	BLASTX
NCBI GI	g4680707
BLAST score	327
E value	6.0e-30
Match length	229
% identity	37
NCBI Description	(AF132968) CGI-34 protein [Homo sapiens]

Seq. No.	130330
Contig ID	41993_1.R1010
5'-most EST	jC-atXP115C248F6T7051d1
Method	BLASTN
NCBI GI	g3800746
BLAST score	42
E value	5.0e-14
Match length	46
% identity	98
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	130331
Contig ID	41993_3.R1010
5'-most EST	LIB3177-066-P1-K1-C11

Seq. No.	130332
Contig ID	42001_1.R1010
5'-most EST	jC-atXP57C192L3T7091a1
Method	BLASTX
NCBI GI	g2191135
BLAST score	877
E value	2.0e-94
Match length	232
% identity	71
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	130333
Contig ID	42035_1.R1010
5'-most EST	LIB3168-086-P1-K1-C12
Method	BLASTN
NCBI GI	g3869071
BLAST score	465
E value	0.0e+00
Match length	536
% identity	97

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	130334
Contig ID	42067_1.R1010
5'-most EST	LIB3176-039-P1-K1-H4
Method	BLASTX
NCBI GI	g4544419
BLAST score	976
E value	1.0e-106
Match length	254
% identity	80
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	130335
Contig ID	42093_1.R1010
5'-most EST	jC-atXP83CG3B4T7028a1
Method	BLASTN
NCBI GI	g4220632
BLAST score	159
E value	6.0e-84
Match length	491
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	130336
Contig ID	42094_1.R1010
5'-most EST	LIB3168-086-P1-K1-H5
Method	BLASTX
NCBI GI	g2160191
BLAST score	97
E value	3.0e-03
Match length	64
% identity	80
NCBI Description	(AC000132) Identical to A. thaliana AtK-1 (gb_X79279). [Arabidopsis thaliana]

Seq. No.	130337
Contig ID	42120_1.R1010
5'-most EST	g906249
Method	BLASTX
NCBI GI	g3021266
BLAST score	143
E value	1.0e-08
Match length	81
% identity	37
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana] >gi_3292840_emb_CAA19830_ (AL031018) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	130338
Contig ID	42123_1.R1010
5'-most EST	LIB3176-047-P1-K1-G10
Method	BLASTX
NCBI GI	g3859696

BLAST score	181
E value	3.0e-13
Match length	132
% identity	33
NCBI Description	(AL033497) unknown hypothetical protein [Candida albicans]

Seq. No.	130339
Contig ID	42173_1.R1010
5'-most EST	LIB3234-089-P1-K1-F11
Method	BLASTX
NCBI GI	g3157937
BLAST score	701
E value	4.0e-74
Match length	151
% identity	87
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	130340
Contig ID	42186_1.R1010
5'-most EST	g2596435
Method	BLASTX
NCBI GI	g1255951
BLAST score	1065
E value	1.0e-116
Match length	245
% identity	79
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	130341
Contig ID	42187_1.R1010
5'-most EST	LIB3168-088-P1-K1-A12
Method	BLASTX
NCBI GI	g1336807
BLAST score	303
E value	2.0e-27
Match length	130
% identity	51
NCBI Description	(S81193) CEN=GTP-binding protein homolog [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum] >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]

Seq. No.	130342
Contig ID	42226_1.R1010
5'-most EST	jC-atXP32C147G17T7d2
Method	BLASTX
NCBI GI	g4586061
BLAST score	772
E value	3.0e-82
Match length	240
% identity	69
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]

Seq. No.	130343

Contig ID	42226_2.R1010
5'-most EST	g1328035
Method	BLASTN
NCBI GI	g2138315
BLAST score	205
E value	1.0e-111
Match length	229
% identity	98
NCBI Description	Arabidopsis thaliana root hair defective 3 (RHD3) gene, complete cds

Seq. No.	130344
Contig ID	42226_3.R1010
5'-most EST	g1053756
Method	BLASTN
NCBI GI	g4585890
BLAST score	133
E value	2.0e-68
Match length	326
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	130345
Contig ID	42226_6.R1010
5'-most EST	jC-atXLIB327438P3f01a2
Method	BLASTN
NCBI GI	g2138315
BLAST score	289
E value	1.0e-161
Match length	571
% identity	97
NCBI Description	Arabidopsis thaliana root hair defective 3 (RHD3) gene, complete cds

Seq. No.	130346
Contig ID	42238_1.R1010
5'-most EST	LIB3177-071-P1-K1-C2
Method	BLASTX
NCBI GI	g2335094
BLAST score	869
E value	9.0e-94
Match length	167
% identity	100
NCBI Description	(AC002339) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	130347
Contig ID	42249_1.R1010
5'-most EST	g3450081

Seq. No.	130348
Contig ID	42249_2.R1010
5'-most EST	LIB3168-088-P1-K1-H11

Seq. No.	130349
Contig ID	42258_1.R1010

5'-most EST	LIB3168-089-P1-K1-A12
Seq. No.	130350
Contig ID	42261_1.R1010
5'-most EST	jC-atXLIB327410P3a12a1
Method	BLASTN
NCBI GI	g4558586
BLAST score	293
E value	1.0e-164
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence
Seq. No.	130351
Contig ID	42280_1.R1010
5'-most EST	LIB3168-089-P1-K1-C12
Seq. No.	130352
Contig ID	42331_1.R1010
5'-most EST	LIB3234-097-P1-K1-C10
Method	BLASTN
NCBI GI	g3859610
BLAST score	158
E value	7.0e-84
Match length	198
% identity	95
NCBI Description	Arabidopsis thaliana BAC T9E19
Seq. No.	130353
Contig ID	42344_1.R1010
5'-most EST	g1053659
Seq. No.	130354
Contig ID	42345_1.R1010
5'-most EST	LIB3168-095-P1-K1-F10
Method	BLASTN
NCBI GI	g3869073
BLAST score	226
E value	1.0e-124
Match length	483
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]
Seq. No.	130355
Contig ID	42353_1.R1010
5'-most EST	LIB3234-040-P1-K1-C12
Method	BLASTX
NCBI GI	g225267
BLAST score	596
E value	1.0e-61
Match length	203
% identity	70
NCBI Description	ORF 1244 [Nicotiana tabacum]
Seq. No.	130356

Contig ID	42366_1.R1010
5'-most EST	LIB3168-090-P1-K1-C6
Seq. No.	130357
Contig ID	42373_1.R1010
5'-most EST	LIB3168-090-P1-K1-D3
Seq. No.	130358
Contig ID	42390_1.R1010
5'-most EST	LIB3168-090-P1-K1-F11
Method	BLASTN
NCBI GI	g2264367
BLAST score	220
E value	1.0e-120
Match length	367
% identity	94
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]
Seq. No.	130359
Contig ID	42391_1.R1010
5'-most EST	LIB3168-090-P1-K1-F3
Method	BLASTN
NCBI GI	g2618683
BLAST score	150
E value	1.0e-78
Match length	465
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130360
Contig ID	42426_1.R1010
5'-most EST	LIB3234-097-P1-K1-A6
Method	BLASTN
NCBI GI	g2618677
BLAST score	271
E value	1.0e-151
Match length	446
% identity	96
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	130361
Contig ID	42454_1.R1010
5'-most EST	LIB3168-091-P1-K1-E6
Method	BLASTN
NCBI GI	g2924505
BLAST score	214
E value	1.0e-117
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)
Seq. No.	130362
Contig ID	42455_1.R1010

5'-most EST	LIB3168-091-P1-K1-E7
Method	BLASTX
NCBI GI	g4544473
BLAST score	1009
E value	1.0e-110
Match length	263
% identity	77
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	130363
Contig ID	42455_2.R1010
5'-most EST	jC-atXP84CG5D10T7b1
Method	BLASTX
NCBI GI	g4544473
BLAST score	508
E value	2.0e-51
Match length	201
% identity	41
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	130364
Contig ID	42484_1.R1010
5'-most EST	LIB3168-100-P1-K1-G2

Seq. No.	130365
Contig ID	42505_1.R1010
5'-most EST	LIB3168-099-P1-K1-E7
Method	BLASTN
NCBI GI	g4589437
BLAST score	239
E value	1.0e-131
Match length	501
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	130366
Contig ID	42511_1.R1010
5'-most EST	LIB3168-100-P1-K1-B8

Seq. No.	130367
Contig ID	42549_1.R1010
5'-most EST	LIB3168-093-P1-K1-F4

Seq. No.	130368
Contig ID	42557_1.R1010
5'-most EST	LIB3234-098-P1-K1-E3
Method	BLASTX
NCBI GI	g3242709
BLAST score	259
E value	2.0e-22
Match length	70
% identity	70
NCBI Description	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]

Seq. No.	130369

Contig ID	42561_1.R1010
5'-most EST	LIB3168-100-P1-K1-E11
Method	BLASTN
NCBI GI	g4584351
BLAST score	75
E value	5.0e-34
Match length	342
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	130370
Contig ID	42565_1.R1010
5'-most EST	LIB3168-093-P1-K1-H10
Method	BLASTN
NCBI GI	g4220510
BLAST score	175
E value	2.0e-93
Match length	553
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	130371
Contig ID	42612_1.R1010
5'-most EST	LIB3168-094-P1-K1-D5
Method	BLASTX
NCBI GI	g4510348
BLAST score	199
E value	5.0e-15
Match length	157
% identity	33
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	130372
Contig ID	42615_1.R1010
5'-most EST	LIB3168-094-P1-K1-E1

Seq. No.	130373
Contig ID	42637_1.R1010
5'-most EST	LIB3168-094-P1-K1-G2
Method	BLASTN
NCBI GI	g2618683
BLAST score	383
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130374
Contig ID	42739_1.R1010
5'-most EST	LIB3168-096-P1-K1-A1
Method	BLASTX
NCBI GI	g2160189
BLAST score	378
E value	3.0e-36

Match length	137
% identity	9
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	130375
Contig ID	42744_1.R1010
5'-most EST	LIB3175-002-Q1-K1-A4
Method	BLASTX
NCBI GI	g2288981
BLAST score	711
E value	3.0e-75
Match length	136
% identity	69
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	130376
Contig ID	42752_1.R1010
5'-most EST	jC-atXLIB327416P4h02a1
Method	BLASTX
NCBI GI	g1296805
BLAST score	204
E value	3.0e-21
Match length	80
% identity	70
NCBI Description	(X90929) C-terminal peptidase of the D1 protein [Hordeum vulgare]

Seq. No.	130377
Contig ID	42762_1.R1010
5'-most EST	jC-atXP63C203G22T7d2
Method	BLASTN
NCBI GI	g4079614
BLAST score	462
E value	0.0e+00
Match length	565
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130378
Contig ID	42804_1.R1010
5'-most EST	LIB3168-096-P1-K1-F6
Method	BLASTN
NCBI GI	g3738275
BLAST score	408
E value	0.0e+00
Match length	553
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130379
Contig ID	42839_1.R1010

5'-most EST	LIB3168-098-P1-K1-A6
Method	BLASTN
NCBI GI	g4678291
BLAST score	282
E value	1.0e-157
Match length	305
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	130380
Contig ID	42882_1.R1010
5'-most EST	jC-atXP87C244G2T7b1
Method	BLASTN
NCBI GI	g4314354
BLAST score	565
E value	0.0e+00
Match length	1024
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130381
Contig ID	42928_1.R1010
5'-most EST	jC-atXLIB327420P4g02a1
Method	BLASTN
NCBI GI	g4567259
BLAST score	137
E value	1.0e-70
Match length	470
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	130382
Contig ID	42936_1.R1010
5'-most EST	LIB3168-099-P1-K1-C2
Method	BLASTN
NCBI GI	g2656029
BLAST score	300
E value	1.0e-168
Match length	517
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	130383
Contig ID	42942_1.R1010
5'-most EST	LIB3168-099-P1-K1-C8
Method	BLASTN
NCBI GI	g4263540
BLAST score	37
E value	3.0e-11
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130384
Contig ID	42944_1.R1010
5'-most EST	LIB3168-100-P1-K1-F1
Method	BLASTX
NCBI GI	g3935148
BLAST score	330
E value	4.0e-71
Match length	147
% identity	96
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	130385
Contig ID	42946_1.R1010
5'-most EST	LIB3234-098-P1-K1-G8

Seq. No.	130386
Contig ID	42957_1.R1010
5'-most EST	jC-atXP61C201B20T7d1
Method	BLASTN
NCBI GI	g3746057
BLAST score	444
E value	0.0e+00
Match length	556
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130387
Contig ID	42968_1.R1010
5'-most EST	jC-atXP34C150I2T7a1
Method	BLASTN
NCBI GI	g2264312
BLAST score	322
E value	0.0e+00
Match length	500
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	130388
Contig ID	42968_3.R1010
5'-most EST	jC-atXL1042Q1E1H07b1
Method	BLASTN
NCBI GI	g2264312
BLAST score	303
E value	1.0e-170
Match length	433
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	130389
Contig ID	42991_1.R1010
5'-most EST	jC-atX25027Q1E1H04a1
Method	BLASTN
NCBI GI	g4580454

BLAST score 413
E value 0.0e+00
Match length 443
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No. 130390
Contig ID 43001_1.R1010
5'-most EST LIB3234-082-Q1-K1-D10
Method BLASTX
NCBI GI g2505876
BLAST score 332
E value 6.0e-31
Match length 72
% identity 86
NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No. 130391
Contig ID 43011_1.R1010
5'-most EST LIB3168-100-P1-K1-B5

Seq. No. 130392
Contig ID 43036_1.R1010
5'-most EST LIB3168-100-P1-K1-D8
Method BLASTX
NCBI GI g2827621
BLAST score 317
E value 3.0e-29
Match length 143
% identity 44
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 130393
Contig ID 43047_1.R1010
5'-most EST LIB3176-105-P1-K1-B5

Seq. No. 130394
Contig ID 43072_1.R1010
5'-most EST g1054095
Method BLASTX
NCBI GI g585165
BLAST score 873
E value 4.0e-94
Match length 192
% identity 84
NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No. 130395
Contig ID 43095_1.R1010
5'-most EST g2047418
Method BLASTX
NCBI GI g2342734

BLAST score	615
E value	4.0e-64
Match length	135
% identity	86
NCBI Description	(AC002341) DNA-binding protein isolog [Arabidopsis thaliana]

Seq. No.	130396
Contig ID	43095_2.R1010
5'-most EST	LIB3175-001-Q1-K1-B11
Method	BLASTX
NCBI GI	g2342734
BLAST score	332
E value	7.0e-60
Match length	122
% identity	94
NCBI Description	(AC002341) DNA-binding protein isolog [Arabidopsis thaliana]

Seq. No.	130397
Contig ID	43098_1.R1010
5'-most EST	jC-atXLIB327428P1g08a2
Method	BLASTN
NCBI GI	g2961335
BLAST score	449
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	130398
Contig ID	43114_1.R1010
5'-most EST	jC-atXLIB327427P1e09b1

Seq. No.	130399
Contig ID	43114_3.R1010
5'-most EST	LIB3175-001-Q1-K1-C7

Seq. No.	130400
Contig ID	43119_1.R1010
5'-most EST	LIB3175-001-Q1-K1-D11
Method	BLASTN
NCBI GI	g4309747
BLAST score	292
E value	1.0e-163
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130401
Contig ID	43124_1.R1010
5'-most EST	g1158694
Method	BLASTN
NCBI GI	g3176695
BLAST score	208

E value	1.0e-113
Match length	522
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	130402
Contig ID	43153_1.R1010
5'-most EST	LIB3175-001-Q1-K1-G10

Seq. No.	130403
Contig ID	43155_1.R1010
5'-most EST	jC-atXP82CG1G7T7d3
Method	BLASTX
NCBI GI	g2982451
BLAST score	880
E value	9.0e-95
Match length	231
% identity	83
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	130404
Contig ID	43155_3.R1010
5'-most EST	jC-atXLIB327421P1h05b1
Method	BLASTN
NCBI GI	g2924653
BLAST score	351
E value	0.0e+00
Match length	363
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	130405
Contig ID	43174_1.R1010
5'-most EST	LIB3175-002-Q1-K1-A11
Method	BLASTN
NCBI GI	g1069997
BLAST score	101
E value	2.0e-49
Match length	372
% identity	94
NCBI Description	B.napus chloroplast accD gene

Seq. No.	130406
Contig ID	43180_1.R1010
5'-most EST	jC-atXLIB327411P3h03a1

Seq. No.	130407
Contig ID	43183_1.R1010
5'-most EST	jC-atXP85C241F10T7b1
Method	BLASTX
NCBI GI	g3582341
BLAST score	435
E value	1.0e-65
Match length	225

% identity 58
NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 130408
Contig ID 43191_1.R1010
5'-most EST LIB3175-002-Q1-K1-B8

Seq. No. 130409
Contig ID 43196_1.R1010
5'-most EST LIB3175-002-Q1-K1-C12
Method BLASTX
NCBI GI g3395588
BLAST score 156
E value 3.0e-10
Match length 80
% identity 39
NCBI Description (AL031179) serine-threonine protein phosphatase [Schizosaccharomyces pombe]

Seq. No. 130410
Contig ID 43218_1.R1010
5'-most EST g2722853
Method BLASTX
NCBI GI g585147
BLAST score 278
E value 2.0e-24
Match length 228
% identity 34
NCBI Description FLUG PROTEIN >gi_1078630_pir__A53186 fluG protein - Emericella nidulans >gi_450258 (L27817) FluG [Emericella nidulans]

Seq. No. 130411
Contig ID 43235_1.R1010
5'-most EST LIB3177-007-P1-K2-F5
Method BLASTN
NCBI GI g3241917
BLAST score 104
E value 3.0e-51
Match length 338
% identity 94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No. 130412
Contig ID 43236_1.R1010
5'-most EST jC-atXP63C204O24T7d2
Method BLASTX
NCBI GI g629669
BLAST score 169
E value 9.0e-12
Match length 124
% identity 42
NCBI Description hypothetical protein - tomato

Seq. No. 130413

Contig ID	43253_1.R1010
5'-most EST	LIB3176-098-P1-K1-F5
Method	BLASTX
NCBI GI	g2244919
BLAST score	514
E value	3.0e-52
Match length	131
% identity	85
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130414
Contig ID	43255_1.R1010
5'-most EST	LIB3175-003-P1-K1-A2
Method	BLASTX
NCBI GI	g4587615
BLAST score	642
E value	5.0e-67
Match length	194
% identity	66
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	130415
Contig ID	43273_1.R1010
5'-most EST	LIB3175-003-P1-K1-B8
Method	BLASTN
NCBI GI	g2947056
BLAST score	273
E value	1.0e-152
Match length	466
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130416
Contig ID	43274_1.R1010
5'-most EST	LIB3175-003-P1-K1-B9
Method	BLASTN
NCBI GI	g2827538
BLAST score	396
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	130417
Contig ID	43295_1.R1010
5'-most EST	jC-atXP41C164H19T7d1

Seq. No.	130418
Contig ID	43298_1.R1010
5'-most EST	g937254
Method	BLASTN
NCBI GI	g4006815
BLAST score	207

E value	1.0e-112
Match length	471
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130419
Contig ID	43302_1.R1010
5'-most EST	LIB3175-003-P1-K1-E2
Method	BLASTX
NCBI GI	g2914703
BLAST score	358
E value	7.0e-34
Match length	146
% identity	47
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	130420
Contig ID	43306_1.R1010
5'-most EST	LIB3175-003-P1-K1-E6
Method	BLASTN
NCBI GI	g3395421
BLAST score	434
E value	0.0e+00
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130421
Contig ID	43313_1.R1010
5'-most EST	LIB3175-043-P1-K1-G1
Method	BLASTX
NCBI GI	g4006827
BLAST score	460
E value	7.0e-46
Match length	177
% identity	50
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	130422
Contig ID	43314_1.R1010
5'-most EST	LIB3176-120-P2-K1-G1
Method	BLASTX
NCBI GI	g2462834
BLAST score	199
E value	2.0e-15
Match length	107
% identity	41
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130423
Contig ID	43318_1.R1010
5'-most EST	LIB3175-003-P1-K1-F7
Method	BLASTX
NCBI GI	g543565
BLAST score	200

E value	2.0e-15
Match length	77
% identity	44
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	130424
Contig ID	43324_1.R1010
5'-most EST	LIB3175-059-P1-K1-B5
Method	BLASTX
NCBI GI	g4467110
BLAST score	815
E value	3.0e-87
Match length	213
% identity	74
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	130425
Contig ID	43351_1.R1010
5'-most EST	jC-atXLIB327431P3e04a1
Method	BLASTN
NCBI GI	g531832
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	130426
Contig ID	43358_1.R1010
5'-most EST	jC-atXP108C190L20T7064d1
Method	BLASTX
NCBI GI	g3785978
BLAST score	741
E value	1.0e-78
Match length	171
% identity	85
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	130427
Contig ID	43365_1.R1010
5'-most EST	LIB3175-004-P1-K1-C12
Method	BLASTX
NCBI GI	g2944446
BLAST score	311
E value	2.0e-28
Match length	77
% identity	77
NCBI Description	(AF050756) cysteine endopeptidase precursor [Ricinus communis]

Seq. No.	130428
Contig ID	43413_1.R1010
5'-most EST	g2062902
Method	BLASTN

NCBI GI	g4263774
BLAST score	424
E value	0.0e+00
Match length	474
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130429
Contig ID	43414_1.R1010
5'-most EST	LIB3175-058-P1-K1-A3
Method	BLASTN
NCBI GI	g2342717
BLAST score	124
E value	4.0e-63
Match length	402
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130430
Contig ID	43427_1.R1010
5'-most EST	jC-atXLIB327410P1c02a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	240
E value	1.0e-132
Match length	414
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	130431
Contig ID	43427_2.R1010
5'-most EST	jC-alXLIB327435P4b09a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	277
E value	1.0e-154
Match length	503
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	130432
Contig ID	43433_1.R1010
5'-most EST	LIB3175-005-P1-K1-A9
Method	BLASTX
NCBI GI	g4140326
BLAST score	239
E value	9.0e-20
Match length	98
% identity	40
NCBI Description	(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins) [Homo sapiens]

Seq. No.	130433
Contig ID	43444_1.R1010
5'-most EST	g2763265
Method	BLASTN
NCBI GI	g3080430
BLAST score	308
E value	1.0e-173
Match length	398
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	130434
Contig ID	43457_1.R1010
5'-most EST	LIB3175-005-P1-K1-D5

Seq. No.	130435
Contig ID	43470_1.R1010
5'-most EST	LIB3175-039-P1-K1-F11
Method	BLASTX
NCBI GI	g3183088
BLAST score	214
E value	4.0e-17
Match length	68
% identity	54
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	130436
Contig ID	43475_1.R1010
5'-most EST	jC-atXLIB327438P2e06a1
Method	BLASTX
NCBI GI	g2317725
BLAST score	180
E value	4.0e-13
Match length	58
% identity	55
NCBI Description	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]

Seq. No.	130437
Contig ID	43479_1.R1010
5'-most EST	g3228577

Seq. No.	130438
Contig ID	43481_1.R1010
5'-most EST	LIB3177-084-P1-K1-B7
Method	BLASTX
NCBI GI	g3850573
BLAST score	2545
E value	0.0e+00
Match length	510
% identity	95
NCBI Description	(AC005278) Similar to gi_1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb_D90908. ESTs

gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from this gene. [Arabidopsis thaliana]

Seq. No.	130439
Contig ID	43481_2.R1010
5'-most EST	jC-atXP49C177I13T7018a1
Method	BLASTN
NCBI GI	g3789706
BLAST score	523
E value	0.0e+00
Match length	587
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130440
Contig ID	43490_1.R1010
5'-most EST	LIB3175-005-P1-K1-H2
Method	BLASTX
NCBI GI	g3953466
BLAST score	865
E value	3.0e-93
Match length	189
% identity	90
NCBI Description	(AC002328) F20N2.11 [Arabidopsis thaliana]

Seq. No.	130441
Contig ID	43510_1.R1010
5'-most EST	jC-atXLIB327431P4d12a1

Seq. No.	130442
Contig ID	43514_1.R1010
5'-most EST	g937344
Method	BLASTN
NCBI GI	g3449334
BLAST score	132
E value	6.0e-68
Match length	460
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	130443
Contig ID	43521_1.R1010
5'-most EST	LIB3175-006-P1-K1-C3
Method	BLASTX
NCBI GI	g3786324
BLAST score	589
E value	6.0e-61
Match length	201
% identity	53
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	130444
Contig ID	43527_1.R1010
5'-most EST	g2748074

Seq. No. 130445
Contig ID 43541_1.R1010
5'-most EST LIB3175-006-P1-K1-E4

Seq. No. 130446
Contig ID 43543_1.R1010
5'-most EST jC-alXLIB327435P4g01b1
Method BLASTN
NCBI GI g2582640
BLAST score 49
E value 3.0e-18
Match length 65
% identity 94
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 130447
Contig ID 43549_1.R1010
5'-most EST LIB3175-006-P1-K1-F2
Method BLASTX
NCBI GI g2829893
BLAST score 610
E value 2.0e-63
Match length 140
% identity 86
NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No. 130448
Contig ID 43551_1.R1010
5'-most EST jC-atXLIB327427P3d06a2
Method BLASTN
NCBI GI g2244901
BLAST score 641
E value 0.0e+00
Match length 698
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 130449
Contig ID 43551_2.R1010
5'-most EST LIB3175-045-P1-K1-F2
Method BLASTX
NCBI GI g3024426
BLAST score 415
E value 6.0e-41
Match length 106
% identity 79
NCBI Description PYRUVATE,PHOSPHATE DIKINASE PRECURSOR (PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi_1084302_pir__S55478 pyruvate,orthophosphate dikinase (EC 2.7.9.1) - common ice plant >gi_854265_emb_CAA57872_ (X82489) pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum]

Seq. No. 130450

Contig ID	43568_1.R1010
5'-most EST	LIB3175-006-P1-K1-H12
Method	BLASTN
NCBI GI	g3608126
BLAST score	441
E value	0.0e+00
Match length	516
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130451
Contig ID	43575_1.R1010
5'-most EST	g2597504
Method	BLASTX
NCBI GI	g3861450
BLAST score	145
E value	6.0e-09
Match length	52
% identity	48
NCBI Description	(Z99260) cps3 complementing, spindle poison sensitivity related protein [Schizosaccharomyces pombe]

Seq. No.	130452
Contig ID	43585_1.R1010
5'-most EST	jC-alXLIB327435P4g12b1
Method	BLASTN
NCBI GI	g4159710
BLAST score	369
E value	0.0e+00
Match length	550
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSD23, complete sequence

Seq. No.	130453
Contig ID	43586_1.R1010
5'-most EST	g493267

Seq. No.	130454
Contig ID	43593_1.R1010
5'-most EST	LIB3175-020-P1-K1-F2
Method	BLASTX
NCBI GI	g4589396
BLAST score	348
E value	1.0e-32
Match length	155
% identity	46
NCBI Description	(D89971) asparaginyl endopeptidase (VmPE-1) [Vigna mungo]

Seq. No.	130455
Contig ID	43607_1.R1010
5'-most EST	LIB3175-007-P1-K1-C5
Method	BLASTX
NCBI GI	g3461838
BLAST score	458
E value	9.0e-46

Match length 142
% identity 58
NCBI Description (AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 130456
Contig ID 43610_1.R1010
5'-most EST LIB3175-007-P1-K1-C8
Method BLASTN
NCBI GI g4512656
BLAST score 409
E value 0.0e+00
Match length 463
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No. 130457
Contig ID 43614_1.R1010
5'-most EST LIB3175-007-P1-K1-D11
Method BLASTN
NCBI GI g2924505
BLAST score 325
E value 0.0e+00
Match length 439
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No. 130458
Contig ID 43628_1.R1010
5'-most EST jC-atXLIB327427P4d10b2
Method BLASTX
NCBI GI g3004547
BLAST score 775
E value 2.0e-82
Match length 167
% identity 91
NCBI Description (AC003673) unknown protein [Arabidopsis thaliana] >gi_4185150 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 130459
Contig ID 43628_2.R1010
5'-most EST LIB3175-063-P1-K1-B4
Method BLASTX
NCBI GI g3004547
BLAST score 307
E value 6.0e-28
Match length 142
% identity 53
NCBI Description (AC003673) unknown protein [Arabidopsis thaliana] >gi_4185150 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 130460
Contig ID 43629_1.R1010

5'-most EST	LIB3234-015-P1-K1-G7
Method	BLASTN
NCBI GI	g4531433
BLAST score	596
E value	0.0e+00
Match length	608
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	130461
Contig ID	43634_1.R1010
5'-most EST	LIB3175-007-P1-K1-F1
Method	BLASTX
NCBI GI	g4538947
BLAST score	472
E value	3.0e-47
Match length	95
% identity	49
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	130462
Contig ID	43636_1.R1010
5'-most EST	LIB3175-007-P1-K1-F12
Method	BLASTN
NCBI GI	g2160155
BLAST score	223
E value	1.0e-122
Match length	423
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	130463
Contig ID	43650_1.R1010
5'-most EST	LIB3177-092-P1-K1-G10
Method	BLASTN
NCBI GI	g2244950
BLAST score	379
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130464
Contig ID	43659_1.R1010
5'-most EST	LIB3175-007-P1-K1-H3
Method	BLASTX
NCBI GI	g2979555
BLAST score	578
E value	4.0e-61
Match length	133
% identity	95
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	130465
Contig ID	43660_1.R1010
5'-most EST	LIB3175-007-P1-K1-H4
Method	BLASTX
NCBI GI	g3785983
BLAST score	382
E value	1.0e-36
Match length	139
% identity	53
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130466
Contig ID	43725_1.R1010
5'-most EST	LIB3175-045-P1-K1-E3
Method	BLASTX
NCBI GI	g2213592
BLAST score	329
E value	1.0e-30
Match length	134
% identity	26
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	130467
Contig ID	43728_1.R1010
5'-most EST	LIB3176-083-P1-K1-G7

Seq. No.	130468
Contig ID	43734_1.R1010
5'-most EST	g2722343
Method	BLASTN
NCBI GI	g3367567
BLAST score	36
E value	2.0e-10
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	130469
Contig ID	43743_1.R1010
5'-most EST	LIB3175-015-P1-K1-E3
Method	BLASTN
NCBI GI	g4760411
BLAST score	357
E value	0.0e+00
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	130470
Contig ID	43744_1.R1010
5'-most EST	LIB35-043-Q1-E1-H11
Method	BLASTX
NCBI GI	g2921094
BLAST score	829
E value	6.0e-89

Match length	177
% identity	92
NCBI Description	(AF018174) thioredoxin-f [Brassica napus]

Seq. No.	130471
Contig ID	43752_1.R1010
5'-most EST	LIB3175-051-P1-K1-A12
Method	BLASTX
NCBI GI	g3063465
BLAST score	606
E value	1.0e-62
Match length	266
% identity	39
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	130472
Contig ID	43753_1.R1010
5'-most EST	LIB3177-014-P1-K2-D3

Seq. No.	130473
Contig ID	43775_1.R1010
5'-most EST	LIB3175-015-P1-K1-H12
Method	BLASTX
NCBI GI	g2160185
BLAST score	350
E value	7.0e-33
Match length	104
% identity	62
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	130474
Contig ID	43780_1.R1010
5'-most EST	LIB3176-091-P1-K1-A2
Method	BLASTN
NCBI GI	g4263694
BLAST score	509
E value	0.0e+00
Match length	558
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130475
Contig ID	43833_1.R1010
5'-most EST	g635102
Method	BLASTX
NCBI GI	g3402692
BLAST score	301
E value	3.0e-27
Match length	88
% identity	67
NCBI Description	(AC004697) putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Arabidopsis thaliana]

Seq. No.	130476

Contig ID	43834_1.R1010
5'-most EST	LIB3177-085-P1-K1-C5
Method	BLASTN
NCBI GI	g3236234
BLAST score	405
E value	0.0e+00
Match length	477
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130477
Contig ID	43837_1.R1010
5'-most EST	jC-atXLIB327423P3d11b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	130478
Contig ID	43848_1.R1010
5'-most EST	LIB3175-016-P1-K1-F8
Method	BLASTX
NCBI GI	g3522946
BLAST score	501
E value	8.0e-51
Match length	105
% identity	90
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	130479
Contig ID	43852_1.R1010
5'-most EST	LIB3175-016-P1-K1-G11

Seq. No.	130480
Contig ID	43861_1.R1010
5'-most EST	LIB35-031-Q1-E1-F11

Seq. No.	130481
Contig ID	43870_1.R1010
5'-most EST	LIB3175-016-P1-K1-H8
Method	BLASTX
NCBI GI	g4454467
BLAST score	272
E value	9.0e-24
Match length	172
% identity	33
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	130482
Contig ID	43874_1.R1010
5'-most EST	g936859

Seq. No.	130483
Contig ID	43881_1.R1010
5'-most EST	jC-atXLIB327420P1g07a1
Method	BLASTX
NCBI GI	g4580394
BLAST score	370
E value	4.0e-35
Match length	128
% identity	56
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	130484
Contig ID	43882_1.R1010
5'-most EST	LIB3175-017-P1-K1-A8
Method	BLASTX
NCBI GI	g4220612
BLAST score	646
E value	1.0e-67
Match length	140
% identity	91
NCBI Description	(AB021934) nicotianamine synthase [Arabidopsis thaliana]

Seq. No.	130485
Contig ID	43884_1.R1010
5'-most EST	jC-atXP5C89E1T7d1
Method	BLASTN
NCBI GI	g4510360
BLAST score	928
E value	0.0e+00
Match length	969
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	130486
Contig ID	43895_1.R1010
5'-most EST	jC-alX25052Q1E1E02a1
Method	BLASTN
NCBI GI	g4589446
BLAST score	260
E value	1.0e-144
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	130487
Contig ID	43896_1.R1010
5'-most EST	LIB3175-017-P1-K1-H6

Seq. No.	130488
Contig ID	43907_1.R1010
5'-most EST	LIB3234-052-P1-K1-E12
Method	BLASTN
NCBI GI	g3046855
BLAST score	223

E value	1.0e-122
Match length	400
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	130489
Contig ID	43918_1.R1010
5'-most EST	jC-atXP123C117P18T7064d1
Method	BLASTN
NCBI GI	g4263774
BLAST score	424
E value	0.0e+00
Match length	536
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130490
Contig ID	43919_1.R1010
5'-most EST	LIB3175-017-P1-K1-E6
Method	BLASTX
NCBI GI	g2129473
BLAST score	393
E value	8.0e-38
Match length	141
% identity	55
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	130491
Contig ID	43953_1.R1010
5'-most EST	LIB3176-017-P1-K1-E8
Method	BLASTX
NCBI GI	g131211
BLAST score	176
E value	9.0e-13
Match length	36
% identity	94
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J) >gi_1363533_pir__S58571 photosystem I protein psaJ - maize chloroplast >gi_552734 (J04502) ORF42 [Zea mays] >gi_902241_emb_CAA60305_ (X86563) psaJ [Zea mays]

Seq. No.	130492
Contig ID	43957_1.R1010
5'-most EST	LIB3175-025-P1-K1-C4
Method	BLASTX
NCBI GI	g3522945
BLAST score	1113
E value	1.0e-122
Match length	222
% identity	97
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	130493
Contig ID	43970_1.R1010

5'-most EST	LIB3175-018-P1-K1-B2
Seq. No.	130494
Contig ID	43981_1.R1010
5'-most EST	LIB3175-018-P1-K1-C12
Seq. No.	130495
Contig ID	43988_1.R1010
5'-most EST	g1159020
Method	BLASTN
NCBI GI	g4417264
BLAST score	346
E value	0.0e+00
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130496
Contig ID	44005_1.R1010
5'-most EST	LIB3175-018-P1-K1-E5
Method	BLASTX
NCBI GI	g2565009
BLAST score	481
E value	3.0e-48
Match length	156
% identity	63
NCBI Description	(AC002983) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	130497
Contig ID	44015_1.R1010
5'-most EST	LIB3175-018-P1-K1-F3
Method	BLASTX
NCBI GI	g541310
BLAST score	146
E value	1.0e-08
Match length	88
% identity	32
NCBI Description	12RNP2 protein - Synechococcus sp. (PCC 6301) >gi_961511_dbj_BAA09863_ (D63794) 12kDa RNA-binding, 12RNP2 [Synechococcus sp.]
Seq. No.	130498
Contig ID	44028_1.R1010
5'-most EST	LIB3175-018-P1-K1-G4
Method	BLASTX
NCBI GI	g4741923
BLAST score	368
E value	3.0e-35
Match length	92
% identity	71
NCBI Description	(AF130849) PIT1 [Arabidopsis thaliana]
Seq. No.	130499
Contig ID	44034_1.R1010
5'-most EST	LIB3175-018-P1-K1-H1

Method	BLASTX
NCBI GI	g1644388
BLAST score	57
E value	1.0e-24
Match length	127
% identity	45
NCBI Description	(U72654) flavonoid 3'5'-hydroxylase [Eustoma grandiflorum]

Seq. No.	130500
Contig ID	44037_1.R1010
5'-most EST	g2446022

Seq. No.	130501
Contig ID	44039_1.R1010
5'-most EST	jC-atXLIB327431P2h06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	130502
Contig ID	44041_1.R1010
5'-most EST	LIB3175-029-P1-K1-A12

Seq. No.	130503
Contig ID	44045_1.R1010
5'-most EST	LIB3175-019-P1-K1-A10
Method	BLASTN
NCBI GI	g4415905
BLAST score	147
E value	6.0e-77
Match length	427
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130504
Contig ID	44048_1.R1010
5'-most EST	jC-atXP54C184O20T7057d1
Method	BLASTX
NCBI GI	g1542941
BLAST score	817
E value	1.0e-87
Match length	180
% identity	93
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	130505
Contig ID	44055_1.R1010
5'-most EST	LIB3175-048-P1-K1-E11

Seq. No.	130506
Contig ID	44068_1.R1010

5'-most EST	jC-alXLIB327436P4e02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	130507
Contig ID	44069_1.R1010
5'-most EST	jC-atXP86CG9D1T7b1
Method	BLASTN
NCBI GI	g2828278
BLAST score	328
E value	0.0e+00
Match length	497
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	130508
Contig ID	44082_1.R1010
5'-most EST	g506589
Method	BLASTX
NCBI GI	g2129675
BLAST score	769
E value	4.0e-82
Match length	174
% identity	85
NCBI Description	probable chlorophyll synthetase G4 - Arabidopsis thaliana >gi_972938 (U19382) putative chlorophyll synthetase [Arabidopsis thaliana] >gi_3068709 (AF049236) putative chlorophyll synthetase [Arabidopsis thaliana]

Seq. No.	130509
Contig ID	44083_1.R1010
5'-most EST	LIB3175-019-P1-K1-D7

Seq. No.	130510
Contig ID	44084_1.R1010
5'-most EST	g936366
Method	BLASTN
NCBI GI	g4757400
BLAST score	249
E value	1.0e-138
Match length	462
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20, complete sequence

Seq. No.	130511
Contig ID	44087_1.R1010
5'-most EST	LIB3175-019-P1-K1-E11
Method	BLASTN
NCBI GI	g4757411

BLAST score	243
E value	1.0e-134
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	130512
Contig ID	44094_1.R1010
5'-most EST	g931057
Method	BLASTN
NCBI GI	g4734003
BLAST score	436
E value	0.0e+00
Match length	470
% identity	65
NCBI Description	Arabidopsis thaliana chromosome II BAC F3L12 genomic sequence, complete sequence

Seq. No.	130513
Contig ID	44100_1.R1010
5'-most EST	LIB3175-019-P1-K1-F2
Method	BLASTX
NCBI GI	g2827699
BLAST score	224
E value	5.0e-41
Match length	150
% identity	65
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	130514
Contig ID	44122_1.R1010
5'-most EST	LIB3175-019-P1-K1-H3
Method	BLASTX
NCBI GI	g3063465
BLAST score	684
E value	3.0e-72
Match length	133
% identity	100
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	130515
Contig ID	44123_1.R1010
5'-most EST	LIB3177-068-P1-K1-B3
Method	BLASTN
NCBI GI	g2760169
BLAST score	245
E value	1.0e-135
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	130516
Contig ID	44130_1.R1010
5'-most EST	LIB3175-042-P1-K1-B4
Method	BLASTX

NCBI GI	g2245087
BLAST score	536
E value	7.0e-55
Match length	125
% identity	81
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130517
Contig ID	44144_1.R1010
5'-most EST	jC-atX22019Q1E1H02a1
Method	BLASTX
NCBI GI	g4506043
BLAST score	234
E value	2.0e-19
Match length	80
% identity	54
NCBI Description	prolyl endopeptidase >gi_1346769_sp_P48147_PPCE_HUMAN PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens]

Seq. No.	130518
Contig ID	44151_1.R1010
5'-most EST	LIB3175-020-P1-K1-B8

Seq. No.	130519
Contig ID	44158_1.R1010
5'-most EST	LIB3175-020-P1-K1-F6
Method	BLASTN
NCBI GI	g3869075
BLAST score	281
E value	1.0e-156
Match length	601
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	130520
Contig ID	44160_1.R1010
5'-most EST	LIB3175-020-P1-K1-C5
Method	BLASTN
NCBI GI	g2828186
BLAST score	175
E value	1.0e-93
Match length	497
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	130521
Contig ID	44198_1.R1010
5'-most EST	g1015438
Method	BLASTX
NCBI GI	g3831446
BLAST score	909
E value	2.0e-98

Match length 178
% identity 99
NCBI Description (AC005819) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 130522
Contig ID 44224_1.R1010
5'-most EST LIB3175-021-P1-K1-A8
Method BLASTN
NCBI GI g4678371
BLAST score 392
E value 0.0e+00
Match length 451
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No. 130523
Contig ID 44225_1.R1010
5'-most EST jC-atXLIB327421P3g11b1
Method BLASTN
NCBI GI g2618602
BLAST score 238
E value 1.0e-131
Match length 604
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 130524
Contig ID 44237_1.R1010
5'-most EST LIB3175-021-P1-K1-B9
Method BLASTX
NCBI GI g82200
BLAST score 309
E value 2.0e-28
Match length 121
% identity 58
NCBI Description hypothetical protein 1244 - common tobacco chloroplast

Seq. No. 130525
Contig ID 44268_1.R1010
5'-most EST jC-atXLIB327426P1e09b1
Method BLASTX
NCBI GI g3482979
BLAST score 636
E value 2.0e-66
Match length 147
% identity 87
NCBI Description (AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 130526
Contig ID 44273_1.R1010
5'-most EST LIB3175-024-P1-K1-B12
Method BLASTX

NCBI GI	g2979544
BLAST score	655
E value	7.0e-69
Match length	128
% identity	98
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	130527
Contig ID	44283_1.R1010
5'-most EST	jC-atXLIB327409P3d10a1
Method	BLASTX
NCBI GI	g2190557
BLAST score	1390
E value	1.0e-154
Match length	275
% identity	97
NCBI Description	(AC001229) F5I14.11 [Arabidopsis thaliana]

Seq. No.	130528
Contig ID	44305_1.R1010
5'-most EST	LIB3234-025-P1-K1-G1
Method	BLASTX
NCBI GI	g2244772
BLAST score	698
E value	7.0e-74
Match length	125
% identity	100
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	130529
Contig ID	44308_1.R1010
5'-most EST	LIB3175-022-P1-K1-A11
Method	BLASTX
NCBI GI	g133788
BLAST score	480
E value	4.0e-48
Match length	100
% identity	90
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S14 >gi_70987_pir__R3NT14 ribosomal protein S14 - common tobacco chloroplast >gi_11828_emb_CAA77350_ (Z00044) ribosomal protein S14 [Nicotiana tabacum] >gi_225196_prf__1211235AA ribosomal protein S14 [Nicotiana tabacum]

Seq. No.	130530
Contig ID	44332_1.R1010
5'-most EST	jC-atXP89CG6C10T7093d1
Method	BLASTX
NCBI GI	g4651202
BLAST score	193
E value	2.0e-14
Match length	125
% identity	34
NCBI Description	(AB026253) copper amine oxidase [Pisum sativum]

Seq. No.	130531
Contig ID	44351_1.R1010

5'-most EST	LIB3175-022-P1-K1-E3
Method	BLASTX
NCBI GI	g3695023
BLAST score	372
E value	1.0e-35
Match length	147
% identity	54
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	130532
Contig ID	44362_1.R1010
5'-most EST	LIB3175-022-P1-K1-F3
Method	BLASTX
NCBI GI	g140299
BLAST score	290
E value	3.0e-66
Match length	214
% identity	62
NCBI Description	CYTOCHROME C BIOGENESIS PROTEIN CCSA >gi_82213_pir__A05213 hypothetical protein 313 - common tobacco chloroplast >gi_1223666_emb_CAA77395_ (Z00044) c-type cytochrome synthesis protein [Nicotiana tabacum] >gi_225254_prf__1211235CN ORF 313 [Nicotiana tabacum]

Seq. No.	130533
Contig ID	44364_1.R1010
5'-most EST	g937820
Method	BLASTX
NCBI GI	g1575752
BLAST score	381
E value	4.0e-44
Match length	125
% identity	74
NCBI Description	(U70672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	130534
Contig ID	44372_1.R1010
5'-most EST	LIB3175-022-P1-K1-G2
Method	BLASTN
NCBI GI	g2182287
BLAST score	373
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	130535
Contig ID	44389_1.R1010
5'-most EST	LIB3175-024-P1-K1-A11
Method	BLASTN
NCBI GI	g3128143
BLAST score	301
E value	1.0e-169
Match length	317
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	130536
Contig ID	44407_1.R1010
5'-most EST	ARABL1-019-Q1-B1-C4
Method	BLASTX
NCBI GI	g4539324
BLAST score	170
E value	8.0e-12
Match length	69
% identity	52
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	130537
Contig ID	44443_1.R1010
5'-most EST	LIB3175-034-P1-K1-A5
Method	BLASTN
NCBI GI	g4757388
BLAST score	409
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	130538
Contig ID	44454_1.R1010
5'-most EST	LIB3234-086-Q1-K1-G10
Method	BLASTX
NCBI GI	g3831443
BLAST score	561
E value	2.0e-57
Match length	121
% identity	89
NCBI Description	(AC005819) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	130539
Contig ID	44469_1.R1010
5'-most EST	LIB3175-024-P1-K1-H12
Method	BLASTN
NCBI GI	g4678266
BLAST score	320
E value	1.0e-180
Match length	388
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	130540
Contig ID	44478_1.R1010
5'-most EST	g2748202

Seq. No.	130541
Contig ID	44491_1.R1010
5'-most EST	jC-atXLIB327402P4c02b1
Method	BLASTX

NCBI GI	g4545231
BLAST score	469
E value	6.0e-56
Match length	118
% identity	95
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	130542
Contig ID	44491_2.R1010
5'-most EST	jC-atXLIB327438P3e07a2
Method	BLASTX
NCBI GI	g4545231
BLAST score	49
E value	7.0e-97
Match length	205
% identity	84
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	130543
Contig ID	44505_1.R1010
5'-most EST	LIB3175-051-P1-K1-A7
Method	BLASTX
NCBI GI	g584865
BLAST score	269
E value	2.0e-23
Match length	132
% identity	36
NCBI Description	CYTOCHROME P450 76A2 (CYPLXXVIA2) (P-450EG7) >gi_542073_pir__S38534 cytochrome P450 76A2 - eggplant >gi_415911_emb_CAA50648_ (X71657) P450 hydroxylase [Solanum melongena]

Seq. No.	130544
Contig ID	44526_1.R1010
5'-most EST	LIB3175-025-P1-K1-E5

Seq. No.	130545
Contig ID	44527_1.R1010
5'-most EST	LIB3175-025-P1-K1-E6
Method	BLASTN
NCBI GI	g3643588
BLAST score	143
E value	1.0e-74
Match length	436
% identity	77
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130546
Contig ID	44529_1.R1010
5'-most EST	jC-atXP94CG11D2T7055d1
Method	BLASTN
NCBI GI	g3985931
BLAST score	360
E value	0.0e+00

Match length	481
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	130547
Contig ID	44537_1.R1010
5'-most EST	jC-atXLIB327420P2d10a2
Method	BLASTX
NCBI GI	g404688
BLAST score	265
E value	8.0e-25
Match length	95
% identity	55
NCBI Description	(L19074) cytochrome P450 [Catharanthus roseus]

Seq. No.	130548
Contig ID	44539_1.R1010
5'-most EST	LIB3175-029-P1-K1-A9
Method	BLASTN
NCBI GI	g3766106
BLAST score	204
E value	1.0e-110
Match length	726
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130549
Contig ID	44540_1.R1010
5'-most EST	LIB3175-025-P1-K1-F9
Method	BLASTX
NCBI GI	g3193316
BLAST score	846
E value	4.0e-91
Match length	174
% identity	94
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	130550
Contig ID	44548_1.R1010
5'-most EST	LIB3175-025-P1-K1-G7
Method	BLASTN
NCBI GI	g2264318
BLAST score	379
E value	0.0e+00
Match length	391
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	130551
Contig ID	44555_2.R1010
5'-most EST	jC-atXP38C158F18T7d1
Method	BLASTN
NCBI GI	g2760165

BLAST score	854
E value	0.0e+00
Match length	1677
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	130552
Contig ID	44600_1.R1010
5'-most EST	jC-atXP115C244E3T7001d1
Method	BLASTX
NCBI GI	g132794
BLAST score	530
E value	7.0e-54
Match length	160
% identity	69
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi_71288_pir__R5NT22 ribosomal protein L22 - common tobacco chloroplast >gi_11866_emb_CAA77382_ (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi_225236_prf__1211235BU ribosomal protein L22 [Nicotiana tabacum]

Seq. No.	130553
Contig ID	44600_2.R1010
5'-most EST	g937771
Method	BLASTX
NCBI GI	g133860
BLAST score	392
E value	8.0e-38
Match length	81
% identity	90
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 >gi_71027_pir__R3SY19 ribosomal protein S19 - soybean chloroplast

Seq. No.	130554
Contig ID	44628_1.R1010
5'-most EST	LIB3175-063-P1-K1-B2

Seq. No.	130555
Contig ID	44633_1.R1010
5'-most EST	LIB3175-026-P1-K1-H12
Method	BLASTX
NCBI GI	g2494130
BLAST score	462
E value	1.0e-53
Match length	140
% identity	81
NCBI Description	(AC002376) Contains similarity to Glycine SRC2 (gb_AB000130). [Arabidopsis thaliana]

Seq. No.	130556
Contig ID	44639_1.R1010
5'-most EST	LIB3175-027-P1-K1-A10
Method	BLASTN
NCBI GI	g2828183
BLAST score	247
E value	1.0e-136

Match length	438
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	130557
Contig ID	44643_1.R1010
5'-most EST	jC-atXP86CG10D8T7b1
Method	BLASTN
NCBI GI	g3985933
BLAST score	430
E value	0.0e+00
Match length	467
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9E15, complete sequence [Arabidopsis thaliana]

Seq. No.	130558
Contig ID	44644_1.R1010
5'-most EST	LIB3175-027-P1-K1-A6
Method	BLASTX
NCBI GI	g4335761
BLAST score	593
E value	2.0e-61
Match length	115
% identity	96
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	130559
Contig ID	44660_1.R1010
5'-most EST	LIB3175-027-P1-K1-C4
Method	BLASTX
NCBI GI	g1762975
BLAST score	160
E value	2.0e-10
Match length	169
% identity	31
NCBI Description	(U67160) p190-B [Mus musculus]

Seq. No.	130560
Contig ID	44660_2.R1010
5'-most EST	jC-atXLIB327431P4f05b1
Method	BLASTN
NCBI GI	g3046847
BLAST score	302
E value	1.0e-169
Match length	375
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	130561
Contig ID	44671_1.R1010
5'-most EST	LIB3176-009-P1-K1-H12

Seq. No.	130562
Contig ID	44738_1.R1010

5'-most EST	LIB3234-053-P1-K1-G10
Seq. No.	130563
Contig ID	44771_1.R1010
5'-most EST	LIB3176-062-P1-K1-C7
Seq. No.	130564
Contig ID	44776_1.R1010
5'-most EST	LIB3175-028-P1-K1-F3
Method	BLASTN
NCBI GI	g2842474
BLAST score	87
E value	5.0e-41
Match length	475
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)
Seq. No.	130565
Contig ID	44792_2.R1010
5'-most EST	LIB3175-028-P1-K1-G8
Method	BLASTX
NCBI GI	g4388726
BLAST score	477
E value	1.0e-115
Match length	214
% identity	95
NCBI Description	(AC006413) putative 12-oxophytodienoate-10,11-reductase [Arabidopsis thaliana]
Seq. No.	130566
Contig ID	44796_1.R1010
5'-most EST	g2596920
Method	BLASTN
NCBI GI	g1402874
BLAST score	305
E value	1.0e-171
Match length	389
% identity	97
NCBI Description	A.thaliana 81kb genomic sequence
Seq. No.	130567
Contig ID	44801_1.R1010
5'-most EST	LIB3175-077-P1-K1-H9
Method	BLASTN
NCBI GI	g4468103
BLAST score	433
E value	0.0e+00
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)
Seq. No.	130568
Contig ID	44844_1.R1010
5'-most EST	LIB3175-029-P1-K1-D4
Method	BLASTX

NCBI GI	g2218152
BLAST score	92
E value	2.0e-77
Match length	150
% identity	91
NCBI Description	(AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No.	130569
Contig ID	44863_1.R1010
5'-most EST	jC-atXLIB327402P4e04b1
Method	BLASTN
NCBI GI	g4582428
BLAST score	255
E value	1.0e-141
Match length	530
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	130570
Contig ID	44869_1.R1010
5'-most EST	LIB3175-029-P1-K1-F7
Method	BLASTX
NCBI GI	g2244825
BLAST score	177
E value	3.0e-35
Match length	124
% identity	71
NCBI Description	(Z97336) light induced protein homolog [Arabidopsis thaliana]

Seq. No.	130571
Contig ID	44870_1.R1010
5'-most EST	g957881
Method	BLASTX
NCBI GI	g3212116
BLAST score	159
E value	1.0e-13
Match length	125
% identity	34
NCBI Description	(Y17393) prefoldin subunit 2 [Mus musculus]

Seq. No.	130572
Contig ID	44872_1.R1010
5'-most EST	g493274
Method	BLASTX
NCBI GI	g1788469
BLAST score	479
E value	1.0e-47
Match length	238
% identity	44
NCBI Description	(AE000303) putative oxidoreductase [Escherichia coli]

Seq. No.	130573
Contig ID	44875_1.R1010
5'-most EST	LIB3175-029-P1-K1-G12

Method	BLASTX
NCBI GI	g2507330
BLAST score	251
E value	3.0e-21
Match length	142
% identity	34
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-II (EIF-4A-II) >gi_90966_pir__S00985 translation initiation factor eIF-4A II - mouse >gi_673434_emb_CAA40269_ (X56953) protein synthesis initiation factor 4A [Mus musculus] >gi_227239_prf__1617105C initiation factor 4AII [Oryctolagus cuniculus]

Seq. No.	130574
Contig ID	44881_1.R1010
5'-most EST	LIB3175-058-P1-K1-C5
Method	BLASTN
NCBI GI	g4757415
BLAST score	416
E value	0.0e+00
Match length	727
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	130575
Contig ID	44899_1.R1010
5'-most EST	g2749438

Seq. No.	130576
Contig ID	44915_1.R1010
5'-most EST	g1053640
Method	BLASTN
NCBI GI	g4567193
BLAST score	373
E value	0.0e+00
Match length	452
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	130577
Contig ID	44941_1.R1010
5'-most EST	jC-atXmonuni27Ca08a1
Method	BLASTX
NCBI GI	g4454481
BLAST score	557
E value	4.0e-57
Match length	108
% identity	98
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana] >gi_4512647_gb_AAD21702.1_ (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	130578
Contig ID	44945_1.R1010
5'-most EST	g1268159

Seq. No.	130579
Contig ID	44950_1.R1010
5'-most EST	jC-atXLIB327417P2e09b1
Method	BLASTX
NCBI GI	g4263519
BLAST score	502
E value	1.0e-50
Match length	99
% identity	100
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	130580
Contig ID	44951_1.R1010
5'-most EST	LIB3175-030-P1-K1-F4
Method	BLASTN
NCBI GI	g4589427
BLAST score	405
E value	0.0e+00
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	130581
Contig ID	44959_1.R1010
5'-most EST	LIB3175-030-P1-K1-G11
Method	BLASTN
NCBI GI	g3702315
BLAST score	204
E value	1.0e-111
Match length	456
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130582
Contig ID	44979_1.R1010
5'-most EST	LIB3175-031-P1-K1-A1
Method	BLASTN
NCBI GI	g2252848
BLAST score	45
E value	4.0e-16
Match length	231
% identity	84
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	130583
Contig ID	44998_1.R1010
5'-most EST	LIB3175-065-P1-K1-G2
Method	BLASTX
NCBI GI	g2435515
BLAST score	366
E value	5.0e-35
Match length	70
% identity	97

NCBI Description	(AF024504) No definition line found [Arabidopsis thaliana]
Seq. No.	130584
Contig ID	45013_1.R1010
5'-most EST	LIB3175-031-P1-K1-D2
Method	BLASTX
NCBI GI	g3435279
BLAST score	639
E value	1.0e-66
Match length	149
% identity	83
NCBI Description	(AF082391) protein kinase homolog [Arabidopsis thaliana]
Seq. No.	130585
Contig ID	45027_1.R1010
5'-most EST	jC-atXP79C239A12T7b1
Method	BLASTN
NCBI GI	g3985957
BLAST score	321
E value	1.0e-180
Match length	588
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.	130586
Contig ID	45040_1.R1010
5'-most EST	g473331
Method	BLASTX
NCBI GI	g2244974
BLAST score	252
E value	2.0e-68
Match length	178
% identity	76
NCBI Description	(Z97340) similarity to pore protein Pisum sativum [Arabidopsis thaliana]
Seq. No.	130587
Contig ID	45044_1.R1010
5'-most EST	LIB3234-060-P1-K1-E2
Seq. No.	130588
Contig ID	45092_1.R1010
5'-most EST	LIB3234-086-Q1-K1-E7
Method	BLASTN
NCBI GI	g3763915
BLAST score	37
E value	6.0e-11
Match length	871
% identity	46
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130589
Contig ID	45092_2.R1010
5'-most EST	g2047486
Method	BLASTN

NCBI GI	g3763915
BLAST score	437
E value	0.0e+00
Match length	469
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130590
Contig ID	45092_4.R1010
5'-most EST	LIB3176-121-P2-K1-D6
Method	BLASTN
NCBI GI	g3763915
BLAST score	42
E value	3.0e-14
Match length	408
% identity	68
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130591
Contig ID	45094_1.R1010
5'-most EST	LIB3175-032-P1-K1-D1
Method	BLASTN
NCBI GI	g4689466
BLAST score	252
E value	1.0e-139
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	130592
Contig ID	45108_1.R1010
5'-most EST	jC-atXP71C221J1T7082d1
Method	BLASTN
NCBI GI	g4191760
BLAST score	371
E value	0.0e+00
Match length	620
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	130593
Contig ID	45108_2.R1010
5'-most EST	LIB3175-052-P1-K1-H10
Method	BLASTX
NCBI GI	g3873710
BLAST score	351
E value	3.0e-33
Match length	101
% identity	61
NCBI Description	(Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409

comes

Seq. No.	130594
Contig ID	45119_1.R1010
5'-most EST	LIB3176-009-P1-K3-C3
Method	BLASTX
NCBI GI	g4309758
BLAST score	307
E value	5.0e-28
Match length	64
% identity	100
NCBI Description	(AC006217) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130595
Contig ID	45128_1.R1010
5'-most EST	LIB3175-032-P1-K1-F8
Method	BLASTX
NCBI GI	g3413714
BLAST score	397
E value	1.0e-38
Match length	122
% identity	22
NCBI Description	(AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	130596
Contig ID	45144_1.R1010
5'-most EST	LIB3175-032-P1-K1-H11
Method	BLASTX
NCBI GI	g131150
BLAST score	860
E value	9.0e-93
Match length	181
% identity	92
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_81515_pir__S00445 photosystem I protein A2 - spinach chloroplast >gi_12271_emb_CAA27745_ (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] >gi_225422_prf__1303218B gene psaB [Spinacia oleracea]

Seq. No.	130597
Contig ID	45157_1.R1010
5'-most EST	LIB35-016-Q1-E1-G12

Seq. No.	130598
Contig ID	45177_1.R1010
5'-most EST	jC-atXP32C147N1T7d2
Method	BLASTX
NCBI GI	g4006888
BLAST score	283
E value	1.0e-24
Match length	241
% identity	30
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	130599

Contig ID	45183_1.R1010
5'-most EST	jC-atXP44C170K13T7038a1
Method	BLASTX
NCBI GI	g297381
BLAST score	461
E value	8.0e-46
Match length	127
% identity	76
NCBI Description	(X67421) extA [Arabidopsis thaliana]

Seq. No.	130600
Contig ID	45183_2.R1010
5'-most EST	g1158613
Method	BLASTX
NCBI GI	g297381
BLAST score	371
E value	2.0e-35
Match length	125
% identity	66
NCBI Description	(X67421) extA [Arabidopsis thaliana]

Seq. No.	130601
Contig ID	45183_5.R1010
5'-most EST	g3449798
Method	BLASTX
NCBI GI	g297381
BLAST score	206
E value	1.0e-35
Match length	91
% identity	87
NCBI Description	(X67421) extA [Arabidopsis thaliana]

Seq. No.	130602
Contig ID	45191_1.R1010
5'-most EST	LIB3175-033-P1-K1-D4
Method	BLASTN
NCBI GI	g3510343
BLAST score	691
E value	0.0e+00
Match length	710
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	130603
Contig ID	45192_1.R1010
5'-most EST	LIB3175-033-P1-K1-D5
Method	BLASTN
NCBI GI	g4220510
BLAST score	211
E value	1.0e-115
Match length	388
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	130604

Contig ID	45205_1.R1010
5'-most EST	LIB3175-035-P1-K1-E3
Method	BLASTX
NCBI GI	g3894172
BLAST score	569
E value	9.0e-59
Match length	109
% identity	100
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	130605
Contig ID	45211_1.R1010
5'-most EST	LIB3175-033-P1-K1-F2
Method	BLASTN
NCBI GI	g2477521
BLAST score	319
E value	1.0e-179
Match length	434
% identity	21
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130606
Contig ID	45219_1.R1010
5'-most EST	LIB3175-033-P1-K1-G9

Seq. No.	130607
Contig ID	45225_1.R1010
5'-most EST	LIB3175-078-P1-K1-B12
Method	BLASTN
NCBI GI	g4757678
BLAST score	47
E value	3.0e-17
Match length	269
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	130608
Contig ID	45239_1.R1010
5'-most EST	LIB3175-034-P1-K1-A11
Method	BLASTX
NCBI GI	g4539319
BLAST score	73
E value	3.0e+00
Match length	198
% identity	43
NCBI Description	(AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	130609
Contig ID	45253_1.R1010
5'-most EST	g2393513
Method	BLASTN
NCBI GI	g2828186
BLAST score	404

E value	0.0e+00
Match length	448
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	130610
Contig ID	45253_2.R1010
5'-most EST	g933545
Method	BLASTN
NCBI GI	g2828186
BLAST score	83
E value	1.0e-38
Match length	412
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	130611
Contig ID	45260_1.R1010
5'-most EST	g2722553
Method	BLASTN
NCBI GI	g3128135
BLAST score	189
E value	1.0e-102
Match length	435
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	130612
Contig ID	45269_1.R1010
5'-most EST	LIB3175-034-P1-K1-C8

Seq. No.	130613
Contig ID	45271_1.R1010
5'-most EST	jC-atXLIB327430P4f10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	130614
Contig ID	45277_1.R1010
5'-most EST	LIB3175-034-P1-K1-D6

Seq. No.	130615
Contig ID	45287_1.R1010
5'-most EST	LIB3177-062-P1-K1-C5
Method	BLASTX
NCBI GI	g1363482
BLAST score	1124
E value	1.0e-123

Match length 246
% identity 90
NCBI Description IAA11 protein - Arabidopsis thaliana >gi_972925 (U18413) IAA11 [Arabidopsis thaliana]

Seq. No. 130616
Contig ID 45288_1.R1010
5'-most EST LIB3175-034-P1-K1-E7

Seq. No. 130617
Contig ID 45288_2.R1010
5'-most EST g2758761

Seq. No. 130618
Contig ID 45296_1.R1010
5'-most EST LIB3175-034-P1-K1-F4

Seq. No. 130619
Contig ID 45313_1.R1010
5'-most EST g2749229
Method BLASTX
NCBI GI g4539335
BLAST score 97
E value 4.0e-16
Match length 65
% identity 58
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 130620
Contig ID 45330_1.R1010
5'-most EST jC-atXLIB327414P2c05a1
Method BLASTN
NCBI GI g2696018
BLAST score 134
E value 4.0e-69
Match length 427
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 130621
Contig ID 45339_1.R1010
5'-most EST LIB3175-035-P1-K1-B12
Method BLASTN
NCBI GI g1419473
BLAST score 227
E value 1.0e-124
Match length 462
% identity 94
NCBI Description A.thaliana chloroplast ndhA gene

Seq. No. 130622
Contig ID 45345_1.R1010
5'-most EST LIB3175-035-P1-K1-B7

Seq. No. 130623
Contig ID 45350_1.R1010

5'-most EST	LIB3175-052-P1-K1-B1
Method	BLASTN
NCBI GI	g2281081
BLAST score	231
E value	1.0e-127
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130624
Contig ID	45355_1.R1010
5'-most EST	LIB3175-035-P1-K1-C7
Method	BLASTN
NCBI GI	g4467094
BLAST score	431
E value	0.0e+00
Match length	496
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	130625
Contig ID	45360_1.R1010
5'-most EST	LIB3175-035-P1-K1-D2
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	9.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	130626
Contig ID	45363_1.R1010
5'-most EST	LIB3175-035-P1-K1-D5
Method	BLASTN
NCBI GI	g4733952
BLAST score	425
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	130627
Contig ID	45368_1.R1010
5'-most EST	LIB3176-071-P1-K1-C7
Method	BLASTX
NCBI GI	g4587615
BLAST score	462
E value	3.0e-60
Match length	172
% identity	63
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	130628
Contig ID	45397_1.R1010
5'-most EST	LIB3175-035-P1-K1-G7

Seq. No.	130629
Contig ID	45401_1.R1010
5'-most EST	LIB3175-035-P1-K1-H10
Method	BLASTX
NCBI GI	g1170606
BLAST score	417
E value	1.0e-40
Match length	148
% identity	53
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	130630
Contig ID	45405_1.R1010
5'-most EST	jC-atXLIB327427P4f02a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	130631
Contig ID	45407_1.R1010
5'-most EST	LIB3175-035-P1-K1-H5
Method	BLASTN
NCBI GI	g3449325
BLAST score	363
E value	0.0e+00
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	130632
Contig ID	45419_1.R1010
5'-most EST	g2393706
Method	BLASTX
NCBI GI	g1065484
BLAST score	147
E value	5.0e-09
Match length	102
% identity	32
NCBI Description	(U40415) similar to S. cerevisiae LAG1 (SP:P38703) [Caenorhabditis elegans]

Seq. No.	130633
Contig ID	45434_1.R1010
5'-most EST	LIB3175-036-P1-K1-C1
Method	BLASTX
NCBI GI	g2842490
BLAST score	646
E value	1.0e-67
Match length	144
% identity	87
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	130634
Contig ID	45442_1.R1010
5'-most EST	LIB3234-048-P1-K1-B4
Method	BLASTN
NCBI GI	g3327922
BLAST score	158
E value	3.0e-83
Match length	720
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130635
Contig ID	45477_1.R1010
5'-most EST	g1033244
Method	BLASTX
NCBI GI	g2829892
BLAST score	1049
E value	1.0e-114
Match length	199
% identity	98
NCBI Description	(AC002311) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	130636
Contig ID	45481_1.R1010
5'-most EST	LIB3175-036-P1-K1-G4

Seq. No.	130637
Contig ID	45498_1.R1010
5'-most EST	g2748510
Method	BLASTN
NCBI GI	g2924257
BLAST score	347
E value	0.0e+00
Match length	430
% identity	48
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	130638
Contig ID	45503_1.R1010
5'-most EST	LIB3177-071-P1-K1-F1
Method	BLASTN
NCBI GI	g2618602
BLAST score	248
E value	1.0e-137

Match length	503
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	130639
Contig ID	45546_1.R1010
5'-most EST	g502061
Method	BLASTX
NCBI GI	g4490292
BLAST score	47
E value	6.0e-89
Match length	202
% identity	86
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	130640
Contig ID	45557_1.R1010
5'-most EST	LIB3175-037-P1-K1-G6
Method	BLASTN
NCBI GI	g3641835
BLAST score	184
E value	6.0e-99
Match length	275
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	130641
Contig ID	45563_1.R1010
5'-most EST	g2757407
Method	BLASTX
NCBI GI	g4586576
BLAST score	312
E value	1.0e-28
Match length	102
% identity	61
NCBI Description	(AB024992) multidrug resistance protein [Cicer arietinum]

Seq. No.	130642
Contig ID	45581_1.R1010
5'-most EST	jC-atXLIB327439P2f10b2
Method	BLASTN
NCBI GI	g402551
BLAST score	236
E value	1.0e-130
Match length	252
% identity	99
NCBI Description	A.thaliana gene for acetohydroxy acid isomeroreductase

Seq. No.	130643
Contig ID	45590_1.R1010
5'-most EST	g1159283
Method	BLASTN
NCBI GI	g3510347
BLAST score	213
E value	1.0e-116

Match length	530
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	130644
Contig ID	45591_1.R1010
5'-most EST	LIB3175-038-P1-K1-C10
Method	BLASTN
NCBI GI	g3702731
BLAST score	177
E value	1.0e-94
Match length	674
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	130645
Contig ID	45613_1.R1010
5'-most EST	g1215991
Method	BLASTN
NCBI GI	g4432829
BLAST score	272
E value	1.0e-151
Match length	478
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130646
Contig ID	45643_1.R1010
5'-most EST	LIB3175-055-P1-K1-A7

Seq. No.	130647
Contig ID	45663_1.R1010
5'-most EST	LIB3175-039-P1-K1-B1
Method	BLASTX
NCBI GI	g167012
BLAST score	636
E value	3.0e-66
Match length	171
% identity	67
NCBI Description	(J03897) carboxypeptidase I precursor [Hordeum vulgare]

Seq. No.	130648
Contig ID	45689_1.R1010
5'-most EST	LIB3175-040-P1-K1-D5
Method	BLASTX
NCBI GI	g3608263
BLAST score	294
E value	2.0e-26
Match length	60
% identity	83
NCBI Description	(AB017565) Dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	130649
Contig ID	45704_1.R1010

5'-most EST	g2733325
Method	BLASTX
NCBI GI	g2506277
BLAST score	633
E value	5.0e-66
Match length	156
% identity	85
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]

Seq. No.	130650
Contig ID	45707_1.R1010
5'-most EST	g2723259
Method	BLASTN
NCBI GI	g4432847
BLAST score	296
E value	1.0e-165
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130651
Contig ID	45707_2.R1010
5'-most EST	LIB3175-039-P1-K1-F12
Method	BLASTN
NCBI GI	g4432847
BLAST score	410
E value	0.0e+00
Match length	503
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130652
Contig ID	45727_1.R1010
5'-most EST	g2596645

Seq. No.	130653
Contig ID	45734_1.R1010
5'-most EST	LIB3175-040-P1-K1-A2
Method	BLASTX
NCBI GI	g4220480
BLAST score	276
E value	2.0e-24
Match length	102
% identity	52
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	130654
Contig ID	45759_1.R1010
5'-most EST	g773534
Method	BLASTX
NCBI GI	g1174718
BLAST score	749
E value	1.0e-79

Match length	182
% identity	76
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	130655
Contig ID	45771_1.R1010
5'-most EST	LIB3176-065-P1-K1-B1
Method	BLASTX
NCBI GI	g3927830
BLAST score	183
E value	2.0e-13
Match length	80
% identity	50
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130656
Contig ID	45784_1.R1010
5'-most EST	LIB3175-051-P1-K1-D7
Method	BLASTX
NCBI GI	g4580394
BLAST score	524
E value	8.0e-60
Match length	213
% identity	53
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	130657
Contig ID	45785_1.R1010
5'-most EST	LIB3175-040-P1-K1-F8
Method	BLASTX
NCBI GI	g4469022
BLAST score	44
E value	3.0e-72
Match length	141
% identity	100
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	130658
Contig ID	45795_1.R1010
5'-most EST	LIB3175-040-P1-K1-H12
Method	BLASTX
NCBI GI	g3859998
BLAST score	302
E value	2.0e-31
Match length	156
% identity	47
NCBI Description	(AF091080) unknown [Homo sapiens]

Seq. No.	130659
Contig ID	45801_1.R1010
5'-most EST	jC-atXP78CF5C4T7b1
Method	BLASTX

NCBI GI	g2832625
BLAST score	204
E value	8.0e-16
Match length	146
% identity	39
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	130660
Contig ID	45801_2.R1010
5'-most EST	g2747464
Method	BLASTX
NCBI GI	g2832625
BLAST score	164
E value	1.0e-56
Match length	147
% identity	83
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	130661
Contig ID	45801_3.R1010
5'-most EST	LIB3234-074-P1-K1-D1
Method	BLASTN
NCBI GI	g2832611
BLAST score	355
E value	0.0e+00
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	130662
Contig ID	45809_1.R1010
5'-most EST	LIB3234-053-P1-K1-G11
Method	BLASTN
NCBI GI	g4589435
BLAST score	515
E value	0.0e+00
Match length	547
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	130663
Contig ID	45810_1.R1010
5'-most EST	g2393329
Method	BLASTN
NCBI GI	g1931636
BLAST score	358
E value	0.0e+00
Match length	455
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	130664
Contig ID	45813_1.R1010
5'-most EST	g2763700

Seq. No.	130665
Contig ID	45815_1.R1010
5'-most EST	LIB3175-041-P1-K1-B2
Method	BLASTX
NCBI GI	g4455192
BLAST score	240
E value	5.0e-20
Match length	127
% identity	24
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	130666
Contig ID	45829_1.R1010
5'-most EST	LIB3177-090-P1-K1-A9

Seq. No.	130667
Contig ID	45832_1.R1010
5'-most EST	jC-atXLIB327421P1f05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	130668
Contig ID	45843_1.R1010
5'-most EST	jC-atXP32C144N22T7d2

Seq. No.	130669
Contig ID	45847_1.R1010
5'-most EST	jC-atXP91C247G2T7b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	775
E value	1.0e-82
Match length	163
% identity	86
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	130670
Contig ID	45847_2.R1010
5'-most EST	jC-atXP98CH8B3T7b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	89
E value	8.0e-59
Match length	130
% identity	84
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	130671
Contig ID	45898_1.R1010
5'-most EST	g906480
Method	BLASTX

NCBI GI	g2827529
BLAST score	1184
E value	1.0e-130
Match length	241
% identity	94
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	130672
Contig ID	45914_1.R1010
5'-most EST	LIB3175-042-P1-K1-C2
Method	BLASTN
NCBI GI	g1865678
BLAST score	270
E value	1.0e-150
Match length	364
% identity	100
NCBI Description	A.thaliana ATB2 gene

Seq. No.	130673
Contig ID	45936_1.R1010
5'-most EST	LIB3175-042-P1-K1-E2
Method	BLASTX
NCBI GI	g4759280
BLAST score	214
E value	5.0e-17
Match length	114
% identity	42
NCBI Description	U5 snRNP-specific protein, 116 kD >gi_434759_dbj_BAA04699_ (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No.	130674
Contig ID	45937_2.R1010
5'-most EST	LIB3176-058-P1-K1-F11
Method	BLASTN
NCBI GI	g4733991
BLAST score	36
E value	1.0e-10
Match length	60
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T4D8 genomic sequence, complete sequence

Seq. No.	130675
Contig ID	45952_1.R1010
5'-most EST	LIB3175-042-P1-K1-G10
Method	BLASTX
NCBI GI	g4587513
BLAST score	654
E value	2.0e-68
Match length	182
% identity	68
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	130676
Contig ID	45956_1.R1010

5'-most EST	LIB3175-042-P1-K1-G3
Method	BLASTX
NCBI GI	g3540185
BLAST score	328
E value	3.0e-30
Match length	137
% identity	44
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	130677
Contig ID	45959_1.R1010
5'-most EST	LIB3175-042-P1-K1-G7
Method	BLASTN
NCBI GI	g3319365
BLAST score	42
E value	5.0e-14
Match length	116
% identity	78
NCBI Description	Arabidopsis thaliana BAC T24M8

Seq. No.	130678
Contig ID	45961_1.R1010
5'-most EST	jC-atXP91CG6H9T7b1
Method	BLASTN
NCBI GI	g2924728
BLAST score	240
E value	1.0e-132
Match length	445
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	130679
Contig ID	45968_1.R1010
5'-most EST	LIB3175-042-P1-K1-H4
Method	BLASTX
NCBI GI	g2983997
BLAST score	325
E value	6.0e-30
Match length	120
% identity	52
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	130680
Contig ID	45973_1.R1010
5'-most EST	LIB35-034-Q1-E1-D1
Method	BLASTN
NCBI GI	g2815404
BLAST score	159
E value	5.0e-84
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No. 130681

Contig ID	45987_1.R1010
5'-most EST	jC-atXLIB327406P2h04a1
Method	BLASTX
NCBI GI	g3157934
BLAST score	322
E value	1.0e-29
Match length	64
% identity	98
NCBI Description	(AC002131) Similar to hypothetical protein F09E5.8 gb_U37429 from C. elegans. ESTs gb_T42019 and gb_N97000 come from this gene. [Arabidopsis thaliana]

Seq. No.	130682
Contig ID	45990_1.R1010
5'-most EST	LIB3175-043-P1-K1-G8
Method	BLASTN
NCBI GI	g2244991
BLAST score	389
E value	0.0e+00
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130683
Contig ID	45998_1.R1010
5'-most EST	LIB3175-056-P1-K1-D8
Method	BLASTN
NCBI GI	g4757395
BLAST score	35
E value	4.0e-10
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	130684
Contig ID	46032_1.R1010
5'-most EST	jC-atXP90C245H19T7d2
Method	BLASTN
NCBI GI	g3510343
BLAST score	489
E value	0.0e+00
Match length	616
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	130685
Contig ID	46063_1.R1010
5'-most EST	g403229
Method	BLASTX
NCBI GI	g2317906
BLAST score	880
E value	4.0e-95
Match length	169
% identity	99

NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]
Seq. No.	130686
Contig ID	46071_1.R1010
5'-most EST	LIB3175-044-P1-K1-B5
Method	BLASTX
NCBI GI	g1931644
BLAST score	272
E value	1.0e-23
Match length	123
% identity	45
NCBI Description	(U95973) membrane protein PTM1 precursor isolog [Arabidopsis thaliana]
Seq. No.	130687
Contig ID	46076_1.R1010
5'-most EST	LIB3177-090-P1-K1-F7
Method	BLASTX
NCBI GI	g1532135
BLAST score	300
E value	4.0e-27
Match length	74
% identity	76
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]
Seq. No.	130688
Contig ID	46080_1.R1010
5'-most EST	LIB3175-044-P1-K1-C5
Method	BLASTN
NCBI GI	g3201608
BLAST score	61
E value	2.0e-25
Match length	89
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	130689
Contig ID	46094_1.R1010
5'-most EST	LIB3175-044-P1-K1-D8
Seq. No.	130690
Contig ID	46106_1.R1010
5'-most EST	jC-atXLIB327431P2b03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	38
E value	1.0e-11
Match length	46
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	130691
Contig ID	46115_1.R1010
5'-most EST	g2593467

Method	BLASTX
NCBI GI	g2894603
BLAST score	547
E value	5.0e-56
Match length	120
% identity	88
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	130692
Contig ID	46129_1.R1010
5'-most EST	LIB3175-044-P1-K1-H9
Method	BLASTX
NCBI GI	g4689316
BLAST score	838
E value	4.0e-90
Match length	170
% identity	51
NCBI Description	(AF130973) peroxisomal targeting signal type 2 receptor [Arabidopsis thaliana]

Seq. No.	130693
Contig ID	46203_1.R1010
5'-most EST	LIB3175-045-P1-K1-G10

Seq. No.	130694
Contig ID	46204_1.R1010
5'-most EST	g2749727
Method	BLASTN
NCBI GI	g4586241
BLAST score	60
E value	7.0e-25
Match length	561
% identity	73
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	130695
Contig ID	46204_2.R1010
5'-most EST	LIB3175-054-P1-K1-H4
Method	BLASTX
NCBI GI	g4586254
BLAST score	797
E value	4.0e-85
Match length	177
% identity	91
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	130696
Contig ID	46207_1.R1010
5'-most EST	g2733309
Method	BLASTX
NCBI GI	g3242730
BLAST score	619
E value	1.0e-64
Match length	139
% identity	91
NCBI Description	(AC003040) putative host response protein (Pir7)

[Arabidopsis thaliana]

Seq. No.	130697
Contig ID	46208_1.R1010
5'-most EST	LIB3175-045-P1-K1-G5
Method	BLASTX
NCBI GI	g4262226
BLAST score	261
E value	2.0e-22
Match length	108
% identity	52
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	130698
Contig ID	46209_1.R1010
5'-most EST	LIB3175-045-P1-K1-G6
Method	BLASTX
NCBI GI	g4760549
BLAST score	243
E value	3.0e-20
Match length	189
% identity	30
NCBI Description	(AB019494) IDN3 [Homo sapiens]

Seq. No.	130699
Contig ID	46238_1.R1010
5'-most EST	LIB3175-046-P1-K1-B3

Seq. No.	130700
Contig ID	46250_1.R1010
5'-most EST	LIB3175-046-P1-K1-C7
Method	BLASTX
NCBI GI	g3928134
BLAST score	536
E value	8.0e-55
Match length	147
% identity	29
NCBI Description	(AJ130956) annexin P38 [Capsicum annuum]

Seq. No.	130701
Contig ID	46281_1.R1010
5'-most EST	g2762259

Seq. No.	130702
Contig ID	46283_1.R1010
5'-most EST	LIB3175-046-P1-K1-F5
Method	BLASTX
NCBI GI	g2623295
BLAST score	63
E value	1.0e-12
Match length	62
% identity	68
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130703
Contig ID	46295_1.R1010
5'-most EST	jC-atXP98CH8D10T7040d1

Seq. No.	130704
Contig ID	46318_1.R1010
5'-most EST	g2759479
Method	BLASTX
NCBI GI	g2529229
BLAST score	279
E value	6.0e-50
Match length	124
% identity	79
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	130705
Contig ID	46319_1.R1010
5'-most EST	g2758124
Method	BLASTX
NCBI GI	g3548811
BLAST score	227
E value	9.0e-19
Match length	94
% identity	59
NCBI Description	(AC005313) kinetochore (SKP1p)-like protein [Arabidopsis thaliana]

Seq. No.	130706
Contig ID	46354_1.R1010
5'-most EST	jC-atXLIB327426P1e03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	4.0e-14
Match length	54
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	130707
Contig ID	46363_1.R1010
5'-most EST	LIB3177-088-P1-K1-F8
Method	BLASTX
NCBI GI	g2832661
BLAST score	365
E value	6.0e-35
Match length	131
% identity	64
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	130708
Contig ID	46368_1.R1010
5'-most EST	LIB3175-048-P1-K1-F10
Method	BLASTX
NCBI GI	g2244954
BLAST score	363
E value	2.0e-34
Match length	71
% identity	93

NCBI Description	(Z97340) strong similarity to ATsEH (EC 3.3.2.3) - Arabidopsis thaliana [Arabidopsis thaliana]

Seq. No.	130709
Contig ID	46398_1.R1010
5'-most EST	LIB3175-049-P1-K1-C12
Method	BLASTX
NCBI GI	g1402904
BLAST score	174
E value	1.0e-12
Match length	69
% identity	57
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	130710
Contig ID	46403_1.R1010
5'-most EST	g1215988
Method	BLASTX
NCBI GI	g2145358
BLAST score	648
E value	5.0e-68
Match length	145
% identity	90
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	130711
Contig ID	46411_1.R1010
5'-most EST	jC-atXLIB327409P2e11a1

Seq. No.	130712
Contig ID	46437_1.R1010
5'-most EST	jC-atXLIB327423P3f03b1
Method	BLASTX
NCBI GI	g553038
BLAST score	205
E value	2.0e-28
Match length	85
% identity	85
NCBI Description	(M58464) beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	130713
Contig ID	46437_2.R1010
5'-most EST	LIB3175-050-P1-K1-F3
Method	BLASTX
NCBI GI	g553038
BLAST score	145
E value	1.0e-59
Match length	127
% identity	97
NCBI Description	(M58464) beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	130714
Contig ID	46438_1.R1010
5'-most EST	LIB3177-002-Q1-K1-B1
Method	BLASTX
NCBI GI	g1524370
BLAST score	603

E value	2.0e-62
Match length	201
% identity	57
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	130715
Contig ID	46455_1.R1010
5'-most EST	LIB3175-051-P1-K1-A3
Method	BLASTN
NCBI GI	g2182285
BLAST score	344
E value	0.0e+00
Match length	579
% identity	97
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	130716
Contig ID	46458_1.R1010
5'-most EST	g2758376
Method	BLASTN
NCBI GI	g3702735
BLAST score	312
E value	1.0e-175
Match length	502
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	130717
Contig ID	46464_1.R1010
5'-most EST	LIB3176-114-P2-K1-D8
Method	BLASTX
NCBI GI	g3925363
BLAST score	132
E value	4.0e-64
Match length	181
% identity	69
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	130718
Contig ID	46471_1.R1010
5'-most EST	g936346

Seq. No.	130719
Contig ID	46484_1.R1010
5'-most EST	LIB3175-051-P1-K1-D3
Method	BLASTN
NCBI GI	g4455168
BLAST score	174
E value	6.0e-93
Match length	550
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	130720

Contig ID	46485_1.R1010
5'-most EST	LIB3175-051-P1-K1-D4
Method	BLASTN
NCBI GI	g4713943
BLAST score	411
E value	0.0e+00
Match length	443
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	130721
Contig ID	46486_1.R1010
5'-most EST	jC-atXP123C117F7T7084d1
Method	BLASTN
NCBI GI	g4159701
BLAST score	460
E value	0.0e+00
Match length	670
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22G18, complete sequence

Seq. No.	130722
Contig ID	46505_1.R1010
5'-most EST	LIB3175-051-P1-K1-F5
Method	BLASTN
NCBI GI	g3449321
BLAST score	407
E value	0.0e+00
Match length	479
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	130723
Contig ID	46509_1.R1010
5'-most EST	LIB3175-051-P1-K1-G10
Method	BLASTX
NCBI GI	g3193285
BLAST score	592
E value	4.0e-61
Match length	142
% identity	80
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	130724
Contig ID	46515_1.R1010
5'-most EST	g16639
Method	BLASTN
NCBI GI	g2924728
BLAST score	173
E value	3.0e-92
Match length	656
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	130725
Contig ID	46516_1.R1010
5'-most EST	LIB3177-017-P1-K2-B6
Method	BLASTN
NCBI GI	g2351073
BLAST score	361
E value	0.0e+00
Match length	938
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	130726
Contig ID	46548_1.R1010
5'-most EST	g931251
Method	BLASTX
NCBI GI	g3386565
BLAST score	701
E value	1.0e-77
Match length	268
% identity	60
NCBI Description	(AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No.	130727
Contig ID	46560_1.R1010
5'-most EST	LIB3176-024-P1-K1-G10
Method	BLASTN
NCBI GI	g3757512
BLAST score	230
E value	1.0e-126
Match length	660
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130728
Contig ID	46566_1.R1010
5'-most EST	LIB3175-052-P1-K1-F1
Method	BLASTX
NCBI GI	g3237304
BLAST score	343
E value	6.0e-32
Match length	115
% identity	56
NCBI Description	(U91561) pyridoxine 5'-phosphate oxidase [Rattus norvegicus]

Seq. No.	130729
Contig ID	46580_1.R1010
5'-most EST	jC-atXP60C198K21T7031d1
Method	BLASTN
NCBI GI	g3449313
BLAST score	742
E value	0.0e+00
Match length	785

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	130730
Contig ID	46601_1.R1010
5'-most EST	jC-atXP119C211N21T7087a1
Method	BLASTX
NCBI GI	g1518540
BLAST score	585
E value	2.0e-60
Match length	120
% identity	87
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	130731
Contig ID	46610_1.R1010
5'-most EST	jC-atXP86CG10C3T7d2
Method	BLASTN
NCBI GI	g2182286
BLAST score	325
E value	0.0e+00
Match length	594
% identity	100
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	130732
Contig ID	46610_2.R1010
5'-most EST	jC-atXLIB327426P2h01b1
Method	BLASTN
NCBI GI	g2182286
BLAST score	152
E value	9.0e-80
Match length	417
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	130733
Contig ID	46621_1.R1010
5'-most EST	LIB3175-062-P1-K1-B4
Method	BLASTN
NCBI GI	g4589410
BLAST score	302
E value	1.0e-169
Match length	466
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	130734
Contig ID	46623_1.R1010
5'-most EST	LIB3175-053-P1-K1-D8
Method	BLASTX
NCBI GI	g1706958
BLAST score	85

E value	2.0e-33
Match length	163
% identity	53
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	130735
Contig ID	46653_1.R1010
5'-most EST	LIB3175-054-P1-K1-A10
Method	BLASTN
NCBI GI	g4580744
BLAST score	277
E value	1.0e-154
Match length	403
% identity	99
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	130736
Contig ID	46659_1.R1010
5'-most EST	jC-atXLIB327421P2f07b1
Method	BLASTX
NCBI GI	g416758
BLAST score	783
E value	8.0e-87
Match length	166
% identity	100
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	130737
Contig ID	46659_2.R1010
5'-most EST	g906989
Method	BLASTX
NCBI GI	g416758
BLAST score	1692
E value	0.0e+00
Match length	347
% identity	93
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	130738
Contig ID	46668_1.R1010
5'-most EST	LIB3175-054-P1-K1-B4
Method	BLASTN
NCBI GI	g4567300
BLAST score	219
E value	1.0e-120
Match length	456
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No. 130739
Contig ID 46673_1.R1010
5'-most EST LIB3175-054-P1-K1-C1

Seq. No. 130740
Contig ID 46696_1.R1010
5'-most EST jC-atXP65C208A13T7029d1
Method BLASTN
NCBI GI g4803835
BLAST score 604
E value 0.0e+00
Match length 673
% identity 97
NCBI Description Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds

Seq. No. 130741
Contig ID 46697_1.R1010
5'-most EST LIB3175-054-P1-K1-E12
Method BLASTX
NCBI GI g1420924
BLAST score 87
E value 3.0e-31
Match length 149
% identity 56
NCBI Description (U57899) IN1 [Zea mays]

Seq. No. 130742
Contig ID 46698_1.R1010
5'-most EST LIB3175-054-P1-K1-E2
Method BLASTN
NCBI GI g2642152
BLAST score 352
E value 0.0e+00
Match length 616
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 130743
Contig ID 46708_1.R1010
5'-most EST LIB3175-054-P1-K1-F4
Method BLASTX
NCBI GI g1652892
BLAST score 477
E value 9.0e-48
Match length 206
% identity 31
NCBI Description (D90909) ABC transporter [Synechocystis sp.]

Seq. No. 130744
Contig ID 46718_1.R1010
5'-most EST jC-atXP91C247G1T7b1
Method BLASTX
NCBI GI g3157944
BLAST score 916
E value 4.0e-99

Match length	188
% identity	95
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	130745
Contig ID	46718_2.R1010
5'-most EST	LIB3175-054-P1-K1-G4
Method	BLASTX
NCBI GI	g3157944
BLAST score	760
E value	4.0e-81
Match length	148
% identity	99
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	130746
Contig ID	46721_1.R1010
5'-most EST	LIB3175-054-P1-K1-G8
Method	BLASTN
NCBI GI	g2245073
BLAST score	310
E value	1.0e-174
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130747
Contig ID	46764_1.R1010
5'-most EST	LIB3176-113-P2-K1-D6
Method	BLASTX
NCBI GI	g3047125
BLAST score	668
E value	2.0e-70
Match length	128
% identity	98
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	130748
Contig ID	46775_1.R1010
5'-most EST	LIB3177-071-P1-K1-H7
Method	BLASTN
NCBI GI	g4544435
BLAST score	143
E value	1.0e-74
Match length	430
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	130749
Contig ID	46799_1.R1010
5'-most EST	LIB3177-042-P1-K2-G1
Method	BLASTX
NCBI GI	g4734010
BLAST score	376
E value	4.0e-36
Match length	159
% identity	46
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130750
Contig ID	46803_1.R1010
5'-most EST	LIB3177-067-P1-K1-B3
Method	BLASTX
NCBI GI	g2654440
BLAST score	283
E value	5.0e-25
Match length	158
% identity	44
NCBI Description	(U70076) Lemir [Lycopersicon esculentum]

Seq. No.	130751
Contig ID	46803_2.R1010
5'-most EST	jC-atXLIB327414P4d09a2
Method	BLASTX
NCBI GI	g1762933
BLAST score	499
E value	3.0e-50
Match length	164
% identity	60
NCBI Description	(U66263) tumor-related protein [Nicotiana tabacum]

Seq. No.	130752
Contig ID	46812_1.R1010
5'-most EST	jC-atXP86CG9G9T7d2
Method	BLASTN
NCBI GI	g4589418
BLAST score	336
E value	0.0e+00
Match length	617
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	130753
Contig ID	46812_2.R1010
5'-most EST	g757603
Method	BLASTN
NCBI GI	g4589418
BLAST score	250
E value	1.0e-138
Match length	521
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	130754
Contig ID	46829_1.R1010
5'-most EST	jC-atXLIB327431P2e10a1

Seq. No.	130755
Contig ID	46829_2.R1010
5'-most EST	LIB3177-079-P1-K1-A9
Method	BLASTX
NCBI GI	g3482928
BLAST score	195
E value	2.0e-14
Match length	117
% identity	44
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana] >gi_3929586 (AF100166) phytochrome interacting factor 3 [Arabidopsis thaliana]

Seq. No.	130756
Contig ID	46830_1.R1010
5'-most EST	jC-atXLIB327427P3f11a2
Method	BLASTN
NCBI GI	g3449324
BLAST score	39
E value	2.0e-12
Match length	70
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12G2, complete sequence

Seq. No.	130757
Contig ID	46839_1.R1010
5'-most EST	LIB3175-056-P1-K1-D11
Method	BLASTN
NCBI GI	g4159707
BLAST score	241
E value	1.0e-133
Match length	535
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	130758
Contig ID	46850_1.R1010
5'-most EST	LIB3177-080-P1-K1-D8
Method	BLASTX
NCBI GI	g4725950
BLAST score	230
E value	5.0e-21
Match length	129
% identity	48
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana] >gi_4725951_emb_CAB41722.1_ (AL049730) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	130759
Contig ID	46850_2.R1010

5'-most EST	jC-atXP111C124L18T7s1
Method	BLASTX
NCBI GI	g4725950
BLAST score	213
E value	4.0e-17
Match length	70
% identity	63
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana] >gi_4725951_emb_CAB41722.1_ (AL049730) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	130760
Contig ID	46853_1.R1010
5'-most EST	LIB3176-005-P1-K1-G4

Seq. No.	130761
Contig ID	46854_1.R1010
5'-most EST	g2763694
Method	BLASTX
NCBI GI	g2979559
BLAST score	244
E value	1.0e-20
Match length	61
% identity	79
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	130762
Contig ID	46860_1.R1010
5'-most EST	jC-atXLIB327414P1b06a1
Method	BLASTX
NCBI GI	g2505874
BLAST score	753
E value	3.0e-80
Match length	153
% identity	95
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	130763
Contig ID	46895_1.R1010
5'-most EST	LIB3175-057-P1-K1-A10
Method	BLASTX
NCBI GI	g1871185
BLAST score	448
E value	2.0e-44
Match length	98
% identity	85
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	130764
Contig ID	46896_1.R1010
5'-most EST	LIB3176-065-P1-K1-B4
Method	BLASTN
NCBI GI	g3738275
BLAST score	315
E value	1.0e-177
Match length	367

% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130765
Contig ID	46900_1.R1010
5'-most EST	jC-atXLIB327421P3d08b1
Method	BLASTX
NCBI GI	g1001294
BLAST score	264
E value	9.0e-23
Match length	104
% identity	42
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	130766
Contig ID	46904_1.R1010
5'-most EST	g1327547
Method	BLASTX
NCBI GI	g3033400
BLAST score	494
E value	1.0e-55
Match length	111
% identity	92
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	130767
Contig ID	46912_1.R1010
5'-most EST	LIB3176-001-Q1-K1-B9

Seq. No.	130768
Contig ID	46920_1.R1010
5'-most EST	jC-atXLIB327422P2d12b2
Method	BLASTX
NCBI GI	g3068713
BLAST score	1237
E value	1.0e-136
Match length	311
% identity	83
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	130769
Contig ID	46961_1.R1010
5'-most EST	LIB3175-057-P1-K1-G7
Method	BLASTN
NCBI GI	g4589446
BLAST score	218
E value	1.0e-119
Match length	376
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	130770
Contig ID	46964_1.R1010
5'-most EST	jC-atXP11C98K15T7067d1

Method	BLASTX
NCBI GI	g3928079
BLAST score	347
E value	3.0e-32
Match length	260
% identity	32
NCBI Description	(AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130771
Contig ID	46966_1.R1010
5'-most EST	g3450074
Method	BLASTX
NCBI GI	g2981475
BLAST score	384
E value	6.0e-37
Match length	95
% identity	74
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	130772
Contig ID	46977_1.R1010
5'-most EST	LIB3177-059-P1-K1-A6

Seq. No.	130773
Contig ID	46992_1.R1010
5'-most EST	g2747526
Method	BLASTN
NCBI GI	g3510343
BLAST score	223
E value	1.0e-122
Match length	452
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	130774
Contig ID	46999_1.R1010
5'-most EST	jC-atXLIB327421P1g10b1

Seq. No.	130775
Contig ID	47000_1.R1010
5'-most EST	g936430
Method	BLASTX
NCBI GI	g2244749
BLAST score	858
E value	3.0e-92
Match length	168
% identity	99
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	130776
Contig ID	47044_1.R1010
5'-most EST	LIB3175-058-P1-K1-H1

Seq. No.	130777
Contig ID	47067_1.R1010

5'-most EST	LIB3175-059-P1-K1-B10
Method	BLASTN
NCBI GI	g3869072
BLAST score	289
E value	1.0e-161
Match length	680
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	130778
Contig ID	47100_1.R1010
5'-most EST	jC-atXP118C144A17T7067d2
Method	BLASTX
NCBI GI	g4490302
BLAST score	1304
E value	1.0e-144
Match length	268
% identity	96
NCBI Description	(AL035678) Tic22-like protein [Arabidopsis thaliana]

Seq. No.	130779
Contig ID	47105_1.R1010
5'-most EST	g1053547
Method	BLASTX
NCBI GI	g3164222
BLAST score	206
E value	3.0e-16
Match length	84
% identity	54
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205_gb_AAD11593.1_AAD11593 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	130780
Contig ID	47181_1.R1010
5'-most EST	LIB3175-077-P1-K1-G9
Method	BLASTX
NCBI GI	g1706376
BLAST score	280
E value	7.0e-25
Match length	121
% identity	43
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_505560_emb_CAA56160_ (X79723) dfrA [Petunia x hybrida]

Seq. No.	130781
Contig ID	47185_1.R1010
5'-most EST	LIB3175-060-P1-K1-F10
Method	BLASTN
NCBI GI	g2760166
BLAST score	313
E value	1.0e-176
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK20, complete sequence [Arabidopsis thaliana]

Seq. No.	130782
Contig ID	47189_1.R1010
5'-most EST	g2756950
Method	BLASTN
NCBI GI	g3135250
BLAST score	375
E value	0.0e+00
Match length	448
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130783
Contig ID	47191_1.R1010
5'-most EST	LIB3175-060-P1-K1-F6
Method	BLASTX
NCBI GI	g2832605
BLAST score	942
E value	1.0e-102
Match length	220
% identity	90
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	130784
Contig ID	47194_1.R1010
5'-most EST	LIB3175-060-P1-K1-F9
Method	BLASTX
NCBI GI	g4455365
BLAST score	76
E value	7.0e-32
Match length	78
% identity	78
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	130785
Contig ID	47194_2.R1010
5'-most EST	ARABL1-031-Q1-B1-H6
Method	BLASTX
NCBI GI	g4455365
BLAST score	305
E value	5.0e-28
Match length	58
% identity	91
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	130786
Contig ID	47196_1.R1010
5'-most EST	LIB3175-060-P1-K1-G12
Method	BLASTX
NCBI GI	g3805765
BLAST score	906
E value	6.0e-98
Match length	206
% identity	88
NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No. 130787
Contig ID 47200_1.R1010
5'-most EST g2048801

Seq. No. 130788
Contig ID 47208_1.R1010
5'-most EST LIB3175-060-P1-K1-H4
Method BLASTN
NCBI GI g3522932
BLAST score 392
E value 0.0e+00
Match length 459
% identity 82
NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 130789
Contig ID 47229_1.R1010
5'-most EST LIB3175-061-P1-K1-B6
Method BLASTX
NCBI GI g3212851
BLAST score 388
E value 2.0e-37
Match length 78
% identity 99
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 130790
Contig ID 47238_1.R1010
5'-most EST LIB3175-061-P1-K1-C7
Method BLASTN
NCBI GI g3805839
BLAST score 300
E value 1.0e-168
Match length 544
% identity 98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No. 130791
Contig ID 47248_1.R1010
5'-most EST g2048674
Method BLASTN
NCBI GI g2290120
BLAST score 56
E value 2.0e-22
Match length 63
% identity 98
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 130792
Contig ID 47252_1.R1010
5'-most EST g2723158
Method BLASTN
NCBI GI g3047100

BLAST score	45
E value	5.0e-16
Match length	192
% identity	95
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	130793
Contig ID	47260_1.R1010
5'-most EST	jC-atXP29C139M22T7086d1
Method	BLASTX
NCBI GI	g4006934
BLAST score	167
E value	3.0e-32
Match length	103
% identity	65
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	130794
Contig ID	47260_2.R1010
5'-most EST	LIB3176-098-P1-K1-G9
Method	BLASTX
NCBI GI	g100302
BLAST score	784
E value	1.0e-83
Match length	218
% identity	65
NCBI Description	auxin-induced protein (clone pCNT107) - common tobacco

Seq. No.	130795
Contig ID	47276_1.R1010
5'-most EST	LIB3175-063-P1-K1-C10
Method	BLASTX
NCBI GI	g1362103
BLAST score	764
E value	3.0e-81
Match length	192
% identity	74
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No.	130796
Contig ID	47308_1.R1010
5'-most EST	g899208
Method	BLASTX
NCBI GI	g4262154
BLAST score	998
E value	1.0e-109
Match length	243
% identity	85
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	130797
Contig ID	47349_1.R1010
5'-most EST	LIB3175-068-P1-K1-C4
Method	BLASTN

NCBI GI g2264318
BLAST score 255
E value 1.0e-141
Match length 458
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No. 130798
Contig ID 47393_1.R1010
5'-most EST LIB3177-056-P1-K1-C2
Method BLASTX
NCBI GI g3831445
BLAST score 792
E value 7.0e-85
Match length 150
% identity 100
NCBI Description (AC005819) unknown protein [Arabidopsis thaliana]

Seq. No. 130799
Contig ID 47410_1.R1010
5'-most EST LIB3175-063-P1-K1-D6
Method BLASTN
NCBI GI g2564049
BLAST score 214
E value 1.0e-117
Match length 409
% identity 95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No. 130800
Contig ID 47411_1.R1010
5'-most EST jC-atXP33C148C13T7d2
Method BLASTX
NCBI GI g3738301
BLAST score 532
E value 2.0e-54
Match length 146
% identity 69
NCBI Description (AC005309) putative zinc-finger protein [Arabidopsis thaliana] >gi_4249397 (AC006072) putative zinc-finger protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No. 130801
Contig ID 47449_1.R1010
5'-most EST LIB3175-063-P1-K1-H11
Method BLASTN
NCBI GI g2196463
BLAST score 390
E value 0.0e+00
Match length 398
% identity 100
NCBI Description Arabidopsis thaliana chloroplast trnC, rpoB & rpoC1 genes

Seq. No. 130802
Contig ID 47463_1.R1010

5'-most EST	LIB3175-064-P1-K1-A9
Method	BLASTX
NCBI GI	g1651459
BLAST score	146
E value	5.0e-09
Match length	124
% identity	31
NCBI Description	(D90732) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	130803
Contig ID	47465_1.R1010
5'-most EST	LIB3234-047-P1-K1-E2
Method	BLASTX
NCBI GI	g729857
BLAST score	360
E value	6.0e-34
Match length	162
% identity	41
NCBI Description	SERINE/THREONINE-PROTEIN KINASE IRE1 PRECURSOR >gi_539088_pir__A47541 protein kinase IRE1 (EC 2.7.1.-) precursor - yeast (Saccharomyces cerevisiae) >gi_393281 (L19640) ERN1 [Saccharomyces cerevisiae]

Seq. No.	130804
Contig ID	47475_1.R1010
5'-most EST	LIB3234-040-P1-K1-C9
Method	BLASTX
NCBI GI	g2673917
BLAST score	636
E value	1.0e-66
Match length	153
% identity	56
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	130805
Contig ID	47478_1.R1010
5'-most EST	LIB3175-064-P1-K1-C6

Seq. No.	130806
Contig ID	47494_1.R1010
5'-most EST	jC-atXP73CF2H9T7d2
Method	BLASTN
NCBI GI	g1070003
BLAST score	44
E value	4.0e-15
Match length	44
% identity	100
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	130807
Contig ID	47494_2.R1010
5'-most EST	LIB3175-064-P1-K1-E12

Seq. No.	130808
Contig ID	47502_1.R1010
5'-most EST	LIB3175-078-P1-K1-F10
Method	BLASTN
NCBI GI	g3413696
BLAST score	279
E value	1.0e-155
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130809
Contig ID	47533_1.R1010
5'-most EST	LIB35-022-Q1-E1-C10

Seq. No.	130810
Contig ID	47533_2.R1010
5'-most EST	jC-atXLIB327438P2h03a1

Seq. No.	130811
Contig ID	47540_1.R1010
5'-most EST	LIB3175-065-P1-K1-B12
Method	BLASTN
NCBI GI	g2264302
BLAST score	390
E value	0.0e+00
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	130812
Contig ID	47549_1.R1010
5'-most EST	LIB3177-073-P1-K1-A11
Method	BLASTX
NCBI GI	g4567267
BLAST score	435
E value	5.0e-43
Match length	81
% identity	98
NCBI Description	(AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	130813
Contig ID	47571_1.R1010
5'-most EST	g2749006
Method	BLASTX
NCBI GI	g4539009
BLAST score	567
E value	5.0e-58
Match length	120
% identity	92
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	130814
Contig ID	47571_2.R1010

5'-most EST	jC-atXLIB327423P4d09b1
Method	BLASTX
NCBI GI	g4539009
BLAST score	957
E value	1.0e-110
Match length	232
% identity	87
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	130815
Contig ID	47584_1.R1010
5'-most EST	g2722145
Method	BLASTX
NCBI GI	g2275217
BLAST score	348
E value	8.0e-36
Match length	131
% identity	69
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	130816
Contig ID	47584_2.R1010
5'-most EST	jC-atXP96C250A11T7b1
Method	BLASTX
NCBI GI	g2275217
BLAST score	416
E value	1.0e-40
Match length	131
% identity	69
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	130817
Contig ID	47593_1.R1010
5'-most EST	LIB3176-067-P1-K1-D2
Method	BLASTX
NCBI GI	g1652105
BLAST score	185
E value	2.0e-13
Match length	55
% identity	58
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	130818
Contig ID	47605_1.R1010
5'-most EST	LIB3175-065-P1-K1-H1
Method	BLASTN
NCBI GI	g3869067
BLAST score	397
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	130819

Contig ID	47605_2.R1010
5'-most EST	LIB3234-056-P1-K1-E6
Method	BLASTN
NCBI GI	g3869067
BLAST score	257
E value	1.0e-142
Match length	414
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	130820
Contig ID	47614_1.R1010
5'-most EST	LIB3176-033-P1-K1-G11

Seq. No.	130821
Contig ID	47653_1.R1010
5'-most EST	LIB3176-047-P1-K1-D6

Seq. No.	130822
Contig ID	47662_1.R1010
5'-most EST	LIB3177-089-P1-K1-G12
Method	BLASTN
NCBI GI	g3386593
BLAST score	230
E value	1.0e-126
Match length	929
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130823
Contig ID	47663_1.R1010
5'-most EST	LIB3175-066-P1-K1-E2
Method	BLASTX
NCBI GI	g1173438
BLAST score	228
E value	8.0e-19
Match length	134
% identity	34
NCBI Description	DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA >gi_280609_pir__A36195 developmental protein sina - fruit fly (Drosophila melanogaster) >gi_158467 (M38384) SEVEN IN ABSTENTIA [Drosophila melanogaster]

Seq. No.	130824
Contig ID	47696_1.R1010
5'-most EST	LIB3175-066-P1-K1-H11

Seq. No.	130825
Contig ID	47697_1.R1010
5'-most EST	LIB3176-045-P1-K1-B12
Method	BLASTX
NCBI GI	g2947067
BLAST score	173
E value	5.0e-23
Match length	111

% identity	68
NCBI Description	(AC002521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130826
Contig ID	47706_1.R1010
5'-most EST	jC-atXLIB327414P3e03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	6.0e-16
Match length	52
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	130827
Contig ID	47709_1.R1010
5'-most EST	LIB3175-068-P1-K1-A4

Seq. No.	130828
Contig ID	47741_1.R1010
5'-most EST	LIB3175-068-P1-K1-D6
Method	BLASTX
NCBI GI	g2739373
BLAST score	245
E value	9.0e-21
Match length	131
% identity	38
NCBI Description	(AC002505) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	130829
Contig ID	47750_1.R1010
5'-most EST	g2748769
Method	BLASTN
NCBI GI	g3461834
BLAST score	502
E value	0.0e+00
Match length	637
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130830
Contig ID	47750_2.R1010
5'-most EST	LIB3175-068-P1-K1-E3
Method	BLASTX
NCBI GI	g3461848
BLAST score	520
E value	5.0e-73
Match length	172
% identity	85
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	130831
Contig ID	47768_1.R1010
5'-most EST	jC-atXP75C226G18T7d1

Seq. No.	130832
Contig ID	47789_1.R1010
5'-most EST	LIB3175-068-P1-K1-H9

Seq. No.	130833
Contig ID	47794_1.R1010
5'-most EST	LIB3175-070-P1-K-A3
Method	BLASTN
NCBI GI	g4519193
BLAST score	159
E value	5.0e-84
Match length	604
% identity	54
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	130834
Contig ID	47813_1.R1010
5'-most EST	LIB3176-051-P1-K1-G4
Method	BLASTX
NCBI GI	g4454464
BLAST score	555
E value	4.0e-57
Match length	127
% identity	85
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	130835
Contig ID	47821_1.R1010
5'-most EST	jC-atXP69C217P3T7068d1
Method	BLASTX
NCBI GI	g4468979
BLAST score	501
E value	2.0e-51
Match length	191
% identity	60
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	130836
Contig ID	47821_2.R1010
5'-most EST	jC-atXLIB327438P2g09a1
Method	BLASTX
NCBI GI	g4468979
BLAST score	334
E value	6.0e-31
Match length	92
% identity	71
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	130837
Contig ID	47822_1.R1010
5'-most EST	LIB3175-070-P1-K-D4

Seq. No.	130838
Contig ID	47832_1.R1010
5'-most EST	LIB3175-070-P1-K-E5
Method	BLASTX

NCBI GI	g4455228
BLAST score	378
E value	4.0e-36
Match length	182
% identity	53
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	130839
Contig ID	47835_1.R1010
5'-most EST	LIB3175-070-P1-K-E8
Method	BLASTX
NCBI GI	g2739366
BLAST score	246
E value	8.0e-21
Match length	117
% identity	45
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	130840
Contig ID	47842_1.R1010
5'-most EST	LIB3175-070-P1-K-F3
Method	BLASTX
NCBI GI	g1707657
BLAST score	209
E value	1.0e-16
Match length	88
% identity	56
NCBI Description	(Z71640) DnaJ homologue [Pisum sativum]

Seq. No.	130841
Contig ID	47856_1.R1010
5'-most EST	LIB3175-070-P1-K-H1

Seq. No.	130842
Contig ID	47877_1.R1010
5'-most EST	LIB3175-075-P1-K1-A9
Method	BLASTN
NCBI GI	g2477521
BLAST score	62
E value	4.0e-26
Match length	179
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130843
Contig ID	47888_1.R1010
5'-most EST	LIB3175-075-P1-K1-B9
Method	BLASTN
NCBI GI	g3063690
BLAST score	266
E value	1.0e-148
Match length	286
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	130844
Contig ID	47892_1.R1010
5'-most EST	LIB3177-045-P1-K2-B11
Method	BLASTX
NCBI GI	g2342727
BLAST score	56
E value	2.0e-59
Match length	125
% identity	93
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130845
Contig ID	47919_1.R1010
5'-most EST	LIB3175-075-P1-K1-E7
Method	BLASTX
NCBI GI	g2829893
BLAST score	316
E value	1.0e-72
Match length	172
% identity	88
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	130846
Contig ID	47919_3.R1010
5'-most EST	jC-atXP67C213L3T7094a1
Method	BLASTX
NCBI GI	g2829893
BLAST score	377
E value	4.0e-36
Match length	78
% identity	97
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	130847
Contig ID	47932_1.R1010
5'-most EST	jC-atXP31C146K17T7d2
Method	BLASTX
NCBI GI	g4468048
BLAST score	565
E value	8.0e-58
Match length	245
% identity	47
NCBI Description	(X78703) catechol O-methyltransferase [Vanilla planifolia]

Seq. No.	130848
Contig ID	47932_2.R1010
5'-most EST	jC-atXP109C220I18T7s1
Method	BLASTX
NCBI GI	g4220447
BLAST score	244
E value	1.0e-20
Match length	93
% identity	48
NCBI Description	(AC006216) Strong similarity to gb_X74814 cafeic acid 3-O-methyl transferase from Eucalyptus gunnii. [Arabidopsis thaliana]

Seq. No.	130849
Contig ID	47932_3.R1010
5'-most EST	ARABL1-036-Q1-E1-G5
Method	BLASTX
NCBI GI	g4220447
BLAST score	245
E value	8.0e-21
Match length	93
% identity	48
NCBI Description	(AC006216) Strong similarity to gb_X74814 cafeic acid 3-O-methyl transferase from Eucalyptus gunnii. [Arabidopsis thaliana]

Seq. No.	130850
Contig ID	47936_1.R1010
5'-most EST	jC-atXLIB327405P3g12a1

Seq. No.	130851
Contig ID	47951_1.R1010
5'-most EST	LIB3176-049-P1-K1-H10
Method	BLASTN
NCBI GI	g2281081
BLAST score	308
E value	1.0e-173
Match length	432
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130852
Contig ID	47959_1.R1010
5'-most EST	g3449657
Method	BLASTX
NCBI GI	g3834326
BLAST score	497
E value	3.0e-50
Match length	95
% identity	98
NCBI Description	(AC005679) Similar to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_T46595 and gb_AI09918 come from this gene. [Arabidopsis thaliana]

Seq. No.	130853
Contig ID	47969_1.R1010
5'-most EST	g502010
Method	BLASTX
NCBI GI	g3850585
BLAST score	111
E value	1.0e-41
Match length	174
% identity	64
NCBI Description	(AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and gb_T20569 come from this gene. [Arabidopsis thaliana]

Seq. No.	130854
Contig ID	47970_1.R1010
5'-most EST	LIB3175-076-P1-K1-B5

Method	BLASTX
NCBI GI	g2244752
BLAST score	245
E value	6.0e-21
Match length	72
% identity	69
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130855
Contig ID	47980_1.R1010
5'-most EST	LIB3175-076-P1-K1-C3
Method	BLASTN
NCBI GI	g12219
BLAST score	156
E value	4.0e-82
Match length	542
% identity	92
NCBI Description	Mustard chloroplast trnk gene for tRNA-Lys(UUU)

Seq. No.	130856
Contig ID	47987_1.R1010
5'-most EST	LIB3175-076-P1-K1-D11
Method	BLASTX
NCBI GI	g419789
BLAST score	313
E value	2.0e-28
Match length	91
% identity	65
NCBI Description	hypothetical protein - potato

Seq. No.	130857
Contig ID	48026_1.R1010
5'-most EST	jC-atXLIB327438P3h12b1

Seq. No.	130858
Contig ID	48041_1.R1010
5'-most EST	g2749015
Method	BLASTN
NCBI GI	g4580454
BLAST score	300
E value	1.0e-168
Match length	361
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	130859
Contig ID	48041_2.R1010
5'-most EST	LIB3175-077-P1-K1-A5
Method	BLASTX
NCBI GI	g4580455
BLAST score	466
E value	2.0e-46
Match length	100
% identity	94
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	130860
Contig ID	48049_1.R1010
5'-most EST	LIB3175-077-P1-K1-B12

Seq. No.	130861
Contig ID	48070_1.R1010
5'-most EST	LIB3175-077-P1-K1-D11
Method	BLASTX
NCBI GI	g3096945
BLAST score	563
E value	8.0e-58
Match length	107
% identity	100
NCBI Description	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	130862
Contig ID	48089_1.R1010
5'-most EST	LIB3175-077-P1-K1-E8

Seq. No.	130863
Contig ID	48092_1.R1010
5'-most EST	LIB3175-077-P1-K1-F11
Method	BLASTN
NCBI GI	g3461834
BLAST score	229
E value	1.0e-126
Match length	440
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130864
Contig ID	48118_1.R1010
5'-most EST	LIB3175-077-P1-K1-H4

Seq. No.	130865
Contig ID	48149_1.R1010
5'-most EST	g1159061
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	3.0e-18
Match length	72
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	130866
Contig ID	48158_1.R1010
5'-most EST	LIB3175-078-P1-K1-D1
Method	BLASTX
NCBI GI	g2754746
BLAST score	520
E value	6.0e-53
Match length	139
% identity	67
NCBI Description	(U85448) sucrose-phosphate synthase [Actinidia deliciosa]

Seq. No.	130867
Contig ID	48165_1.R1010
5'-most EST	jC-atXLIB327407P1c01b2
Method	BLASTN
NCBI GI	g4263774
BLAST score	380
E value	0.0e+00
Match length	574
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130868
Contig ID	48176_1.R1010
5'-most EST	LIB3175-078-P1-K1-E5
Method	BLASTX
NCBI GI	g4567197
BLAST score	249
E value	4.0e-21
Match length	135
% identity	41
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	130869
Contig ID	48180_1.R1010
5'-most EST	LIB3175-078-P1-K1-E9

Seq. No.	130870
Contig ID	48222_1.R1010
5'-most EST	g550255

Seq. No.	130871
Contig ID	48224_1.R1010
5'-most EST	LIB3177-088-P1-K1-F6
Method	BLASTX
NCBI GI	g3785997
BLAST score	678
E value	2.0e-71
Match length	134
% identity	99
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]

Seq. No.	130872
Contig ID	48224_2.R1010
5'-most EST	g2042805
Method	BLASTN
NCBI GI	g3785992
BLAST score	156
E value	2.0e-82
Match length	233
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130873
Contig ID	48227_1.R1010

5'-most EST	LIB3175-079-P1-K1-B10
Method	BLASTX
NCBI GI	g3249065
BLAST score	641
E value	3.0e-67
Match length	141
% identity	93
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	130874
Contig ID	48254_1.R1010
5'-most EST	LIB3175-079-P1-K1-D2
Method	BLASTX
NCBI GI	g4704766
BLAST score	237
E value	3.0e-67
Match length	194
% identity	61
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	130875
Contig ID	48260_1.R1010
5'-most EST	LIB3175-079-P1-K1-D8
Method	BLASTX
NCBI GI	g3236240
BLAST score	85
E value	9.0e-76
Match length	209
% identity	66
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	130876
Contig ID	48263_1.R1010
5'-most EST	LIB3175-079-P1-K1-E10

Seq. No.	130877
Contig ID	48282_1.R1010
5'-most EST	LIB3177-094-P1-K1-D9
Method	BLASTX
NCBI GI	g3367590
BLAST score	603
E value	8.0e-63
Match length	124
% identity	100
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	130878
Contig ID	48291_1.R1010
5'-most EST	jC-atXP102CE2G6T7b1
Method	BLASTX
NCBI GI	g3355475
BLAST score	522
E value	7.0e-53
Match length	151

% identity	72
NCBI Description	(AC004218) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	130879
Contig ID	48291_2.R1010
5'-most EST	LIB3177-021-P1-K2-F2
Method	BLASTX
NCBI GI	g2654122
BLAST score	219
E value	1.0e-17
Match length	74
% identity	62
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	130880
Contig ID	48291_3.R1010
5'-most EST	g2763197
Method	BLASTX
NCBI GI	g2654122
BLAST score	337
E value	1.0e-31
Match length	106
% identity	68
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	130881
Contig ID	48301_1.R1010
5'-most EST	jC-atXP119C211N18T7079a1
Method	BLASTX
NCBI GI	g1652057
BLAST score	628
E value	2.0e-65
Match length	191
% identity	65
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	130882
Contig ID	48326_1.R1010
5'-most EST	ARABL1-036-Q1-B1-A12
Method	BLASTN
NCBI GI	g4538972
BLAST score	201
E value	1.0e-109
Match length	269
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M11 (ESSA project)

Seq. No.	130883
Contig ID	48354_1.R1010
5'-most EST	LIB3175-080-P1-K1-E10
Method	BLASTN
NCBI GI	g3080430
BLAST score	178
E value	2.0e-95
Match length	391
% identity	98

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	130884
Contig ID	48355_1.R1010
5'-most EST	jC-atXP12C102B12T7041a1
Method	BLASTX
NCBI GI	g4115925
BLAST score	260
E value	3.0e-22
Match length	69
% identity	44
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	130885
Contig ID	48408_1.R1010
5'-most EST	g936379
Method	BLASTN
NCBI GI	g4733953
BLAST score	232
E value	1.0e-127
Match length	399
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	130886
Contig ID	48436_1.R1010
5'-most EST	LIB3175-081-P1-K1-D8

Seq. No.	130887
Contig ID	48474_1.R1010
5'-most EST	g2576800
Method	BLASTN
NCBI GI	g4519193
BLAST score	236
E value	1.0e-130
Match length	431
% identity	66
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	130888
Contig ID	48483_1.R1010
5'-most EST	g1565735
Method	BLASTN
NCBI GI	g2864607
BLAST score	91
E value	2.0e-43
Match length	167
% identity	32
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	130889
Contig ID	48500_1.R1010
5'-most EST	jC-atXLIB327438P2e08a1
Method	BLASTN
NCBI GI	g2264314
BLAST score	431
E value	0.0e+00
Match length	479
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	130890
Contig ID	48512_1.R1010
5'-most EST	LIB3175-082-P1-K1-C2
Method	BLASTX
NCBI GI	g3413700
BLAST score	691
E value	7.0e-73
Match length	180
% identity	78
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	130891
Contig ID	48529_1.R1010
5'-most EST	g1520507
Method	BLASTN
NCBI GI	g4376087
BLAST score	366
E value	0.0e+00
Match length	472
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	130892
Contig ID	48541_1.R1010
5'-most EST	LIB3175-082-P1-K1-H2
Method	BLASTN
NCBI GI	g2264310
BLAST score	349
E value	0.0e+00
Match length	396
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	130893
Contig ID	48548_1.R1010
5'-most EST	LIB3175-082-P1-K1-F5
Method	BLASTN
NCBI GI	g3873174
BLAST score	303
E value	1.0e-170
Match length	610
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No.	130894
Contig ID	48549_1.R1010
5'-most EST	LIB3175-082-P1-K1-F6
Method	BLASTN
NCBI GI	g4589443
BLAST score	174
E value	5.0e-93
Match length	345
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	130895
Contig ID	48572_1.R1010
5'-most EST	jC-atXLIB327408P1g03a1
Method	BLASTN
NCBI GI	g3426033
BLAST score	279
E value	1.0e-155
Match length	469
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130896
Contig ID	48572_2.R1010
5'-most EST	jC-atXLIB327415P3c07a1
Method	BLASTN
NCBI GI	g3426033
BLAST score	339
E value	0.0e+00
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130897
Contig ID	48599_1.R1010
5'-most EST	g1517417
Method	BLASTN
NCBI GI	g2702261
BLAST score	258
E value	1.0e-143
Match length	502
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130898
Contig ID	48602_1.R1010
5'-most EST	jC-atXP102CE5C9T7062d1
Method	BLASTX
NCBI GI	g4584110
BLAST score	830
E value	4.0e-89

Match length	159
% identity	100
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	130899
Contig ID	48645_1.R1010
5'-most EST	g2748045
Method	BLASTX
NCBI GI	g1705930
BLAST score	60
E value	2.0e-25
Match length	95
% identity	65
NCBI Description	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 (ENDOPEPTIDASE CLP 1) >gi_1001349_dbj_BAA10836_ (D64006) ATP-dependent protease ClpP [Synechocystis sp.]

Seq. No.	130900
Contig ID	48650_1.R1010
5'-most EST	LIB3177-090-P1-K1-A7
Method	BLASTX
NCBI GI	g4006883
BLAST score	1171
E value	1.0e-129
Match length	245
% identity	91
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	130901
Contig ID	48650_4.R1010
5'-most EST	LIB3176-021-P1-K1-H6
Method	BLASTX
NCBI GI	g4006883
BLAST score	129
E value	3.0e-48
Match length	124
% identity	81
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	130902
Contig ID	48657_1.R1010
5'-most EST	LIB3176-069-P1-K1-C1
Method	BLASTN
NCBI GI	g4585890
BLAST score	168
E value	2.0e-89
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	130903
Contig ID	48671_1.R1010
5'-most EST	LIB3176-002-Q1-K1-B10
Method	BLASTX
NCBI GI	g2253010
BLAST score	578

E value	2.0e-59
Match length	152
% identity	73
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	130904
Contig ID	48677_1.R1010
5'-most EST	g905949

Seq. No.	130905
Contig ID	48681_1.R1010
5'-most EST	g501936
Method	BLASTX
NCBI GI	g2642158
BLAST score	339
E value	1.0e-31
Match length	138
% identity	50
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130906
Contig ID	48707_1.R1010
5'-most EST	LIB3176-002-Q1-K1-E11
Method	BLASTN
NCBI GI	g3869067
BLAST score	332
E value	0.0e+00
Match length	440
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	130907
Contig ID	48710_1.R1010
5'-most EST	jC-atXP34C150P18T7a1
Method	BLASTX
NCBI GI	g3269301
BLAST score	350
E value	1.0e-32
Match length	114
% identity	64
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	130908
Contig ID	48710_2.R1010
5'-most EST	jC-atXP74C225A15T7005d1
Method	BLASTX
NCBI GI	g1350543
BLAST score	140
E value	3.0e-43
Match length	319
% identity	36
NCBI Description	(L47117) late embryogenesis abundant protein [Picea glauca]

Seq. No.	130909
Contig ID	48725_1.R1010

5'-most EST	LIB35-042-Q1-E1-D10
Method	BLASTX
NCBI GI	g3953481
BLAST score	1053
E value	1.0e-115
Match length	200
% identity	61
NCBI Description	(AC002328) F22O2.26 [Arabidopsis thaliana]

Seq. No.	130910
Contig ID	48748_1.R1010
5'-most EST	LIB3176-002-Q1-K1-H8
Method	BLASTX
NCBI GI	g3402676
BLAST score	148
E value	9.0e-34
Match length	78
% identity	43
NCBI Description	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	130911
Contig ID	48749_1.R1010
5'-most EST	jC-atXP15C107E15T7043a1
Method	BLASTN
NCBI GI	g3046851
BLAST score	374
E value	0.0e+00
Match length	790
% identity	63
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	130912
Contig ID	48749_2.R1010
5'-most EST	jC-atXLIB327408P1h02a1
Method	BLASTN
NCBI GI	g3046851
BLAST score	438
E value	0.0e+00
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	130913
Contig ID	48754_1.R1010
5'-most EST	g2733608

Seq. No.	130914
Contig ID	48777_1.R1010
5'-most EST	LIB3176-003-P1-K1-D6
Method	BLASTN
NCBI GI	g2264311
BLAST score	617
E value	0.0e+00
Match length	802

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	130915
Contig ID	48793_1.R1010
5'-most EST	LIB3176-003-P1-K1-F12
Method	BLASTN
NCBI GI	g2244829
BLAST score	395
E value	0.0e+00
Match length	475
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130916
Contig ID	48807_1.R1010
5'-most EST	LIB3176-003-P1-K1-G4
Method	BLASTN
NCBI GI	g4468801
BLAST score	322
E value	0.0e+00
Match length	451
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	130917
Contig ID	48817_1.R1010
5'-most EST	jC-atXLIB327404P3f11a1
Method	BLASTX
NCBI GI	g2827709
BLAST score	426
E value	9.0e-42
Match length	94
% identity	86
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	130918
Contig ID	48829_1.R1010
5'-most EST	LIB3176-004-P1-K1-A6

Seq. No.	130919
Contig ID	48833_1.R1010
5'-most EST	LIB3176-004-P1-K1-B10
Method	BLASTN
NCBI GI	g1871173
BLAST score	469
E value	0.0e+00
Match length	497
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	130920
Contig ID	48841_1.R1010

5'-most EST	LIB3176-004-P1-K1-B8
Method	BLASTN
NCBI GI	g2656030
BLAST score	273
E value	1.0e-152
Match length	399
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	130921
Contig ID	48842_1.R1010
5'-most EST	g2759686
Method	BLASTN
NCBI GI	g4835223
BLAST score	172
E value	9.0e-92
Match length	389
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	130922
Contig ID	48853_1.R1010
5'-most EST	LIB3176-004-P1-K1-C8
Method	BLASTX
NCBI GI	g3367568
BLAST score	406
E value	8.0e-40
Match length	115
% identity	64
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	130923
Contig ID	48854_1.R1010
5'-most EST	g934754
Method	BLASTN
NCBI GI	g4559344
BLAST score	392
E value	0.0e+00
Match length	724
% identity	14
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	130924
Contig ID	48855_1.R1010
5'-most EST	LIB3176-010-P1-K1-F9
Method	BLASTN
NCBI GI	g2264321
BLAST score	246
E value	1.0e-136
Match length	571
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 130925
Contig ID 48861_1.R1010
5'-most EST g2748750

Seq. No. 130926
Contig ID 48867_1.R1010
5'-most EST LIB3177-022-P1-K2-C12
Method BLASTX
NCBI GI g4204285
BLAST score 1039
E value 1.0e-113
Match length 198
% identity 99
NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 130927
Contig ID 48868_1.R1010
5'-most EST LIB3177-049-P1-K2-H4

Seq. No. 130928
Contig ID 48883_1.R1010
5'-most EST LIB3177-084-P1-K1-A8
Method BLASTX
NCBI GI g2245131
BLAST score 290
E value 9.0e-26
Match length 117
% identity 60
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 130929
Contig ID 48897_1.R1010
5'-most EST LIB3176-004-P1-K1-G6
Method BLASTX
NCBI GI g2829883
BLAST score 632
E value 9.0e-66
Match length 142
% identity 88
NCBI Description (AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No. 130930
Contig ID 48900_1.R1010
5'-most EST LIB3176-004-P1-K1-G9
Method BLASTX
NCBI GI g66618
BLAST score 745
E value 3.0e-79
Match length 189
% identity 79
NCBI Description 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - Arabidopsis thaliana

Seq. No. 130931
Contig ID 48905_1.R1010

5'-most EST	LIB3176-004-P1-K1-H3
Method	BLASTN
NCBI GI	g4586024
BLAST score	198
E value	1.0e-107
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13C7 genomic sequence, complete sequence

Seq. No.	130932
Contig ID	48909_1.R1010
5'-most EST	jC-atX24024Q1E1C07a1
Method	BLASTX
NCBI GI	g461999
BLAST score	79
E value	2.0e-35
Match length	83
% identity	85
NCBI Description	ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No.	130933
Contig ID	48910_1.R1010
5'-most EST	g4714029
Method	BLASTX
NCBI GI	g4324597
BLAST score	784
E value	9.0e-85
Match length	217
% identity	64
NCBI Description	(AF106324) sodium proton exchanger Nhx1 [Arabidopsis thaliana]

Seq. No.	130934
Contig ID	48936_1.R1010
5'-most EST	LIB3176-005-P1-K1-C12
Method	BLASTX
NCBI GI	g2245107
BLAST score	250
E value	2.0e-76
Match length	217
% identity	39
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No.	130935
Contig ID	48941_1.R1010
5'-most EST	LIB3176-005-P1-K1-C6
Method	BLASTX
NCBI GI	g1652057
BLAST score	449
E value	3.0e-44
Match length	221
% identity	38
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	130936
Contig ID	48959_1.R1010

5'-most EST	LIB3176-005-P1-K1-E12
Seq. No.	130937
Contig ID	48979_1.R1010
5'-most EST	jC-atXLIB327426P2g06b1
Seq. No.	130938
Contig ID	48979_2.R1010
5'-most EST	LIB35-050-Q1-E1-B3
Method	BLASTX
NCBI GI	g627469
BLAST score	214
E value	7.0e-17
Match length	182
% identity	8
NCBI Description	hypothetical protein 2 - human (fragment)
Seq. No.	130939
Contig ID	48992_1.R1010
5'-most EST	g948547
Method	BLASTX
NCBI GI	g3129952
BLAST score	497
E value	5.0e-50
Match length	161
% identity	58
NCBI Description	(AJ006052) copper amine oxidase [Cicer arietinum]
Seq. No.	130940
Contig ID	49002_1.R1010
5'-most EST	LIB3176-006-P1-K1-A10
Seq. No.	130941
Contig ID	49036_1.R1010
5'-most EST	LIB3176-006-P1-K1-D11
Method	BLASTX
NCBI GI	g2388583
BLAST score	1002
E value	1.0e-109
Match length	240
% identity	86
NCBI Description	(AC000098) Similar to Synechocystis hypothetical protein (gb_D90908). [Arabidopsis thaliana]
Seq. No.	130942
Contig ID	49050_1.R1010
5'-most EST	LIB3176-052-P1-K1-F7
Method	BLASTX
NCBI GI	g2829862
BLAST score	231
E value	6.0e-19
Match length	151
% identity	42
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]
Seq. No.	130943

Contig ID	49050_3.R1010
5'-most EST	g1053678
Method	BLASTX
NCBI GI	g2829862
BLAST score	146
E value	4.0e-09
Match length	66
% identity	45
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	130944
Contig ID	49078_1.R1010
5'-most EST	LIB3176-030-P1-K1-C7
Method	BLASTN
NCBI GI	g4519183
BLAST score	48
E value	8.0e-18
Match length	439
% identity	50
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	130945
Contig ID	49084_1.R1010
5'-most EST	LIB3176-006-P1-K1-H5
Method	BLASTX
NCBI GI	g3297813
BLAST score	624
E value	4.0e-65
Match length	140
% identity	88
NCBI Description	(AL031032) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130946
Contig ID	49109_1.R1010
5'-most EST	g2413022
Method	BLASTN
NCBI GI	g572514
BLAST score	251
E value	1.0e-139
Match length	255
% identity	100
NCBI Description	A.thaliana gene At7SL-1 for 7SL RNA

Seq. No.	130947
Contig ID	49135_1.R1010
5'-most EST	LIB3176-007-P1-K1-E3
Method	BLASTX
NCBI GI	g4432855
BLAST score	467
E value	9.0e-47
Match length	96
% identity	100
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 130948

Contig ID 49142_1.R1010
5'-most EST LIB3176-007-P1-K1-F10
Method BLASTX
NCBI GI g507808
BLAST score 330
E value 1.0e-103
Match length 201
% identity 97
NCBI Description (D13987) phosphoenolpyruvate carboxylase [Brassica napus] >gi_743641_prf__2013218A phosphoenolpyruvate carboxylase [Brassica napus]

Seq. No. 130949
Contig ID 49158_1.R1010
5'-most EST g2763110
Method BLASTX
NCBI GI g4335737
BLAST score 567
E value 7.0e-58
Match length 280
% identity 43
NCBI Description (AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 130950
Contig ID 49163_1.R1010
5'-most EST g906047
Method BLASTX
NCBI GI g2809246
BLAST score 530
E value 1.0e-60
Match length 169
% identity 66
NCBI Description (AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 130951
Contig ID 49175_1.R1010
5'-most EST LIB3176-008-P1-K3-B7
Method BLASTX
NCBI GI g3337361
BLAST score 805
E value 3.0e-86
Match length 201
% identity 72
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 130952
Contig ID 49195_1.R1010
5'-most EST LIB3176-008-P1-K2-C6
Method BLASTX
NCBI GI g2342728
BLAST score 749
E value 2.0e-79
Match length 238
% identity 61
NCBI Description (AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	130953
Contig ID	49202_1.R1010
5'-most EST	jC-atXP15C106K8T7026a1
Method	BLASTX
NCBI GI	g2982303
BLAST score	639
E value	1.0e-66
Match length	141
% identity	87
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	130954
Contig ID	49202_2.R1010
5'-most EST	jC-atXLIB327415P4g08a1
Method	BLASTN
NCBI GI	g4581084
BLAST score	341
E value	0.0e+00
Match length	473
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	130955
Contig ID	49207_1.R1010
5'-most EST	LIB3176-008-P1-K1-D6
Method	BLASTX
NCBI GI	g4309731
BLAST score	196
E value	8.0e-15
Match length	104
% identity	39
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130956
Contig ID	49208_1.R1010
5'-most EST	LIB3176-008-P1-K3-D7
Method	BLASTX
NCBI GI	g2224911
BLAST score	94
E value	4.0e-03
Match length	136
% identity	62
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	130957
Contig ID	49221_1.R1010
5'-most EST	LIB3176-008-P1-K1-E8

Seq. No.	130958
Contig ID	49233_1.R1010
5'-most EST	LIB3176-008-P1-K1-F8
Method	BLASTX
NCBI GI	g2583128
BLAST score	298

E value	5.0e-27
Match length	131
% identity	43
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	130959
Contig ID	49238_1.R1010
5'-most EST	LIB3176-008-P1-K4-G12
Method	BLASTX
NCBI GI	g3080371
BLAST score	1011
E value	1.0e-110
Match length	227
% identity	80
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	130960
Contig ID	49239_1.R1010
5'-most EST	LIB3176-008-P1-K4-G2
Method	BLASTX
NCBI GI	g3540219
BLAST score	412
E value	2.0e-40
Match length	141
% identity	55
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]

Seq. No.	130961
Contig ID	49248_1.R1010
5'-most EST	LIB3176-008-P1-K3-H11
Method	BLASTN
NCBI GI	g4455168
BLAST score	324
E value	0.0e+00
Match length	649
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	130962
Contig ID	49248_2.R1010
5'-most EST	jC-atXP34C150K20T7a1
Method	BLASTN
NCBI GI	g4455168
BLAST score	123
E value	2.0e-62
Match length	560
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	130963
Contig ID	49252_1.R1010
5'-most EST	LIB35-028-Q1-E1-H12
Method	BLASTN
NCBI GI	g3688169

BLAST score	268
E value	1.0e-149
Match length	717
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	130964
Contig ID	49270_1.R1010
5'-most EST	LIB3176-008-P1-K2-B10
Method	BLASTN
NCBI GI	g2182289
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	130965
Contig ID	49517_1.R1010
5'-most EST	LIB3176-009-P1-K2-A1
Method	BLASTX
NCBI GI	g2244851
BLAST score	530
E value	5.0e-54
Match length	191
% identity	50
NCBI Description	(Z97337) amine oxidase [Arabidopsis thaliana]

Seq. No.	130966
Contig ID	49519_1.R1010
5'-most EST	LIB3176-009-P1-K2-A11
Method	BLASTX
NCBI GI	g4490336
BLAST score	257
E value	4.0e-22
Match length	88
% identity	60
NCBI Description	(AL035656) auxin-induced protein-like [Arabidopsis thaliana]

Seq. No.	130967
Contig ID	49524_1.R1010
5'-most EST	LIB3176-009-P1-K1-A5

Seq. No.	130968
Contig ID	49525_1.R1010
5'-most EST	LIB3176-009-P1-K2-A6
Method	BLASTX
NCBI GI	g4454010
BLAST score	410
E value	3.0e-52
Match length	131
% identity	87
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	130969
Contig ID	49531_1.R1010
5'-most EST	LIB3176-009-P1-K2-B11
Method	BLASTX
NCBI GI	g2244846
BLAST score	614
E value	5.0e-64
Match length	130
% identity	93
NCBI Description	(Z97337) ferredoxin [Arabidopsis thaliana]

Seq. No.	130970
Contig ID	49533_1.R1010
5'-most EST	LIB3176-009-P1-K2-B2
Method	BLASTN
NCBI GI	g4757678
BLAST score	125
E value	1.0e-63
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	130971
Contig ID	49534_1.R1010
5'-most EST	LIB3176-009-P1-K3-B3
Method	BLASTN
NCBI GI	g3869066
BLAST score	414
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	130972
Contig ID	49539_1.R1010
5'-most EST	LIB3176-009-P1-K2-B8
Method	BLASTN
NCBI GI	g3510346
BLAST score	466
E value	0.0e+00
Match length	491
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]

Seq. No.	130973
Contig ID	49551_1.R1010
5'-most EST	LIB3176-009-P1-K3-C8
Method	BLASTX
NCBI GI	g1351438
BLAST score	229
E value	7.0e-19
Match length	129
% identity	44
NCBI Description	XANTHINE DEHYDROGENASE (XD) (CONTAINS: XANTHINE OXIDASE

(XO)) >gi_2144325_pir__XOCHDH xanthine dehydrogenase (EC 1.1.1.204) - chicken >gi_507880_dbj_BAA02502_ (D13221) xanthine dehydrogenase [Gallus gallus]

Seq. No.	130974
Contig ID	49552_1.R1010
5'-most EST	LIB3176-009-P1-K2-C9
Method	BLASTN
NCBI GI	g2244788
BLAST score	552
E value	0.0e+00
Match length	564
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	130975
Contig ID	49557_1.R1010
5'-most EST	LIB3176-009-P1-K2-D2
Method	BLASTX
NCBI GI	g1723480
BLAST score	101
E value	2.0e-03
Match length	114
% identity	16
NCBI Description	HYPOTHETICAL 31.3 KD PROTEIN C17G8.08C IN CHROMOSOME I >gi_1213257_emb_CAA93691_ (Z69795) unknown [Schizosaccharomyces pombe]

Seq. No.	130976
Contig ID	49560_2.R1010
5'-most EST	g935360
Method	BLASTX
NCBI GI	g2980788
BLAST score	237
E value	2.0e-19
Match length	98
% identity	57
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	130977
Contig ID	49564_1.R1010
5'-most EST	LIB3176-009-P1-K2-D9
Method	BLASTX
NCBI GI	g1685005
BLAST score	306
E value	6.0e-28
Match length	128
% identity	48
NCBI Description	(U32644) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No.	130978
Contig ID	49568_1.R1010
5'-most EST	LIB3176-009-P1-K3-E12
Method	BLASTN
NCBI GI	g2623294

BLAST score 426
E value 0.0e+00
Match length 457
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 130979
Contig ID 49605_1.R1010
5'-most EST g936650
Method BLASTN
NCBI GI g2182286
BLAST score 369
E value 0.0e+00
Match length 472
% identity 99
NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 130980
Contig ID 49607_1.R1010
5'-most EST LIB3176-019-P1-K1-H1
Method BLASTN
NCBI GI g3510342
BLAST score 144
E value 5.0e-75
Match length 605
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No. 130981
Contig ID 49808_1.R1010
5'-most EST LIB3176-010-P1-K1-B4
Method BLASTX
NCBI GI g1707012
BLAST score 422
E value 2.0e-41
Match length 126
% identity 69
NCBI Description (U78721) tyrosyl-tRNA synthetase isolog [Arabidopsis thaliana]

Seq. No. 130982
Contig ID 49858_1.R1010
5'-most EST LIB3176-083-P1-K1-A5

Seq. No. 130983
Contig ID 49863_1.R1010
5'-most EST LIB3176-010-P1-K1-H1

Seq. No. 130984
Contig ID 49877_1.R1010
5'-most EST LIB3176-011-P1-K1-A12

Seq. No. 130985
Contig ID 49888_1.R1010

5'-most EST	LIB3176-011-P1-K1-B12
Seq. No.	130986
Contig ID	49893_1.R1010
5'-most EST	LIB3176-011-P1-K1-B6
Method	BLASTN
NCBI GI	g4757392
BLAST score	194
E value	1.0e-105
Match length	484
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence
Seq. No.	130987
Contig ID	49909_1.R1010
5'-most EST	LIB3176-011-P1-K1-D12
Method	BLASTN
NCBI GI	g3985958
BLAST score	480
E value	0.0e+00
Match length	528
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.	130988
Contig ID	49933_1.R1010
5'-most EST	jC-atXP25C125F16T7d1
Method	BLASTN
NCBI GI	g4510360
BLAST score	741
E value	0.0e+00
Match length	858
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence
Seq. No.	130989
Contig ID	49936_1.R1010
5'-most EST	LIB3176-042-P1-K1-A7
Method	BLASTX
NCBI GI	g3075392
BLAST score	491
E value	1.0e-49
Match length	112
% identity	85
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]
Seq. No.	130990
Contig ID	49938_1.R1010
5'-most EST	LIB3176-011-P1-K1-F9
Method	BLASTN
NCBI GI	g3046851
BLAST score	243
E value	1.0e-134

Match length 519
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 130991
Contig ID 49945_1.R1010
5'-most EST jC-atXP74C224M19T7055d1
Method BLASTN
NCBI GI g3763915
BLAST score 947
E value 0.0e+00
Match length 988
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 130992
Contig ID 49945_2.R1010
5'-most EST jC-atX24036Q1E1G08a1
Method BLASTN
NCBI GI g3763915
BLAST score 231
E value 1.0e-127
Match length 454
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 130993
Contig ID 49955_1.R1010
5'-most EST g46051 7
Method BLASTN
NCBI GI g3241923
BLAST score 365
E value 0.0e+00
Match length 417
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No. 130994
Contig ID 49994_1.R1010
5'-most EST LIB31 6-012-P1-K1-E12
Method BLASTX
NCBI GI g1931650
BLAST score 156
E value 2.0e-10
Match length 84
% identity 46
NCBI Description (U95973) disease resistance protein RPM1 isolog [Arabidopsis thaliana]

Seq. No. 130995
Contig ID 50015_1.R1010
5'-most EST LIB31 6-117-P2-K1-H8
Method BLASTX

NCBI GI	g3080411
BLAST score	209
E value	1.0e-16
Match length	77
% identity	47
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	130996
Contig ID	50025_1.R1010
5'-most EST	LIB3176-012-P1-K1-H8
Method	BLASTN
NCBI GI	g4580744
BLAST score	306
E value	1.0e-172
Match length	374
% identity	97
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	130997
Contig ID	50058_1.R1010
5'-most EST	jC-atXLIB327404P3a12a1

Seq. No.	130998
Contig ID	50068_1.R1010
5'-most EST	LIB3176-104-P1-K1-A7
Method	BLASTN
NCBI GI	g2264313
BLAST score	105
E value	6.0e-52
Match length	257
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	130999
Contig ID	50072_1.R1010
5'-most EST	LIB3177-070-P1-K1-G2
Method	BLASTN
NCBI GI	g4756963
BLAST score	333
E value	0.0e+00
Match length	561
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	131000
Contig ID	50086_1.R1010
5'-most EST	jC-atX25028Q1E1A05a2

Seq. No.	131001
Contig ID	50092_1.R1010
5'-most EST	LIB35-043-Q1-E1-A1
Method	BLASTX
NCBI GI	g2341033
BLAST score	46

E value	3.0e-61
Match length	138
% identity	99
NCBI Description	(AC000104) Similar to Babesia aldo-keto reductase (gb_M93122). [Arabidopsis thaliana]

Seq. No.	131002
Contig ID	50094_1.R1010
5'-most EST	LIB3176-014-P1-K1-H8
Method	BLASTX
NCBI GI	g4262240
BLAST score	648
E value	5.0e-68
Match length	153
% identity	77
NCBI Description	(AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No.	131003
Contig ID	50099_1.R1010
5'-most EST	jC-atXLIB327421P3c06a1
Method	BLASTX
NCBI GI	g4586449
BLAST score	224
E value	2.0e-23
Match length	63
% identity	64
NCBI Description	(AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No.	131004
Contig ID	50128_1.R1010
5'-most EST	LIB3176-053-P1-K1-B2
Method	BLASTN
NCBI GI	g2795802
BLAST score	289
E value	1.0e-161
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131005
Contig ID	50155_1.R1010
5'-most EST	LIB3176-015-P1-K1-F8

Seq. No.	131006
Contig ID	50183_1.R1010
5'-most EST	LIB3176-016-P1-K1-A12
Method	BLASTN
NCBI GI	g2182286
BLAST score	283
E value	1.0e-158
Match length	549
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	131007

Contig ID	50227_1.R1010
5'-most EST	LIB3176-016-P1-K1-H2
Method	BLASTN
NCBI GI	g4757662
BLAST score	289
E value	1.0e-161
Match length	418
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	131008
Contig ID	50228_2.R1010
5'-most EST	LIB3176-016-P1-K1-H4
Method	BLASTX
NCBI GI	g4455338
BLAST score	571
E value	8.0e-59
Match length	195
% identity	55
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	131009
Contig ID	50238_1.R1010
5'-most EST	LIB3176-017-P1-K1-A4
Method	BLASTX
NCBI GI	g2462744
BLAST score	290
E value	1.0e-25
Match length	155
% identity	38
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	131010
Contig ID	50248_1.R1010
5'-most EST	LIB3176-017-P1-K1-B4

Seq. No.	131011
Contig ID	50255_1.R1010
5'-most EST	jC-atXLIB327427P4h02a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	131012
Contig ID	50274_1.R1010
5'-most EST	LIB3177-063-P1-K1-B11
Method	BLASTX
NCBI GI	g3080404
BLAST score	447
E value	2.0e-44
Match length	83
% identity	92

NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455268_emb_CAB36804.1_ (AL035527) putative bifunctional nuclease [Arabidopsis thaliana]

Seq. No.	131013
Contig ID	50293_1.R1010
5'-most EST	LIB3176-017-P1-K1-F8
Method	BLASTX
NCBI GI	g3668080
BLAST score	784
E value	1.0e-83
Match length	224
% identity	75
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	131014
Contig ID	50307_1.R1010
5'-most EST	LIB3176-058-P1-K1-D6
Method	BLASTX
NCBI GI	g2980806
BLAST score	537
E value	5.0e-55
Match length	113
% identity	87
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	131015
Contig ID	50336_1.R1010
5'-most EST	g957728
Method	BLASTX
NCBI GI	g4006934
BLAST score	477
E value	8.0e-48
Match length	112
% identity	75
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	131016
Contig ID	50402_1.R1010
5'-most EST	jC-atXP61C201G3T7d1
Method	BLASTX
NCBI GI	g2190554
BLAST score	378
E value	6.0e-36
Match length	203
% identity	34
NCBI Description	(AC001229) Similar to Arabidopsis cytochrome P450 CYP90 (gb_X87367). [Arabidopsis thaliana]

Seq. No.	131017
Contig ID	50423_1.R1010
5'-most EST	LIB3176-019-P1-K1-F2
Method	BLASTX
NCBI GI	g4582451
BLAST score	310
E value	2.0e-28
Match length	95

% identity	72
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana]

Seq. No.	131018
Contig ID	50470_1.R1010
5'-most EST	g947804
Method	BLASTN
NCBI GI	g3033373
BLAST score	202
E value	1.0e-109
Match length	777
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131019
Contig ID	50476_1.R1010
5'-most EST	LIB3176-086-P1-K1-F5

Seq. No.	131020
Contig ID	50487_1.R1010
5'-most EST	LIB3177-049-P1-K2-E10
Method	BLASTX
NCBI GI	g4585966
BLAST score	120
E value	1.0e-121
Match length	255
% identity	87
NCBI Description	(AC005287) Putative dihyrdolipoamide acetyltransferase [Arabidopsis thaliana]

Seq. No.	131021
Contig ID	50504_1.R1010
5'-most EST	g2062886
Method	BLASTN
NCBI GI	g4220638
BLAST score	181
E value	4.0e-97
Match length	430
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	131022
Contig ID	50504_2.R1010
5'-most EST	g906006
Method	BLASTX
NCBI GI	g1542941
BLAST score	477
E value	1.0e-47
Match length	129
% identity	81
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	131023
Contig ID	50505_1.R1010
5'-most EST	LIB3176-020-P1-K1-G1

Method	BLASTX
NCBI GI	g2462834
BLAST score	484
E value	9.0e-49
Match length	132
% identity	69
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131024
Contig ID	50506_1.R1010
5'-most EST	LIB3176-020-P1-K1-G10
Method	BLASTN
NCBI GI	g2264309
BLAST score	133
E value	1.0e-68
Match length	323
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	131025
Contig ID	50530_1.R1010
5'-most EST	g2412914
Method	BLASTX
NCBI GI	g4586113
BLAST score	390
E value	1.0e-37
Match length	117
% identity	70
NCBI Description	(AL049638) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	131026
Contig ID	50543_1.R1010
5'-most EST	jC-atXLIB327438P1g05a1
Method	BLASTX
NCBI GI	g1931639
BLAST score	298
E value	9.0e-27
Match length	139
% identity	42
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	131027
Contig ID	50548_1.R1010
5'-most EST	LIB3234-090-P1-K1-D12

Seq. No.	131028
Contig ID	50585_1.R1010
5'-most EST	LIB3176-021-P1-K1-F5
Method	BLASTX
NCBI GI	g3386614
BLAST score	435
E value	4.0e-43
Match length	99
% identity	48
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis

thaliana]

Seq. No.	131029
Contig ID	50587_1.R1010
5'-most EST	LIB3176-021-P1-K1-F7
Method	BLASTX
NCBI GI	g2832625
BLAST score	369
E value	7.0e-35
Match length	267
% identity	35
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	131030
Contig ID	50626_1.R1010
5'-most EST	g2748108

Seq. No.	131031
Contig ID	50630_1.R1010
5'-most EST	LIB3176-060-P1-K1-D12
Method	BLASTX
NCBI GI	g4678342
BLAST score	757
E value	1.0e-80
Match length	148
% identity	99
NCBI Description	(AL049659) lipase-like protein [Arabidopsis thaliana]

Seq. No.	131032
Contig ID	50635_1.R1010
5'-most EST	jC-atXP22C116K22T7053a1
Method	BLASTN
NCBI GI	g4510323
BLAST score	152
E value	1.0e-79
Match length	531
% identity	94
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	131033
Contig ID	50635_3.R1010
5'-most EST	g905717
Method	BLASTX
NCBI GI	g4558550
BLAST score	101
E value	1.0e-107
Match length	249
% identity	86
NCBI Description	(AC007138) putative protein transport factor [Arabidopsis thaliana]

Seq. No.	131034
Contig ID	50642_2.R1010
5'-most EST	LIB3176-022-P1-K1-D9
Method	BLASTN
NCBI GI	g4558521

BLAST score 247
E value 1.0e-136
Match length 824
% identity 95
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No. 131035
Contig ID 50643_1.R1010
5'-most EST LIB3176-022-P1-K1-E12

Seq. No. 131036
Contig ID 50646_1.R1010
5'-most EST jC-atXP20C114B24T7052a1
Method BLASTX
NCBI GI g419760
BLAST score 471
E value 6.0e-47
Match length 113
% identity 45
NCBI Description P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No. 131037
Contig ID 50660_1.R1010
5'-most EST ARABL1-023-Q1-B1-C2
Method BLASTX
NCBI GI g3298441
BLAST score 300
E value 2.0e-27
Match length 86
% identity 69
NCBI Description (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No. 131038
Contig ID 50673_1.R1010
5'-most EST LIB3176-067-P1-K1-F11
Method BLASTN
NCBI GI g2264315
BLAST score 316
E value 1.0e-178
Match length 332
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No. 131039
Contig ID 50676_1.R1010
5'-most EST LIB35-033-Q1-E1-C6
Method BLASTX
NCBI GI g2565275
BLAST score 219
E value 2.0e-17
Match length 135
% identity 35

NCBI Description	(AF023611) Dim1p homolog [Homo sapiens]
Seq. No.	131040
Contig ID	50685_1.R1010
5'-most EST	LIB3177-043-P1-K2-D1
Method	BLASTN
NCBI GI	g4314374
BLAST score	24
E value	2.0e-03
Match length	439
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	131041
Contig ID	50689_2.R1010
5'-most EST	g2739516
Method	BLASTX
NCBI GI	g169363
BLAST score	257
E value	6.0e-22
Match length	56
% identity	77
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]
Seq. No.	131042
Contig ID	50715_1.R1010
5'-most EST	g406721
Seq. No.	131043
Contig ID	50718_1.R1010
5'-most EST	jC-atXP20C115E24T7d2
Method	BLASTX
NCBI GI	g4249402
BLAST score	529
E value	5.0e-54
Match length	150
% identity	75
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]
Seq. No.	131044
Contig ID	50724_1.R1010
5'-most EST	LIB3176-023-P1-K1-F1
Method	BLASTX
NCBI GI	g3341687
BLAST score	368
E value	5.0e-35
Match length	91
% identity	78
NCBI Description	(AC003672) putative ras protein [Arabidopsis thaliana]
Seq. No.	131045
Contig ID	50745_1.R1010
5'-most EST	jC-atXLIB327423P3d08b1
Method	BLASTX
NCBI GI	g3080425
BLAST score	611

E value	2.0e-63
Match length	181
% identity	71
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	131046
Contig ID	50750_1.R1010
5'-most EST	jC-atXP53C183L10T7082d1
Method	BLASTX
NCBI GI	g3550519
BLAST score	254
E value	8.0e-65
Match length	166
% identity	71
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	131047
Contig ID	50750_2.R1010
5'-most EST	g2446184
Method	BLASTX
NCBI GI	g3550519
BLAST score	113
E value	2.0e-34
Match length	95
% identity	73
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	131048
Contig ID	50750_3.R1010
5'-most EST	LIB3176-024-P1-K1-A1
Method	BLASTX
NCBI GI	g3550519
BLAST score	514
E value	2.0e-82
Match length	233
% identity	65
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	131049
Contig ID	50752_1.R1010
5'-most EST	LIB3176-024-P1-K1-A12
Method	BLASTX
NCBI GI	g4454468
BLAST score	492
E value	1.0e-49
Match length	146
% identity	66
NCBI Description	(AC006234) putative NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	131050
Contig ID	50753_1.R1010
5'-most EST	LIB3176-061-P1-K1-D2
Method	BLASTX
NCBI GI	g1001309
BLAST score	313
E value	2.0e-28

Match length	229
% identity	32
NCBI Description	(D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No.	131051
Contig ID	50781_1.R1010
5'-most EST	ARABLI-05-Q1-B1-B7

Seq. No.	131052
Contig ID	50785_1.R1010
5'-most EST	ARABLI-18-Q1-B1-D8
Method	BLASTX
NCBI GI	g4455235
BLAST score	274
E value	4.0e-24
Match length	69
% identity	83
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]

Seq. No.	131053
Contig ID	50787_1.R1010
5'-most EST	LIB3176-024-P1-K1-D2
Method	BLASTX
NCBI GI	g3892708
BLAST score	65
E value	1.0e-53
Match length	136
% identity	74
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	131054
Contig ID	50799_1.R1010
5'-most EST	jC-atXP115C248N15T7d1

Seq. No.	131055
Contig ID	50803_1.R1010
5'-most EST	LIB3176-056-P1-K1-F1
Method	BLASTN
NCBI GI	g3228389
BLAST score	288
E value	1.0e-161
Match length	593
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	131056
Contig ID	50815_2.R1010
5'-most EST	LIB3176-066-P1-K1-F4
Method	BLASTX
NCBI GI	g3021270
BLAST score	223
E value	6.0e-18
Match length	138
% identity	39
NCBI Description	(AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

Seq. No.	131057
Contig ID	50872_1.R1010
5'-most EST	LIB3177-039-P1-K2-C2

Seq. No.	131058
Contig ID	50892_1.R1010
5'-most EST	jC-atXLIB327411P1f11b1
Method	BLASTN
NCBI GI	g2351061
BLAST score	337
E value	0.0e+00
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	131059
Contig ID	50915_1.R1010
5'-most EST	jC-atXLIB327414P3b10a1
Method	BLASTX
NCBI GI	g4539371
BLAST score	873
E value	9.0e-95
Match length	216
% identity	87
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	131060
Contig ID	50938_1.R1010
5'-most EST	jC-atXLIB327408P3c04a1
Method	BLASTX
NCBI GI	g2979551
BLAST score	692
E value	8.0e-73
Match length	176
% identity	81
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	131061
Contig ID	50948_1.R1010
5'-most EST	LIB3176-092-P1-K1-A3

Seq. No.	131062
Contig ID	50954_1.R1010
5'-most EST	g2759223
Method	BLASTX
NCBI GI	g4586034
BLAST score	647
E value	1.0e-67
Match length	127
% identity	100
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 131063

Contig ID	50956_1.R1010
5'-most EST	LIB3176-042-P1-K1-B4
Method	BLASTX
NCBI GI	g3292828
BLAST score	584
E value	2.0e-60
Match length	132
% identity	88
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131064
Contig ID	50983_1.R1010
5'-most EST	LIB3176-027-P1-K1-A8

Seq. No.	131065
Contig ID	50988_1.R1010
5'-most EST	g935852
Method	BLASTN
NCBI GI	g4417264
BLAST score	180
E value	2.0e-96
Match length	443
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131066
Contig ID	51023_1.R1010
5'-most EST	LIB3176-120-P2-K1-F4
Method	BLASTX
NCBI GI	g2982283
BLAST score	155
E value	5.0e-10
Match length	74
% identity	45
NCBI Description	(AF051226) PREG-like protein [Picea mariana]

Seq. No.	131067
Contig ID	51023_2.R1010
5'-most EST	g1159064
Method	BLASTX
NCBI GI	g3341694
BLAST score	294
E value	3.0e-26
Match length	103
% identity	58
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	131068
Contig ID	51036_1.R1010
5'-most EST	jC-atXLIB327423P1d07a1

Seq. No.	131069
Contig ID	51036_2.R1010
5'-most EST	jC-atXLIB327423P1d07b1
Method	BLASTX
NCBI GI	g3335378

BLAST score 221
E value 1.0e-17
Match length 117
% identity 44
NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No. 131070
Contig ID 51048_1.R1010
5'-most EST LIB3176-027-P1-K1-G5
Method BLASTN
NCBI GI g3980374
BLAST score 294
E value 1.0e-164
Match length 656
% identity 69
NCBI Description Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 131071
Contig ID 51054_1.R1010
5'-most EST LIB3176-027-P1-K1-H11
Method BLASTX
NCBI GI g4314378
BLAST score 626
E value 2.0e-65
Match length 151
% identity 81
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 131072
Contig ID 51074_1.R1010
5'-most EST g2748396
Method BLASTX
NCBI GI g2708532
BLAST score 352
E value 1.0e-33
Match length 119
% identity 28
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No. 131073
Contig ID 51091_1.R1010
5'-most EST LIB3176-028-P1-K1-C6
Method BLASTX
NCBI GI g118492
BLAST score 257
E value 9.0e-22
Match length 224
% identity 71
NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi_99532_pir__A35994 betaine-aldehyde dehydrogenase (EC 1.2.1.8) precursor - spinach >gi_170100 (M31480) betaine-aldehyde dehydrogenase (BADH) (EC 1.2.1.8) [Spinacia oleracea]

Seq. No. 131074

Contig ID	51095_1.R1010
5'-most EST	LIB3176-071-P1-K1-H3
Method	BLASTX
NCBI GI	g4191788
BLAST score	747
E value	1.0e-79
Match length	146
% identity	98
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	131075
Contig ID	51104_1.R1010
5'-most EST	LIB3176-028-P1-K1-D8
Method	BLASTX
NCBI GI	g4220454
BLAST score	300
E value	6.0e-51
Match length	110
% identity	58
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. ESTs gb_65870 and gb_T20812 come from this gene. [Arabidopsis thaliana]

Seq. No.	131076
Contig ID	51109_1.R1010
5'-most EST	g947540
Method	BLASTX
NCBI GI	g3283435
BLAST score	593
E value	2.0e-61
Match length	147
% identity	80
NCBI Description	(AF069495) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	131077
Contig ID	51109_2.R1010
5'-most EST	LIB3176-028-P1-K1-E12
Method	BLASTX
NCBI GI	g4490746
BLAST score	252
E value	1.0e-66
Match length	145
% identity	94
NCBI Description	(AL035708) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	131078
Contig ID	51112_1.R1010
5'-most EST	g2048400
Method	BLASTX
NCBI GI	g2160182
BLAST score	433
E value	1.0e-42
Match length	86
% identity	100

NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	131079
Contig ID	51112_2.R1010
5'-most EST	LIB3176-028-P1-K1-E5
Method	BLASTX
NCBI GI	g2160182
BLAST score	682
E value	8.0e-72
Match length	172
% identity	82
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	131080
Contig ID	51113_1.R1010
5'-most EST	LIB3176-028-P1-K1-E6
Method	BLASTX
NCBI GI	g3650030
BLAST score	648
E value	6.0e-68
Match length	141
% identity	90
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	131081
Contig ID	51135_1.R1010
5'-most EST	LIB3176-114-P2-K1-E3
Method	BLASTN
NCBI GI	g3869075
BLAST score	256
E value	1.0e-142
Match length	449
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	131082
Contig ID	51137_1.R1010
5'-most EST	jC-atXLIB327438P2h07a1
Method	BLASTX
NCBI GI	g4531444
BLAST score	488
E value	3.0e-67
Match length	181
% identity	67
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	131083
Contig ID	51154_1.R1010
5'-most EST	jC-atXP110CG7D6T7021a1
Method	BLASTX
NCBI GI	g3293551
BLAST score	152
E value	1.0e-09
Match length	127

% identity	33
NCBI Description	(AF072697) SHYC [Mus musculus]

Seq. No.	131084
Contig ID	51177_1.R1010
5'-most EST	g3450204
Method	BLASTX
NCBI GI	g1170169
BLAST score	470
E value	7.0e-47
Match length	106
% identity	84
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT2 (HD-ZIP PROTEIN 2) >gi_549886 (U09335) homeobox protein [Arabidopsis thaliana]

Seq. No.	131085
Contig ID	51191_1.R1010
5'-most EST	LIB3176-029-P1-K1-E1
Method	BLASTN
NCBI GI	g4589414
BLAST score	282
E value	1.0e-157
Match length	1002
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No.	131086
Contig ID	51206_1.R1010
5'-most EST	LIB3176-029-P1-K1-F12
Method	BLASTX
NCBI GI	g4454010
BLAST score	598
E value	7.0e-62
Match length	162
% identity	72
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	131087
Contig ID	51220_2.R1010
5'-most EST	LIB3176-029-P1-K1-G4
Method	BLASTX
NCBI GI	g399942
BLAST score	198
E value	3.0e-15
Match length	87
% identity	56
NCBI Description	CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No.	131088
Contig ID	51227_2.R1010
5'-most EST	LIB3176-029-P1-K1-H11

Seq. No.	131089
Contig ID	51228_1.R1010
5'-most EST	g2756814
Method	BLASTN
NCBI GI	g2979540
BLAST score	446
E value	0.0e+00
Match length	1318
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131090
Contig ID	51231_1.R1010
5'-most EST	g496830
Method	BLASTN
NCBI GI	g4589423
BLAST score	286
E value	1.0e-160
Match length	559
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence

Seq. No.	131091
Contig ID	51251_1.R1010
5'-most EST	LIB3177-065-P1-K1-F4
Method	BLASTX
NCBI GI	g4006879
BLAST score	725
E value	4.0e-77
Match length	139
% identity	100
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131092
Contig ID	51254_1.R1010
5'-most EST	ARABL1-031-Q1-E1-H10

Seq. No.	131093
Contig ID	51255_1.R1010
5'-most EST	LIB3176-030-P1-K1-B8
Method	BLASTX
NCBI GI	g3608139
BLAST score	535
E value	2.0e-54
Match length	171
% identity	67
NCBI Description	(AC005314) putative fibrillin [Arabidopsis thaliana]

Seq. No.	131094
Contig ID	51284_1.R1010
5'-most EST	g905622
Method	BLASTX
NCBI GI	g3928543
BLAST score	692
E value	4.0e-73

Match length	174
% identity	74
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	131095
Contig ID	51285_1.R1010
5'-most EST	LIB3176-106-P1-K1-A1
Method	BLASTN
NCBI GI	g3869071
BLAST score	178
E value	2.0e-95
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	131096
Contig ID	51287_1.R1010
5'-most EST	g2733495
Method	BLASTN
NCBI GI	g3297806
BLAST score	341
E value	0.0e+00
Match length	380
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	131097
Contig ID	51288_1.R1010
5'-most EST	LIB3176-030-P1-K1-E5

Seq. No.	131098
Contig ID	51291_1.R1010
5'-most EST	g2739592
Method	BLASTN
NCBI GI	g2264305
BLAST score	128
E value	2.0e-65
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	131099
Contig ID	51298_1.R1010
5'-most EST	LIB3176-030-P1-K1-F4
Method	BLASTN
NCBI GI	g3449331
BLAST score	227
E value	1.0e-124
Match length	459
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	131100
Contig ID	51309_1.R1010
5'-most EST	LIB3176-030-P1-K1-G3
Method	BLASTX
NCBI GI	g2760332
BLAST score	779
E value	3.0e-83
Match length	160
% identity	96
NCBI Description	(AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No.	131101
Contig ID	51310_1.R1010
5'-most EST	LIB3176-030-P1-K1-G4

Seq. No.	131102
Contig ID	51315_1.R1010
5'-most EST	LIB3176-030-P1-K1-G9
Method	BLASTX
NCBI GI	g4689366
BLAST score	146
E value	9.0e-09
Match length	60
% identity	45
NCBI Description	(AF134155) RING finger protein [Arabidopsis thaliana]

Seq. No.	131103
Contig ID	51317_1.R1010
5'-most EST	LIB3177-070-P1-K1-D11
Method	BLASTX
NCBI GI	g2244874
BLAST score	113
E value	8.0e-05
Match length	122
% identity	83
NCBI Description	(Z97338) coll wall protein homolog [Arabidopsis thaliana]

Seq. No.	131104
Contig ID	51318_1.R1010
5'-most EST	LIB3176-030-P1-K1-H11
Method	BLASTX
NCBI GI	g4678328
BLAST score	387
E value	2.0e-50
Match length	217
% identity	52
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	131105
Contig ID	51319_1.R1010
5'-most EST	LIB3176-030-P1-K1-H12
Method	BLASTX
NCBI GI	g818849
BLAST score	662
E value	2.0e-69
Match length	172

% identity	72
NCBI Description	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]

Seq. No.	131106
Contig ID	51323_1.R1010
5'-most EST	g2757450
Method	BLASTX
NCBI GI	g3522936
BLAST score	142
E value	1.0e-08
Match length	132
% identity	21
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	131107
Contig ID	51323_2.R1010
5'-most EST	LIB3176-030-P1-K1-H5
Method	BLASTX
NCBI GI	g3522935
BLAST score	475
E value	2.0e-47
Match length	138
% identity	70
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	131108
Contig ID	51352_2.R1010
5'-most EST	LIB3234-048-P1-K1-C5
Method	BLASTN
NCBI GI	g3046856
BLAST score	308
E value	1.0e-173
Match length	371
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	131109
Contig ID	51380_1.R1010
5'-most EST	LIB3176-032-P1-K1-F1
Method	BLASTX
NCBI GI	g4678353
BLAST score	747
E value	1.0e-79
Match length	143
% identity	99
NCBI Description	(AL049659) cysteine endopeptidase precursor-like protein [Arabidopsis thaliana]

Seq. No.	131110
Contig ID	51411_1.R1010
5'-most EST	g2393672
Method	BLASTX
NCBI GI	g2493810

BLAST score 291
E value 5.0e-26
Match length 62
% identity 85
NCBI Description COPROPORPHYRINOGEN III OXIDASE PRECURSOR (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) >gi_1213067_emb_CAA58038_ (X82831) coproporphyrinogen oxidase [Nicotiana tabacum]

Seq. No. 131111
Contig ID 51413_1.R1010
5'-most EST g930969
Method BLASTX
NCBI GI g4091806
BLAST score 87
E value 5.0e-64
Match length 202
% identity 64
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No. 131112
Contig ID 51456_1.R1010
5'-most EST jC-atXLIB327438P4f05a2
Method BLASTN
NCBI GI g531828
BLAST score 39
E value 5.0e-12
Match length 43
% identity 98
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 131113
Contig ID 51457_1.R1010
5'-most EST LIB3234-009-P1-K1-F8

Seq. No. 131114
Contig ID 51486_1.R1010
5'-most EST jC-atXLIB327426P2d03b1
Method BLASTN
NCBI GI g2182287
BLAST score 279
E value 1.0e-155
Match length 417
% identity 100
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No. 131115
Contig ID 51486_2.R1010
5'-most EST LIB3176-033-P1-K1-H3
Method BLASTN
NCBI GI g2182287
BLAST score 337
E value 0.0e+00
Match length 404
% identity 98
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,

complete sequence [Arabidopsis thaliana]

Seq. No.	131116
Contig ID	51486_3.R1010
5'-most EST	jC-atXLIB327405P1g04a2
Method	BLASTN
NCBI GI	g2182287
BLAST score	366
E value	0.0e+00
Match length	406
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	131117
Contig ID	51489_1.R1010
5'-most EST	LIB3176-033-P1-K1-H8
Method	BLASTX
NCBI GI	g2829751
BLAST score	203
E value	1.0e-15
Match length	115
% identity	38
NCBI Description	MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) >gi_1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi_2190976 (AF002699) macrophage migration inhibitory factor [Brugia malayi]

Seq. No.	131118
Contig ID	51495_1.R1010
5'-most EST	LIB3176-034-P1-K1-A3
Method	BLASTX
NCBI GI	g417360
BLAST score	323
E value	6.0e-30
Match length	115
% identity	55
NCBI Description	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 >gi_2131280_pir__S67767 high mobility group-like protein NHP2 - yeast (Saccharomyces cerevisiae) >gi_666101_emb_CAA40885_ (X57714) high mobility group-like nuclear protein 2 [Saccharomyces cerevisiae] >gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like protein [Saccharomyces cerevisiae] >gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w [Saccharomyces cerevisiae]

Seq. No.	131119
Contig ID	51523_1.R1010
5'-most EST	LIB3177-014-P1-K2-E4
Method	BLASTN
NCBI GI	g4678219
BLAST score	346
E value	0.0e+00
Match length	477
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic

sequence, complete sequence

Seq. No.	131120
Contig ID	51528_1.R1010
5'-most EST	LIB3176-034-P1-K1-D7
Method	BLASTX
NCBI GI	g3025470
BLAST score	58
E value	3.0e-37
Match length	147
% identity	52
NCBI Description	(U76756) endo-beta-1,4-glucanase [Pinus radiata]

Seq. No.	131121
Contig ID	51529_1.R1010
5'-most EST	LIB3176-034-P1-K1-D8
Method	BLASTX
NCBI GI	g3123244
BLAST score	49
E value	4.0e-23
Match length	182
% identity	41
NCBI Description	ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX) >gi_1132479_dbj_BAA09510_ (D55649) alpha mannosidase II isozyme [Homo sapiens]

Seq. No.	131122
Contig ID	51532_1.R1010
5'-most EST	jC-atXP22C119C22T7007a1

Seq. No.	131123
Contig ID	51563_1.R1010
5'-most EST	LIB3176-034-P1-K1-H11
Method	BLASTX
NCBI GI	g3377802
BLAST score	281
E value	6.0e-25
Match length	148
% identity	31
NCBI Description	(AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis thaliana]

Seq. No.	131124
Contig ID	51615_1.R1010
5'-most EST	LIB3176-035-P1-K1-E5

Seq. No.	131125
Contig ID	51673_1.R1010
5'-most EST	LIB3176-036-P1-K1-C8
Method	BLASTN
NCBI GI	g4757405
BLAST score	296
E value	1.0e-166
Match length	332
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOJ10, complete sequence

Seq. No.	131126
Contig ID	51681_1.R1010
5'-most EST	g4210235
Method	BLASTN
NCBI GI	g4584531
BLAST score	483
E value	0.0e+00
Match length	483
% identity	31
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	131127
Contig ID	51693_1.R1010
5'-most EST	LIB3176-085-P1-K1-H12
Method	BLASTN
NCBI GI	g3449326
BLAST score	454
E value	0.0e+00
Match length	498
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	131128
Contig ID	51703_1.R1010
5'-most EST	LIB3176-036-P1-K1-G10
Method	BLASTX
NCBI GI	g4725941
BLAST score	561
E value	8.0e-58
Match length	137
% identity	85
NCBI Description	(AL049730) putative pollen-specific protein [Arabidopsis thaliana]

Seq. No.	131129
Contig ID	51704_1.R1010
5'-most EST	LIB3176-036-P1-K1-G2
Method	BLASTX
NCBI GI	g3894194
BLAST score	52
E value	9.0e-16
Match length	132
% identity	44
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	131130
Contig ID	51711_1.R1010
5'-most EST	g1054433
Method	BLASTX
NCBI GI	g2832625
BLAST score	534
E value	1.0e-54

Match length	116
% identity	83
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	131131
Contig ID	51726_1.R1010
5'-most EST	jC-atXLIB327429P4g09a2
Method	BLASTN
NCBI GI	g531828
BLAST score	40
E value	7.0e-13
Match length	43
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	131132
Contig ID	51762_1.R1010
5'-most EST	LIB3176-074-P1-K1-H9

Seq. No.	131133
Contig ID	51773_1.R1010
5'-most EST	LIB3176-037-P1-K1-G5
Method	BLASTX
NCBI GI	g4544409
BLAST score	729
E value	4.0e-77
Match length	190
% identity	71
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211_2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana]

Seq. No.	131134
Contig ID	51804_1.R1010
5'-most EST	jC-atXLIB327408P3h03a1
Method	BLASTX
NCBI GI	g3913240
BLAST score	281
E value	2.0e-81
Match length	179
% identity	91
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase subunit [Nicotiana tabacum]

Seq. No.	131135
Contig ID	51850_1.R1010
5'-most EST	jC-atXmonuni26Dc12b1
Method	BLASTX
NCBI GI	g3341699
BLAST score	510
E value	1.0e-51
Match length	140
% identity	69
NCBI Description	(AC003672) putative giberellin beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	131136
Contig ID	51851_1.R1010
5'-most EST	LIB3176-038-P1-K1-H1

Seq. No.	131137
Contig ID	51855_1.R1010
5'-most EST	LIB3176-038-P1-K1-H2
Method	BLASTN
NCBI GI	g3056579
BLAST score	234
E value	1.0e-129
Match length	401
% identity	90
NCBI Description	Arabidopsis thaliana BAC T1F9 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	131138
Contig ID	51877_1.R1010
5'-most EST	jC-atXP102CE3H7T7b1

Seq. No.	131139
Contig ID	51888_1.R1010
5'-most EST	jC-atXP20C114C13T7d2
Method	BLASTX
NCBI GI	g4220523
BLAST score	311
E value	1.0e-28
Match length	132
% identity	52
NCBI Description	(AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No.	131140
Contig ID	51892_1.R1010
5'-most EST	LIB3176-039-P1-K1-C4
Method	BLASTX
NCBI GI	g4006848
BLAST score	177
E value	2.0e-13
Match length	83
% identity	49
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	131141
Contig ID	51899_1.R1010
5'-most EST	LIB3176-039-P1-K1-D10

Seq. No.	131142
Contig ID	51900_1.R1010
5'-most EST	LIB3176-088-P1-K1-F9
Method	BLASTN
NCBI GI	g4376087
BLAST score	433
E value	0.0e+00
Match length	441
% identity	100

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	131143
Contig ID	51920_1.R1010
5'-most EST	LIB3176-040-P1-K1-C4
Seq. No.	131144
Contig ID	51936_1.R1010
5'-most EST	LIB3176-119-P2-K1-C10
Method	BLASTX
NCBI GI	g4539297
BLAST score	375
E value	4.0e-72
Match length	208
% identity	66
NCBI Description	(AL049480) putative pathogenesis-related protein [Arabidopsis thaliana]
Seq. No.	131145
Contig ID	51983_1.R1010
5'-most EST	jC-atXmonuni26Ac01b1
Method	BLASTN
NCBI GI	g3449324
BLAST score	159
E value	4.0e-84
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12G2, complete sequence
Seq. No.	131146
Contig ID	51984_1.R1010
5'-most EST	LIB3176-040-P1-K1-D3
Method	BLASTN
NCBI GI	g1877523
BLAST score	185
E value	1.0e-99
Match length	376
% identity	99
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]
Seq. No.	131147
Contig ID	52030_2.R1010
5'-most EST	jC-atXP36C156D3T7d1
Method	BLASTN
NCBI GI	g4589412
BLAST score	374
E value	0.0e+00
Match length	632
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence
Seq. No.	131148
Contig ID	52049_1.R1010

5'-most EST	g2048956
Seq. No.	131149
Contig ID	52050_1.R1010
5'-most EST	LIB3176-041-P1-K1-C3
Method	BLASTX
NCBI GI	g2342722
BLAST score	372
E value	2.0e-42
Match length	125
% identity	74
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.	131150
Contig ID	52058_1.R1010
5'-most EST	LIB3176-041-P1-K1-D2
Method	BLASTN
NCBI GI	g2098816
BLAST score	444
E value	0.0e+00
Match length	737
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence
Seq. No.	131151
Contig ID	52070_1.R1010
5'-most EST	jC-atXLIB327401P3a02b2
Method	BLASTN
NCBI GI	g2656030
BLAST score	191
E value	1.0e-103
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
Seq. No.	131152
Contig ID	52099_1.R1010
5'-most EST	LIB3176-041-P1-K1-H11
Method	BLASTN
NCBI GI	g4027862
BLAST score	316
E value	1.0e-178
Match length	372
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	131153
Contig ID	52106_1.R1010
5'-most EST	LIB35-036-Q1-E2-B2
Method	BLASTX
NCBI GI	g2832672
BLAST score	708
E value	7.0e-75
Match length	149
% identity	93

NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.	131154
Contig ID	52117_1.R1010
5'-most EST	g1158617
Method	BLASTN
NCBI GI	g3688169
BLAST score	204
E value	1.0e-111
Match length	461
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)
Seq. No.	131155
Contig ID	52137_1.R1010
5'-most EST	jC-atXP31C146I7T7d2
Method	BLASTX
NCBI GI	g549061
BLAST score	569
E value	1.0e-58
Match length	168
% identity	64
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi_468554_emb_CAA83432_ (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus]
Seq. No.	131156
Contig ID	52145_1.R1010
5'-most EST	LIB3176-042-P1-K1-D6
Method	BLASTX
NCBI GI	g2244775
BLAST score	630
E value	1.0e-65
Match length	120
% identity	98
NCBI Description	(Z97335) salt-inducible protein homolog [Arabidopsis thaliana]
Seq. No.	131157
Contig ID	52151_1.R1010
5'-most EST	LIB3177-072-P1-K1-G6
Method	BLASTN
NCBI GI	g4469002
BLAST score	124
E value	3.0e-63
Match length	463
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)
Seq. No.	131158
Contig ID	52206_1.R1010
5'-most EST	jC-atXP123C117C23T7091a1
Method	BLASTX

NCBI GI g1881585
BLAST score 46
E value 3.0e-25
Match length 161
% identity 44
NCBI Description (U72489) remorin [Solanum tuberosum]

Seq. No. 131159
Contig ID 52206_2.R1010
5'-most EST jC-atXP107C117C22T7d1
Method BLASTX
NCBI GI g4731573
BLAST score 165
E value 3.0e-11
Match length 62
% identity 58
NCBI Description (AF123265) remorin 1 [Lycopersicon esculentum]

Seq. No. 131160
Contig ID 52221_1.R1010
5'-most EST LIB3176-043-P1-K1-E3
Method BLASTX
NCBI GI g2160169
BLAST score 176
E value 2.0e-12
Match length 72
% identity 51
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 131161
Contig ID 52254_1.R1010
5'-most EST jC-atXLIB327421P3g10b1
Method BLASTN
NCBI GI g3063438
BLAST score 280
E value 1.0e-156
Match length 606
% identity 100
NCBI Description Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No. 131162
Contig ID 52315_1.R1010
5'-most EST LIB3176-044-P1-K1-G6
Method BLASTX
NCBI GI g3426039
BLAST score 1104
E value 1.0e-121
Match length 315
% identity 64
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 131163
Contig ID 52316_1.R1010
5'-most EST LIB3176-044-P1-K1-G7

Seq. No. 131164

Contig ID	52324_1.R1010
5'-most EST	LIB3177-017-P1-K2-E7
Method	BLASTX
NCBI GI	g3193296
BLAST score	716
E value	9.0e-76
Match length	206
% identity	65
NCBI Description	(AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No.	131165
Contig ID	52330_1.R1010
5'-most EST	jC-atXLIB327402P3b11b1
Method	BLASTX
NCBI GI	g418507
BLAST score	177
E value	1.0e-12
Match length	70
% identity	50
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	131166
Contig ID	52380_1.R1010
5'-most EST	LIB3176-045-P1-K1-H1
Method	BLASTX
NCBI GI	g2558662
BLAST score	197
E value	6.0e-15
Match length	204
% identity	7
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	131167
Contig ID	52386_1.R1010
5'-most EST	LIB3177-039-P1-K2-F10

Seq. No.	131168
Contig ID	52440_1.R1010
5'-most EST	LIB3176-046-P1-K1-G1

Seq. No.	131169
Contig ID	52484_1.R1010
5'-most EST	jC-atXLIB327409P2b06a1
Method	BLASTX
NCBI GI	g2982303
BLAST score	329
E value	2.0e-66
Match length	155
% identity	82
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	131170
Contig ID	52490_1.R1010
5'-most EST	g2747396
Seq. No.	131171
Contig ID	52506_1.R1010
5'-most EST	g957961
Method	BLASTX
NCBI GI	g2529674
BLAST score	308
E value	7.0e-28
Match length	120
% identity	50
NCBI Description	(AC002535) hypothetical protein [Arabidopsis thaliana]
Seq. No.	131172
Contig ID	52510_1.R1010
5'-most EST	jC-atXP18C115B20T7d2
Seq. No.	131173
Contig ID	52510_2.R1010
5'-most EST	LIB3177-099-P1-K1-H9
Seq. No.	131174
Contig ID	52513_1.R1010
5'-most EST	LIB35-039-Q1-E1-C11
Method	BLASTX
NCBI GI	g4335763
BLAST score	414
E value	3.0e-40
Match length	161
% identity	50
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.	131175
Contig ID	52513_2.R1010
5'-most EST	jC-atXLIB327401P2a03a1
Method	BLASTN
NCBI GI	g3510344
BLAST score	63
E value	1.0e-26
Match length	143
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
Seq. No.	131176
Contig ID	52516_1.R1010
5'-most EST	LIB3176-047-P1-K1-F12
Method	BLASTN
NCBI GI	g4454447
BLAST score	516
E value	0.0e+00
Match length	979
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131177
Contig ID	52553_1.R1010
5'-most EST	g2048702
Method	BLASTN
NCBI GI	g2342717
BLAST score	326
E value	0.0e+00
Match length	421
% identity	56
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131178
Contig ID	52572_2.R1010
5'-most EST	jC-atXP34C149I19T7a1
Method	BLASTX
NCBI GI	g2244772
BLAST score	138
E value	1.0e-11
Match length	69
% identity	70
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	131179
Contig ID	52572_3.R1010
5'-most EST	LIB3176-048-P1-K1-C6
Method	BLASTX
NCBI GI	g2244772
BLAST score	494
E value	1.0e-49
Match length	129
% identity	82
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	131180
Contig ID	52573_1.R1010
5'-most EST	LIB3176-048-P1-K1-C7
Method	BLASTX
NCBI GI	g4633656
BLAST score	273
E value	8.0e-24
Match length	115
% identity	47
NCBI Description	(AF123263) phenylalanyl tRNA synthetase beta subunit [Mus musculus]

Seq. No.	131181
Contig ID	52584_1.R1010
5'-most EST	jC-atXP19C113B4T7064a1
Method	BLASTX
NCBI GI	g4185143
BLAST score	579
E value	1.0e-59
Match length	130
% identity	84
NCBI Description	(AC005724) putative signal recognition particle receptor

beta subunit [Arabidopsis thaliana]

Seq. No.	131182
Contig ID	52588_1.R1010
5'-most EST	LIB3177-026-P1-K2-B2
Method	BLASTX
NCBI GI	g4220528
BLAST score	745
E value	4.0e-79
Match length	151
% identity	98
NCBI Description	(AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	131183
Contig ID	52592_1.R1010
5'-most EST	LIB3176-048-P1-K1-E2
Method	BLASTX
NCBI GI	g1906830
BLAST score	499
E value	2.0e-50
Match length	172
% identity	57
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	131184
Contig ID	52617_1.R1010
5'-most EST	LIB3176-050-P1-K1-B5
Method	BLASTX
NCBI GI	g4335773
BLAST score	267
E value	4.0e-23
Match length	74
% identity	73
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	131185
Contig ID	52618_1.R1010
5'-most EST	LIB3176-048-P1-K1-G6

Seq. No.	131186
Contig ID	52645_1.R1010
5'-most EST	g2446013
Method	BLASTX
NCBI GI	g4218151
BLAST score	189
E value	4.0e-14
Match length	83
% identity	42
NCBI Description	(AJ132705) hypothetical protein [Anabaena variabilis]

Seq. No.	131187
Contig ID	52645_2.R1010
5'-most EST	g958196
Method	BLASTN
NCBI GI	g3702734
BLAST score	449

E value	0.0e+00
Match length	472
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	131188
Contig ID	52666_1.R1010
5'-most EST	LIB3176-049-P1-K1-D2
Method	BLASTX
NCBI GI	g4454038
BLAST score	588
E value	1.0e-60
Match length	168
% identity	67
NCBI Description	(AL035394) putative disease resistance response protein [Arabidopsis thaliana]

Seq. No.	131189
Contig ID	52679_1.R1010
5'-most EST	jC-atXP66C211B6T7d1
Method	BLASTX
NCBI GI	g4510384
BLAST score	235
E value	2.0e-19
Match length	70
% identity	71
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	131190
Contig ID	52679_2.R1010
5'-most EST	jC-atXP66C211B6T7087a1

Seq. No.	131191
Contig ID	52693_1.R1010
5'-most EST	LIB3176-101-P1-K1-C11
Method	BLASTX
NCBI GI	g113363
BLAST score	432
E value	2.0e-42
Match length	155
% identity	52
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_279445_pir__DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia >gi_20506_emb_CAA38039_ (X54106) alcohol dehydrogenase [Petunia x hybrida]

Seq. No.	131192
Contig ID	52728_1.R1010
5'-most EST	LIB3176-050-P1-K1-B8
Method	BLASTX
NCBI GI	g1729980
BLAST score	681
E value	9.0e-72
Match length	151
% identity	81
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175

thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	131193
Contig ID	52739_1.R1010
5'-most EST	LIB3176-050-P1-K1-C9
Method	BLASTX
NCBI GI	g3420751
BLAST score	203
E value	2.0e-26
Match length	122
% identity	52
NCBI Description	(AF079448) cytochrome c oxidase assembly protein [Dictyostelium discoideum]

Seq. No.	131194
Contig ID	52762_1.R1010
5'-most EST	jC-atXP39C162G2T7s1
Method	BLASTX
NCBI GI	g2842490
BLAST score	238
E value	2.0e-47
Match length	102
% identity	94
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	131195
Contig ID	52790_1.R1010
5'-most EST	LIB3176-050-P1-K1-H3
Method	BLASTX
NCBI GI	g4733981
BLAST score	558
E value	2.0e-57
Match length	151
% identity	72
NCBI Description	(AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	131196
Contig ID	52792_2.R1010
5'-most EST	LIB3234-078-P1-K1-B2
Method	BLASTX
NCBI GI	g4337188
BLAST score	505
E value	5.0e-51
Match length	127
% identity	83
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131197
Contig ID	52809_1.R1010
5'-most EST	LIB3176-051-P1-K1-B4
Method	BLASTX
NCBI GI	g2244910
BLAST score	165

E value	4.0e-11
Match length	103
% identity	40
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	131198
Contig ID	52883_1.R1010
5'-most EST	g2763952
Method	BLASTX
NCBI GI	g2982262
BLAST score	386
E value	4.0e-37
Match length	124
% identity	57
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	131199
Contig ID	52907_1.R1010
5'-most EST	g1565711
Method	BLASTX
NCBI GI	g1781338
BLAST score	301
E value	3.0e-27
Match length	117
% identity	55
NCBI Description	(Y10470) peroxidase [Spinacia oleracea]

Seq. No.	131200
Contig ID	52926_1.R1010
5'-most EST	LIB3176-052-P1-K1-G7
Method	BLASTX
NCBI GI	g2982331
BLAST score	654
E value	1.0e-68
Match length	142
% identity	93
NCBI Description	(AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No.	131201
Contig ID	52939_1.R1010
5'-most EST	LIB3176-053-P1-K1-B1
Method	BLASTX
NCBI GI	g140508
BLAST score	533
E value	1.0e-79
Match length	157
% identity	89
NCBI Description	PROBABLE INTRON MATURASE >gi_99852_pir__S07168 probable maturase, 63K - white mustard chloroplast >gi_12220_emb_CAA28509_ (X04826) ycf14 (AA1-324) [Sinapis alba]

Seq. No.	131202
Contig ID	52947_1.R1010
5'-most EST	LIB3176-053-P1-K1-B8
Method	BLASTX

NCBI GI	g1346875
BLAST score	323
E value	1.0e-29
Match length	104
% identity	57
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN >gi_1185169_emb_CAA91652_ (Z67753) PSII, protein W, 13 kDa [Odontella sinensis]

Seq. No.	131203
Contig ID	52960_1.R1010
5'-most EST	jC-atXLIB327413P4f11a1
Method	BLASTX
NCBI GI	g4538905
BLAST score	966
E value	1.0e-105
Match length	191
% identity	98
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	131204
Contig ID	52965_1.R1010
5'-most EST	g2062810
Method	BLASTN
NCBI GI	g2880038
BLAST score	292
E value	1.0e-163
Match length	402
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131205
Contig ID	52971_1.R1010
5'-most EST	LIB3176-053-P1-K1-F8
Method	BLASTN
NCBI GI	g2828185
BLAST score	164
E value	5.0e-87
Match length	412
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	131206
Contig ID	52974_1.R1010
5'-most EST	LIB3176-053-P1-K1-G2
Method	BLASTX
NCBI GI	g4314392
BLAST score	518
E value	7.0e-53
Match length	105
% identity	99
NCBI Description	(AC006232) putative ferredoxin [Arabidopsis thaliana]

Seq. No.	131207
Contig ID	53025_1.R1010

5'-most EST	jC-atXP10C97B15T7d1
Method	BLASTX
NCBI GI	g3242715
BLAST score	319
E value	2.0e-29
Match length	136
% identity	65
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131208
Contig ID	53079_1.R1010
5'-most EST	LIB3177-050-P1-K1-G4
Method	BLASTX
NCBI GI	g1934726
BLAST score	297
E value	8.0e-27
Match length	120
% identity	57
NCBI Description	(U95034) germin-like protein [Arabidopsis thaliana]

Seq. No.	131209
Contig ID	53097_1.R1010
5'-most EST	LIB3177-043-P1-K2-G7
Method	BLASTX
NCBI GI	g3142289
BLAST score	502
E value	1.0e-74
Match length	184
% identity	82
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	131210
Contig ID	53108_1.R1010
5'-most EST	g16934
Method	BLASTX
NCBI GI	g3063701
BLAST score	736
E value	5.0e-78
Match length	144
% identity	98
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	131211
Contig ID	53110_2.R1010
5'-most EST	jC-atXL1040Q1E1E07b1
Method	BLASTN
NCBI GI	g4510323
BLAST score	221
E value	1.0e-121
Match length	428
% identity	96
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	131212
Contig ID	53110_3.R1010

5'-most EST	jC-atXLIB327414P2f09a1
Method	BLASTN
NCBI GI	g4510323
BLAST score	418
E value	0.0e+00
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	131213
Contig ID	53113_1.R1010
5'-most EST	g2733153
Method	BLASTX
NCBI GI	g3193287
BLAST score	666
E value	2.0e-72
Match length	183
% identity	66
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	131214
Contig ID	53126_1.R1010
5'-most EST	jC-atXP82CG1F5T7b1

Seq. No.	131215
Contig ID	53147_1.R1010
5'-most EST	LIB3176-056-P1-K1-H9
Method	BLASTX
NCBI GI	g1769907
BLAST score	475
E value	1.0e-47
Match length	135
% identity	61
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	131216
Contig ID	53155_1.R1010
5'-most EST	jC-atXP19C113A18T7032a1
Method	BLASTX
NCBI GI	g2688839
BLAST score	597
E value	1.0e-61
Match length	153
% identity	76
NCBI Description	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]

Seq. No.	131217
Contig ID	53155_2.R1010
5'-most EST	jC-atXLI11Q1B1H11a1
Method	BLASTX
NCBI GI	g2688839
BLAST score	522
E value	4.0e-53

Match length	143
% identity	80
NCBI Description	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]

Seq. No.	131218
Contig ID	53163_1.R1010
5'-most EST	LIB3176-057-P1-K1-B6
Method	BLASTN
NCBI GI	g4567300
BLAST score	400
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	131219
Contig ID	53164_1.R1010
5'-most EST	jC-atXLIB327438P4f08a2
Method	BLASTX
NCBI GI	g4455169
BLAST score	324
E value	6.0e-30
Match length	154
% identity	49
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	131220
Contig ID	53164_2.R1010
5'-most EST	LIB3176-057-P1-K1-B7
Method	BLASTN
NCBI GI	g4455168
BLAST score	202
E value	1.0e-110
Match length	388
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	131221
Contig ID	53167_1.R1010
5'-most EST	jC-atXP85C241B24T7b1
Method	BLASTN
NCBI GI	g4220636
BLAST score	276
E value	1.0e-153
Match length	630
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	131222
Contig ID	53181_1.R1010
5'-most EST	g2722166
Method	BLASTX

NCBI GI	g4455295
BLAST score	383
E value	8.0e-37
Match length	117
% identity	68
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	131223
Contig ID	53216_1.R1010
5'-most EST	LIB3176-057-P1-K1-G6
Method	BLASTX
NCBI GI	g3522956
BLAST score	297
E value	7.0e-27
Match length	84
% identity	69
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	131224
Contig ID	53239_1.R1010
5'-most EST	jC-atXP98CH2H7T7b1
Method	BLASTX
NCBI GI	g4314369
BLAST score	658
E value	7.0e-69
Match length	184
% identity	77
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131225
Contig ID	53257_1.R1010
5'-most EST	LIB3177-020-P1-K2-H3
Method	BLASTX
NCBI GI	g1653444
BLAST score	209
E value	4.0e-16
Match length	175
% identity	31
NCBI Description	(D90913) hypothetical protein [Synechocystis sp.]

Seq. No.	131226
Contig ID	53262_1.R1010
5'-most EST	g458793
Method	BLASTX
NCBI GI	g4115918
BLAST score	66
E value	3.0e-10
Match length	52
% identity	92
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	131227
Contig ID	53290_1.R1010
5'-most EST	LIB3176-064-P1-K1-A1

Method	BLASTN
NCBI GI	g4589439
BLAST score	175
E value	1.0e-93
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	131228
Contig ID	53301_1.R1010
5'-most EST	LIB3177-055-P1-K1-A1
Method	BLASTX
NCBI GI	g4262241
BLAST score	292
E value	4.0e-26
Match length	142
% identity	52
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	131229
Contig ID	53302_1.R1010
5'-most EST	jC-atXP90C245N5T7s2
Method	BLASTX
NCBI GI	g99698
BLAST score	662
E value	2.0e-69
Match length	125
% identity	99
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgskb6) - Arabidopsis thaliana

Seq. No.	131230
Contig ID	53302_2.R1010
5'-most EST	jC-atXLIB327403P1b09a1
Method	BLASTX
NCBI GI	g1076473
BLAST score	343
E value	3.0e-32
Match length	72
% identity	92
NCBI Description	Gln 1.1 protein - radish >gi_1526562_dbj_BAA04994_ (D25324) glutamine synthetase [Raphanus sativus]

Seq. No.	131231
Contig ID	53307_1.R1010
5'-most EST	LIB3176-058-P1-K1-H3
Method	BLASTX
NCBI GI	g4733973
BLAST score	216
E value	4.0e-17
Match length	85
% identity	48
NCBI Description	(AC007264) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131232
Contig ID	53412_1.R1010

5'-most EST	LIB3177-020-P1-K2-A9
Method	BLASTX
NCBI GI	g133409
BLAST score	404
E value	4.0e-39
Match length	89
% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_66962_pir__RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi_11860_emb_CAA77376_ (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi_225228_prf__1211235BK RNA polymerase alpha [Nicotiana tabacum]

Seq. No.	131233
Contig ID	53418_1.R1010
5'-most EST	LIB3176-060-P1-K1-F6
Method	BLASTX
NCBI GI	g1362162
BLAST score	872
E value	8.0e-94
Match length	262
% identity	61
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	131234
Contig ID	53427_1.R1010
5'-most EST	g2413801
Method	BLASTX
NCBI GI	g3738291
BLAST score	328
E value	2.0e-60
Match length	126
% identity	98
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	131235
Contig ID	53427_3.R1010
5'-most EST	LIB3176-060-P1-K1-G8
Method	BLASTX
NCBI GI	g3738291
BLAST score	544
E value	1.0e-55
Match length	150
% identity	77
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	131236
Contig ID	53444_1.R1010
5'-most EST	g2759180
Method	BLASTX
NCBI GI	g3335347
BLAST score	443
E value	7.0e-44
Match length	125
% identity	72

NCBI Description	(AC004512) Contains similarity to ARI, RING finger protein gb_X98309 from Drosophila melanogaster. ESTs gb_T44383, gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and gb_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No.	131237
Contig ID	53450_1.R1010
5'-most EST	jC-atXLIB327408P3a03a1
Method	BLASTN
NCBI GI	g3873174
BLAST score	77
E value	6.0e-35
Match length	267
% identity	87
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	131238
Contig ID	53493_1.R1010
5'-most EST	LIB3176-087-P1-K1-A11
Method	BLASTX
NCBI GI	g3738091
BLAST score	890
E value	4.0e-96
Match length	250
% identity	74
NCBI Description	(AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana]

Seq. No.	131239
Contig ID	53534_1.R1010
5'-most EST	LIB3177-025-P1-K2-E12
Method	BLASTN
NCBI GI	g3702734
BLAST score	437
E value	0.0e+00
Match length	501
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	131240
Contig ID	53546_1.R1010
5'-most EST	ARABL1-06-Q1-B1-F7

Seq. No.	131241
Contig ID	53556_1.R1010
5'-most EST	g2446133
Method	BLASTN
NCBI GI	g3128134
BLAST score	574
E value	0.0e+00
Match length	623
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	131242
Contig ID	53559_1.R1010
5'-most EST	ARABLI-022-Q1-B1-G11
Method	BLASTN
NCBI GI	g2264319
BLAST score	54
E value	3.0e-21
Match length	348
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	131243
Contig ID	53580_1.R1010
5'-most EST	LIB3234-009-P1-K1-A5
Method	BLASTX
NCBI GI	g1731078
BLAST score	191
E value	3.0e-14
Match length	138
% identity	37
NCBI Description	HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION >gi_1303968_dbj_BAA12623_ (D84432) YqjQ [Bacillus subtilis] >gi_2634813_emb_CAB14310_ (Z99116) similar to ketoacyl reductase [Bacillus subtilis]

Seq. No.	131244
Contig ID	53622_1.R1010
5'-most EST	ARABLI-044-Q1-B1-C7

Seq. No.	131245
Contig ID	53638_1.R1010
5'-most EST	LIB3176-064-P1-K1-E3

Seq. No.	131246
Contig ID	53676_1.R1010
5'-most EST	jC-atXP82CG2A1T7b1
Method	BLASTX
NCBI GI	g2914703
BLAST score	181
E value	5.0e-59
Match length	132
% identity	92
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	131247
Contig ID	53702_1.R1010
5'-most EST	jC-atXP85C241C10T7b1
Method	BLASTX
NCBI GI	g3242077
BLAST score	472
E value	4.0e-47
Match length	150
% identity	65
NCBI Description	(AJ003119) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 131248

Contig ID	53720_1.R1010
5'-most EST	LIB3176-065-P1-K1-E6
Method	BLASTX
NCBI GI	g2706450
BLAST score	376
E value	5.0e-36
Match length	93
% identity	77
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	131249
Contig ID	53721_1.R1010
5'-most EST	LIB3176-065-P1-K1-E7
Method	BLASTN
NCBI GI	g3241917
BLAST score	235
E value	1.0e-129
Match length	712
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	131250
Contig ID	53727_1.R1010
5'-most EST	LIB3176-065-P1-K1-F2

Seq. No.	131251
Contig ID	53731_1.R1010
5'-most EST	LIB3176-065-P1-K1-F6
Method	BLASTX
NCBI GI	g4581108
BLAST score	306
E value	3.0e-28
Match length	142
% identity	50
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	131252
Contig ID	53740_1.R1010
5'-most EST	LIB3176-065-P1-K1-G4
Method	BLASTN
NCBI GI	g3337347
BLAST score	290
E value	1.0e-162
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131253
Contig ID	53750_1.R1010
5'-most EST	g2749608

Seq. No.	131254

Contig ID 53750_3.R1010
5'-most EST jC-atXLIB327427P3a05b2

Seq. No. 131255
Contig ID 53750_4.R1010
5'-most EST jC-atXP52C181O22T7d2

Seq. No. 131256
Contig ID 53761_1.R1010
5'-most EST jC-atXLIB327416P1h04a1
Method BLASTN
NCBI GI g4263694
BLAST score 225
E value 1.0e-123
Match length 304
% identity 96
NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 131257
Contig ID 53761_2.R1010
5'-most EST g2393383
Method BLASTN
NCBI GI g4263694
BLAST score 345
E value 0.0e+00
Match length 417
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 131258
Contig ID 53812_1.R1010
5'-most EST LIB3176-067-P1-K1-A10
Method BLASTX
NCBI GI g3297824
BLAST score 223
E value 6.0e-18
Match length 45
% identity 100
NCBI Description (AL031032) bZIP transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 131259
Contig ID 53825_1.R1010
5'-most EST LIB3176-067-P1-K1-B5
Method BLASTX
NCBI GI g3096935
BLAST score 42
E value 7.0e-21
Match length 195
% identity 37
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 131260
Contig ID 53846_1.R1010
5'-most EST LIB3176-067-P1-K1-D5

Method	BLASTX
NCBI GI	g3540206
BLAST score	197
E value	6.0e-15
Match length	87
% identity	45
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	131261
Contig ID	53849_1.R1010
5'-most EST	jC-atXP33C151A11T7d2
Method	BLASTX
NCBI GI	g2245136
BLAST score	629
E value	1.0e-65
Match length	178
% identity	66
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	131262
Contig ID	53874_1.R1010
5'-most EST	LIB3177-041-P1-K2-H7
Method	BLASTX
NCBI GI	g2160175
BLAST score	634
E value	2.0e-66
Match length	121
% identity	99
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No.	131263
Contig ID	53883_1.R1010
5'-most EST	LIB3176-067-P1-K1-H1
Method	BLASTN
NCBI GI	g4580745
BLAST score	176
E value	3.0e-94
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	131264
Contig ID	53915_1.R1010
5'-most EST	g906387

Seq. No.	131265
Contig ID	53931_1.R1010
5'-most EST	LIB3176-068-P1-K1-E2
Method	BLASTN
NCBI GI	g4559344
BLAST score	154
E value	5.0e-81
Match length	476
% identity	6

NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence
Seq. No.	131266
Contig ID	54002_1.R1010
5'-most EST	jC-atXP70C222F15T7080a1
Method	BLASTX
NCBI GI	g2244759
BLAST score	950
E value	1.0e-103
Match length	206
% identity	83
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.	131267
Contig ID	54004_1.R1010
5'-most EST	LIB3176-069-P1-K1-F11
Method	BLASTN
NCBI GI	g4589434
BLAST score	300
E value	1.0e-168
Match length	754
% identity	62
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence
Seq. No.	131268
Contig ID	54005_1.R1010
5'-most EST	LIB3176-069-P1-K1-F12
Method	BLASTX
NCBI GI	g4539388
BLAST score	86
E value	2.0e-14
Match length	46
% identity	96
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]
Seq. No.	131269
Contig ID	54006_1.R1010
5'-most EST	jC-atXP96C248H6T7b1
Method	BLASTN
NCBI GI	g3241927
BLAST score	456
E value	0.0e+00
Match length	906
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.	131270
Contig ID	54017_1.R1010
5'-most EST	LIB35-055-Q1-E2-H9
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62

% identity	98
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	131271
Contig ID	54022_1.R1010
5'-most EST	jC-atXP15C108F4T7094a1
Seq. No.	131272
Contig ID	54076_1.R1010
5'-most EST	jC-atXP84CG5F9T7b1
Method	BLASTN
NCBI GI	g2264312
BLAST score	195
E value	1.0e-105
Match length	271
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
Seq. No.	131273
Contig ID	54087_1.R1010
5'-most EST	LIB3176-070-P1-K1-F2
Seq. No.	131274
Contig ID	54117_1.R1010
5'-most EST	LIB3176-071-P1-K1-A2
Method	BLASTN
NCBI GI	g2702261
BLAST score	314
E value	1.0e-176
Match length	397
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	131275
Contig ID	54169_1.R1010
5'-most EST	LIB3176-106-P1-K1-D12
Seq. No.	131276
Contig ID	54184_1.R1010
5'-most EST	LIB3176-073-P1-K1-A11
Method	BLASTX
NCBI GI	g4415931
BLAST score	314
E value	3.0e-58
Match length	170
% identity	65
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]
Seq. No.	131277
Contig ID	54184_2.R1010
5'-most EST	g928959
Seq. No.	131278

Contig ID	54193_1.R1010
5'-most EST	g2722134
Method	BLASTX
NCBI GI	g4335745
BLAST score	407
E value	3.0e-39
Match length	310
% identity	54
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	131279
Contig ID	54219_1.R1010
5'-most EST	jC-atXLIB327426P1e10a1
Method	BLASTX
NCBI GI	g2583130
BLAST score	390
E value	1.0e-37
Match length	137
% identity	58
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	131280
Contig ID	54227_1.R1010
5'-most EST	LIB3176-073-P1-K1-E1
Method	BLASTN
NCBI GI	g3128134
BLAST score	452
E value	0.0e+00
Match length	515
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	131281
Contig ID	54244_1.R1010
5'-most EST	LIB3176-073-P1-K1-F8
Method	BLASTX
NCBI GI	g3367521
BLAST score	132
E value	8.0e-60
Match length	117
% identity	91
NCBI Description	(AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana]

Seq. No.	131282
Contig ID	54268_1.R1010
5'-most EST	LIB3176-073-P1-K1-H8

Seq. No.	131283
Contig ID	54269_1.R1010
5'-most EST	jC-atXLIB327426P2f01b1

Seq. No.	131284
Contig ID	54279_1.R1010
5'-most EST	LIB3176-074-P1-K1-A9
Method	BLASTN
NCBI GI	g2477521
BLAST score	231
E value	1.0e-127
Match length	468
% identity	56
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131285
Contig ID	54355_1.R1010
5'-most EST	g1215874
Method	BLASTN
NCBI GI	g4371278
BLAST score	373
E value	0.0e+00
Match length	531
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131286
Contig ID	54376_1.R1010
5'-most EST	g460356
Method	BLASTN
NCBI GI	g4159711
BLAST score	207
E value	1.0e-112
Match length	443
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD12, complete sequence

Seq. No.	131287
Contig ID	54383_1.R1010
5'-most EST	LIB3176-083-P1-K1-C6

Seq. No.	131288
Contig ID	54385_1.R1010
5'-most EST	jC-atXP115C248G2T7075d1
Method	BLASTX
NCBI GI	g2558663
BLAST score	175
E value	3.0e-12
Match length	166
% identity	30
NCBI Description	(AC002354) F6P23.10.1 [Arabidopsis thaliana]

Seq. No.	131289
Contig ID	54423_1.R1010
5'-most EST	g406640

Seq. No.	131290

Contig ID	54448_1.R1010
5'-most EST	LIB3176-084-P1-K1-A2

Seq. No.	131291
Contig ID	54457_1.R1010
5'-most EST	LIB3176-121-P2-K1-C4
Method	BLASTX
NCBI GI	g3377808
BLAST score	782
E value	2.0e-83
Match length	165
% identity	90
NCBI Description	(AF075597) contains similarity to Nicotiana alata pistil extensin-like protein (GB:U45958) [Arabidopsis thaliana]

Seq. No.	131292
Contig ID	54462_2.R1010
5'-most EST	jC-atXLIB327423P4d05b1
Method	BLASTX
NCBI GI	g4455203
BLAST score	270
E value	2.0e-23
Match length	225
% identity	7
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	131293
Contig ID	54470_1.R1010
5'-most EST	jC-atXP8C92M10T7s1
Method	BLASTX
NCBI GI	g4732123
BLAST score	456
E value	2.0e-45
Match length	132
% identity	65
NCBI Description	(AF129087) mitogen-activated protein kinase homologue [Medicago sativa]

Seq. No.	131294
Contig ID	54478_1.R1010
5'-most EST	g2749629
Method	BLASTX
NCBI GI	g2961389
BLAST score	239
E value	6.0e-20
Match length	73
% identity	53
NCBI Description	(AL022141) purple acid phosphatase like protein [Arabidopsis thaliana] >gi_4006925_emb_CAB16853.1_ (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No.	131295
Contig ID	54500_1.R1010
5'-most EST	LIB3176-090-P1-K1-C4

Seq. No.	131296
Contig ID	54532_1.R1010

5'-most EST	LIB3176-085-P1-K1-A2
Method	BLASTN
NCBI GI	g3869068
BLAST score	488
E value	0.0e+00
Match length	500
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	131297
Contig ID	54557_1.R1010
5'-most EST	g1268148
Method	BLASTX
NCBI GI	g4507047
BLAST score	210
E value	4.0e-16
Match length	138
% identity	48
NCBI Description	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 >gi_1706185_sp_P30825_CTR1_HUMAN HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) >gi_107594_pir__A40775 retroviral receptor - human >gi_36161_emb_CAA41869_ (X59155) retroviral receptor [Homo sapiens] >gi_3342908 (AF078107) cationic amino acid transporter [Homo sapiens]

Seq. No.	131298
Contig ID	54559_1.R1010
5'-most EST	LIB3176-085-P1-K1-C6
Method	BLASTX
NCBI GI	g4469020
BLAST score	951
E value	1.0e-103
Match length	200
% identity	92
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	131299
Contig ID	54574_1.R1010
5'-most EST	jC-atXP89C242K8T7057d1
Method	BLASTX
NCBI GI	g1944132
BLAST score	565
E value	5.0e-58
Match length	155
% identity	68
NCBI Description	(AB002560) CUC2 [Arabidopsis thaliana]

Seq. No.	131300
Contig ID	54594_1.R1010
5'-most EST	LIB35-011-Q1-E1-D5

Seq. No.	131301

Contig ID	54611_1.R1010
5'-most EST	LIB3176-085-P1-K1-H2

Seq. No.	131302
Contig ID	54638_1.R1010
5'-most EST	LIB3176-101-P1-K1-H5
Method	BLASTX
NCBI GI	g3776575
BLAST score	629
E value	1.0e-65
Match length	140
% identity	88
NCBI Description	(AC005388) Similar to Schizosaccharomyces CCAAT-binding factor F7G19.16 gi_1922964 from Arabidopsis thaliana BAC gb_AC000106. EST gb_H36963 comes from this gene. [Arabidopsis thaliana]

Seq. No.	131303
Contig ID	54654_1.R1010
5'-most EST	g2749439
Method	BLASTN
NCBI GI	g4249393
BLAST score	377
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131304
Contig ID	54654_2.R1010
5'-most EST	jC-atXLIB327414P4e09a2
Method	BLASTN
NCBI GI	g4249393
BLAST score	600
E value	0.0e+00
Match length	629
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131305
Contig ID	54663_1.R1010
5'-most EST	LIB3234-041-P1-K1-D12

Seq. No.	131306
Contig ID	54677_1.R1010
5'-most EST	g906447
Method	BLASTX
NCBI GI	g3063451
BLAST score	618
E value	3.0e-64
Match length	130
% identity	90
NCBI Description	(AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No. 131307

Contig ID	54705_1.R1010
5'-most EST	g2762588
Seq. No.	131308
Contig ID	54758_1.R1010
5'-most EST	LIB3176-087-P1-K1-E4
Seq. No.	131309
Contig ID	54779_1.R1010
5'-most EST	jC-atXLIB327414P3c02a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	368
E value	0.0e+00
Match length	580
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	131310
Contig ID	54781_1.R1010
5'-most EST	LIB3176-087-P1-K1-G5
Method	BLASTX
NCBI GI	g3786324
BLAST score	271
E value	1.0e-23
Match length	73
% identity	59
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]
Seq. No.	131311
Contig ID	54782_1.R1010
5'-most EST	LIB3176-087-P1-K1-G6
Method	BLASTX
NCBI GI	g3242722
BLAST score	1268
E value	1.0e-140
Match length	257
% identity	95
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]
Seq. No.	131312
Contig ID	54830_1.R1010
5'-most EST	LIB3176-088-P1-K1-D11
Method	BLASTX
NCBI GI	g841208
BLAST score	438
E value	5.0e-43
Match length	208
% identity	52
NCBI Description	(U18995) trypsin inhibitor propeptide [Brassica oleracea]
Seq. No.	131313
Contig ID	54855_1.R1010
5'-most EST	g906240

Method	BLASTN
NCBI GI	g3869074
BLAST score	244
E value	1.0e-135
Match length	419
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	131314
Contig ID	54867_1.R1010
5'-most EST	jC-atXLIB327408P4c07a1
Method	BLASTN
NCBI GI	g3402695
BLAST score	417
E value	0.0e+00
Match length	465
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131315
Contig ID	54875_1.R1010
5'-most EST	LIB3176-088-P1-K1-H3
Method	BLASTX
NCBI GI	g3080401
BLAST score	1109
E value	1.0e-122
Match length	213
% identity	100
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	131316
Contig ID	54892_1.R1010
5'-most EST	LIB3176-089-P1-K1-B12
Method	BLASTN
NCBI GI	g2924733
BLAST score	161
E value	2.0e-85
Match length	302
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	131317
Contig ID	54900_1.R1010
5'-most EST	g948572
Method	BLASTN
NCBI GI	g3135250
BLAST score	710
E value	0.0e+00
Match length	730
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131318
Contig ID	54927_1.R1010
5'-most EST	g2722784
Method	BLASTX
NCBI GI	g2979561
BLAST score	376
E value	5.0e-36
Match length	84
% identity	85
NCBI Description	(AC003680) putative ribosomal protein S27 [Arabidopsis thaliana] >gi_3386624 (AC004665) putative ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	131319
Contig ID	54951_1.R1010
5'-most EST	LIB3176-089-P1-K1-H12
Method	BLASTN
NCBI GI	g4572664
BLAST score	446
E value	0.0e+00
Match length	466
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	131320
Contig ID	54957_1.R1010
5'-most EST	LIB3177-085-P1-K1-C7
Method	BLASTN
NCBI GI	g4220627
BLAST score	136
E value	2.0e-70
Match length	468
% identity	6
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	131321
Contig ID	54957_2.R1010
5'-most EST	g438304
Method	BLASTN
NCBI GI	g4220627
BLAST score	83
E value	1.0e-38
Match length	186
% identity	5
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	131322
Contig ID	54957_3.R1010
5'-most EST	LIB3176-108-P1-K1-H11
Method	BLASTN
NCBI GI	g4559344
BLAST score	33
E value	8.0e-09

Match length	151
% identity	7
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	131323
Contig ID	54960_1.R1010
5'-most EST	jC-atXP53C184I1T7085a1
Method	BLASTN
NCBI GI	g4490324
BLAST score	330
E value	0.0e+00
Match length	488
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	131324
Contig ID	54960_2.R1010
5'-most EST	LIB3176-090-P1-K1-A10
Method	BLASTN
NCBI GI	g4490324
BLAST score	289
E value	1.0e-161
Match length	397
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	131325
Contig ID	54983_1.R1010
5'-most EST	LIB3176-090-P1-K1-C7

Seq. No.	131326
Contig ID	54984_1.R1010
5'-most EST	LIB3176-090-P1-K1-C3
Method	BLASTX
NCBI GI	g3386615
BLAST score	507
E value	2.0e-51
Match length	99
% identity	94
NCBI Description	(AC004665) putative phosphomannomutase [Arabidopsis thaliana]

Seq. No.	131327
Contig ID	55023_1.R1010
5'-most EST	g937202

Seq. No.	131328
Contig ID	55087_1.R1010
5'-most EST	g2733618
Method	BLASTX
NCBI GI	g2498397
BLAST score	153
E value	9.0e-10
Match length	40

% identity	68
NCBI Description	FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A)

Seq. No.	131329
Contig ID	55088_1.R1010
5'-most EST	g2763218

Seq. No.	131330
Contig ID	55147_1.R1010
5'-most EST	g907024
Method	BLASTN
NCBI GI	g3402671
BLAST score	355
E value	0.0e+00
Match length	355
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131331
Contig ID	55189_1.R1010
5'-most EST	g1054027
Method	BLASTX
NCBI GI	g3522943
BLAST score	599
E value	3.0e-62
Match length	149
% identity	68
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	131332
Contig ID	55200_1.R1010
5'-most EST	jC-atXP117C141A17T7a1
Method	BLASTN
NCBI GI	g4490291
BLAST score	259
E value	1.0e-143
Match length	485
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	131333
Contig ID	55200_3.R1010
5'-most EST	g2763355
Method	BLASTX
NCBI GI	g4490303
BLAST score	619
E value	1.0e-140
Match length	298
% identity	89
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	131334
Contig ID	55207_1.R1010
5'-most EST	LIB3176-093-P1-K1-B12

Method	BLASTX
NCBI GI	g4337192
BLAST score	319
E value	2.0e-29
Match length	63
% identity	100
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131335
Contig ID	55230_1.R1010
5'-most EST	g937970
Method	BLASTX
NCBI GI	g4775270
BLAST score	393
E value	5.0e-38
Match length	85
% identity	88
NCBI Description	(AJ131214) SF2/ASF-like splicing modulator Srp30 [Arabidopsis thaliana]

Seq. No.	131336
Contig ID	55264_1.R1010
5'-most EST	LIB3234-088-Q1-K1-C2
Method	BLASTX
NCBI GI	g4567286
BLAST score	693
E value	3.0e-73
Match length	156
% identity	88
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	131337
Contig ID	55267_1.R1010
5'-most EST	LIB3177-097-P1-K1-E4
Method	BLASTN
NCBI GI	g4263774
BLAST score	284
E value	1.0e-158
Match length	632
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131338
Contig ID	55302_1.R1010
5'-most EST	jC-atXP89CG6E4T7078d1
Method	BLASTX
NCBI GI	g2342723
BLAST score	366
E value	7.0e-41
Match length	152
% identity	61
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	131339
Contig ID	55313_1.R1010

5'-most EST	jC-atXP64C207I17T7d1
Method	BLASTX
NCBI GI	g3292824
BLAST score	364
E value	1.0e-34
Match length	170
% identity	41
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	131340
Contig ID	55339_1.R1010
5'-most EST	g1053988

Seq. No.	131341
Contig ID	55421_1.R1010
5'-most EST	g396611
Method	BLASTX
NCBI GI	g4249382
BLAST score	150
E value	4.0e-98
Match length	213
% identity	82
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	131342
Contig ID	55421_2.R1010
5'-most EST	g2445893
Method	BLASTN
NCBI GI	g2656029
BLAST score	399
E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	131343
Contig ID	55428_1.R1010
5'-most EST	g2756881
Method	BLASTX
NCBI GI	g4559396
BLAST score	650
E value	3.0e-68
Match length	138
% identity	97
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	131344
Contig ID	55467_1.R1010
5'-most EST	LIB3176-097-P1-K1-D8
Method	BLASTN
NCBI GI	g4220627
BLAST score	201
E value	1.0e-109
Match length	462

% identity	8
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	131345
Contig ID	55480_1.R1010
5'-most EST	LIB3177-083-P1-K1-G11
Method	BLASTN
NCBI GI	g4585890
BLAST score	102
E value	1.0e-50
Match length	142
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	131346
Contig ID	55486_1.R1010
5'-most EST	g1159019
Method	BLASTN
NCBI GI	g3873174
BLAST score	321
E value	1.0e-180
Match length	664
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	131347
Contig ID	55490_1.R1010
5'-most EST	jC-atXLIB327409P2f05a1

Seq. No.	131348
Contig ID	55509_1.R1010
5'-most EST	g2596393
Method	BLASTX
NCBI GI	g2392763
BLAST score	179
E value	5.0e-13
Match length	84
% identity	54
NCBI Description	(AC002534) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131349
Contig ID	55555_1.R1010
5'-most EST	jC-atXLIB327417P4f09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	131350
Contig ID	55555_2.R1010

5'-most EST	jC-atXLIB327414P2d10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13
Match length	82
% identity	99
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	131351
Contig ID	55616_1.R1010
5'-most EST	jC-atXP4C87H8T7038a1
Method	BLASTX
NCBI GI	g4337192
BLAST score	151
E value	2.0e-09
Match length	80
% identity	45
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131352
Contig ID	55630_1.R1010
5'-most EST	g1269309
Method	BLASTX
NCBI GI	g1161167
BLAST score	326
E value	6.0e-30
Match length	140
% identity	41
NCBI Description	(L42466) ethylene-forming enzyme [Picea glauca]

Seq. No.	131353
Contig ID	55696_1.R1010
5'-most EST	LIB3176-101-P1-K1-D11
Method	BLASTX
NCBI GI	g2911071
BLAST score	301
E value	3.0e-27
Match length	110
% identity	60
NCBI Description	(AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131354
Contig ID	55696_2.R1010
5'-most EST	g3868964
Method	BLASTX
NCBI GI	g2191171
BLAST score	530
E value	9.0e-54
Match length	148
% identity	73
NCBI Description	(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) [Arabidopsis thaliana]

Seq. No.	131355
Contig ID	55696_5.R1010
5'-most EST	g4713996

Method	BLASTN
NCBI GI	g2191157
BLAST score	108
E value	9.0e-54
Match length	211
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	131356
Contig ID	55718_1.R1010
5'-most EST	LIB3176-101-P1-K1-F12
Method	BLASTN
NCBI GI	g2275194
BLAST score	106
E value	1.0e-52
Match length	274
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131357
Contig ID	55747_1.R1010
5'-most EST	LIB3176-102-P1-K1-A1
Method	BLASTX
NCBI GI	g2911068
BLAST score	350
E value	9.0e-81
Match length	144
% identity	99
NCBI Description	(AL021960) G10-like protein [Arabidopsis thaliana]

Seq. No.	131358
Contig ID	55786_1.R1010
5'-most EST	g2047827
Method	BLASTN
NCBI GI	g3449326
BLAST score	279
E value	1.0e-155
Match length	445
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	131359
Contig ID	55786_2.R1010
5'-most EST	jC-atXP36C152G13T7d1
Method	BLASTN
NCBI GI	g3449326
BLAST score	303
E value	1.0e-170
Match length	528
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	131360
Contig ID	55788_1.R1010

5'-most EST	LIB3176-102-P1-K1-D8
Seq. No.	131361
Contig ID	55793_1.R1010
5'-most EST	jC-atXP112C129E13T7d2
Method	BLASTX
NCBI GI	g4263509
BLAST score	995
E value	1.0e-108
Match length	194
% identity	100
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.	131362
Contig ID	55829_1.R1010
5'-most EST	jC-atXLIB327409P3b09a1
Method	BLASTX
NCBI GI	g4586041
BLAST score	932
E value	1.0e-101
Match length	191
% identity	62
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana] >gi_4587998_gb_AAD25939.1_AF085279_12 (AF085279) hypothetical protein [Arabidopsis thaliana]
Seq. No.	131363
Contig ID	55849_1.R1010
5'-most EST	g2757426
Method	BLASTN
NCBI GI	g2244747
BLAST score	317
E value	1.0e-178
Match length	333
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	131364
Contig ID	55880_1.R1010
5'-most EST	g2756976
Method	BLASTN
NCBI GI	g4678291
BLAST score	221
E value	1.0e-121
Match length	310
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)
Seq. No.	131365
Contig ID	55881_1.R1010
5'-most EST	jC-atXP30C143K6T7s2
Method	BLASTX
NCBI GI	g2492952
BLAST score	299
E value	4.0e-27

Match length	65
% identity	89
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	131366
Contig ID	55893_1.R1010
5'-most EST	LIB3177-014-P1-K2-E5
Method	BLASTX
NCBI GI	g2827039
BLAST score	501
E value	5.0e-51
Match length	109
% identity	89
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	131367
Contig ID	55903_1.R1010
5'-most EST	LIB3176-103-P1-K1-G8
Method	BLASTX
NCBI GI	g2129636
BLAST score	384
E value	6.0e-67
Match length	197
% identity	59
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	131368
Contig ID	55907_1.R1010
5'-most EST	LIB3177-063-P1-K1-G12

Seq. No.	131369
Contig ID	55916_1.R1010
5'-most EST	LIB3176-104-P1-K1-A11

Seq. No.	131370
Contig ID	55929_1.R1010
5'-most EST	LIB3176-104-P1-K1-B12

Seq. No.	131371
Contig ID	55934_1.R1010
5'-most EST	LIB3176-104-P1-K1-B8

Seq. No.	131372
Contig ID	56022_1.R1010
5'-most EST	jC-atXP29C140H2T7048d1
Method	BLASTX
NCBI GI	g4539468
BLAST score	176
E value	1.0e-41
Match length	249
% identity	43

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 131373
Contig ID 56034_1.R1010
5'-most EST LIB3176-105-P1-K1-F12
Method BLASTX
NCBI GI g3550519
BLAST score 414
E value 9.0e-41
Match length 113
% identity 67
NCBI Description (AJ007630) oxygenase [Nicotiana tabacum]

Seq. No. 131374
Contig ID 56069_1.R1010
5'-most EST LIB3234-077-P1-K1-G6

Seq. No. 131375
Contig ID 56072_1.R1010
5'-most EST jC-atXP80C232C22T7d1
Method BLASTX
NCBI GI g3080435
BLAST score 693
E value 4.0e-73
Match length 189
% identity 78
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 131376
Contig ID 56117_1.R1010
5'-most EST jC-atXLIB327426P2e03b1

Seq. No. 131377
Contig ID 56117_3.R1010
5'-most EST jC-atXP43C170C10T7061d1

Seq. No. 131378
Contig ID 56182_1.R1010
5'-most EST LIB3176-108-P1-K1-E10

Seq. No. 131379
Contig ID 56208_1.R1010
5'-most EST LIB3177-098-P1-K1-G12
Method BLASTX
NCBI GI g4204295
BLAST score 94
E value 2.0e-61
Match length 135
% identity 83
NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 131380
Contig ID 56211_1.R1010
5'-most EST g45320
Method BLASTN
NCBI GI g4220643

BLAST score 336
E value 0.0e+00
Match length 372
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 131381
Contig ID 56231_1.R1010
5'-most EST LIB3176-109-P1-K1-A8
Method BLASTN
NCBI GI g4417264
BLAST score 254
E value 1.0e-141
Match length 384
% identity 96
NCBI Description Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 131382
Contig ID 56236_1.R1010
5'-most EST jC-atXP13C103P10T7d2
Method BLASTX
NCBI GI g4220535
BLAST score 545
E value 7.0e-56
Match length 110
% identity 95
NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No. 131383
Contig ID 56239_1.R1010
5'-most EST g1054378
Method BLASTX
NCBI GI g2160152
BLAST score 548
E value 4.0e-56
Match length 168
% identity 72
NCBI Description (AC000375) ESTs gb_U75592,gb_T13956,gb_T43869 come from from this gene. [Arabidopsis thaliana]

Seq. No. 131384
Contig ID 56239_2.R1010
5'-most EST LIB3176-109-P1-K1-B6
Method BLASTN
NCBI GI g2160132
BLAST score 387
E value 0.0e+00
Match length 457
% identity 96
NCBI Description Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 131385
Contig ID 56239_4.R1010

5'-most EST	g2446040
Method	BLASTX
NCBI GI	g2160152
BLAST score	380
E value	3.0e-36
Match length	125
% identity	63
NCBI Description	(AC000375) ESTs gb_U75592,gb_T13956,gb_T43869 come from from this gene. [Arabidopsis thaliana]

Seq. No.	131386
Contig ID	56288_1.R1010
5'-most EST	jC-atXP118C155H2T7079d2
Method	BLASTN
NCBI GI	g3941523
BLAST score	38
E value	2.0e-11
Match length	77
% identity	99
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	131387
Contig ID	56288_2.R1010
5'-most EST	g935927
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	8.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	131388
Contig ID	56288_4.R1010
5'-most EST	LIB3176-110-P1-K1-A12

Seq. No.	131389
Contig ID	56343_1.R1010
5'-most EST	LIB3176-110-P1-K1-G6
Method	BLASTN
NCBI GI	g3193311
BLAST score	222
E value	1.0e-122
Match length	296
% identity	94
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	131390
Contig ID	56349_1.R1010
5'-most EST	g315679
Method	BLASTX
NCBI GI	g3451071
BLAST score	282
E value	3.0e-25
Match length	93

% identity	68
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	131391
Contig ID	56374_1.R1010
5'-most EST	LIB3176-111-P1-K1-D4
Method	BLASTX
NCBI GI	g482131
BLAST score	143
E value	1.0e-09
Match length	97
% identity	38
NCBI Description	hypothetical protein ZK512.2 - Caenorhabditis elegans

Seq. No.	131392
Contig ID	56375_1.R1010
5'-most EST	jC-atXP34C149L5T7a1
Method	BLASTX
NCBI GI	g2708749
BLAST score	305
E value	2.0e-27
Match length	106
% identity	52
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	131393
Contig ID	56378_1.R1010
5'-most EST	LIB3176-111-P1-K1-C8
Method	BLASTX
NCBI GI	g4325343
BLAST score	706
E value	8.0e-75
Match length	154
% identity	94
NCBI Description	(AF128393) contains similarity to homeobox domains (Pfam: PF00046, Score,36.5, E=6.9e-08, N=1) [Arabidopsis thaliana]

Seq. No.	131394
Contig ID	56383_1.R1010
5'-most EST	jC-atXP9C93F17T7d1
Method	BLASTX
NCBI GI	g3249099
BLAST score	410
E value	4.0e-40
Match length	134
% identity	74
NCBI Description	(AC003114) EST gb_T21244 comes from this gene. [Arabidopsis thaliana] >gi_4220616_dbj_BAA74591_ (AB021936) nicotianamine synthase [Arabidopsis thaliana]

Seq. No.	131395
Contig ID	56466_1.R1010
5'-most EST	LIB3176-112-P1-K1-F10
Method	BLASTX
NCBI GI	g2959767

BLAST score 626
E value 1.0e-109
Match length 224
% identity 87
NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No. 131396
Contig ID 56519_1.R1010
5'-most EST g931240
Method BLASTX
NCBI GI g4583546
BLAST score 503
E value 6.0e-51
Match length 104
% identity 97
NCBI Description (AJ010819) GrpE protein [Arabidopsis thaliana]

Seq. No. 131397
Contig ID 56519_2.R1010
5'-most EST jC-atXLIB327419P1a12a2
Method BLASTN
NCBI GI g4583545
BLAST score 382
E value 0.0e+00
Match length 419
% identity 98
NCBI Description Arabidopsis thaliana mRNA for chloroplast GrpE protein

Seq. No. 131398
Contig ID 56527_1.R1010
5'-most EST LIB3176-113-P2-K1-E5
Method BLASTX
NCBI GI g107350
BLAST score 249
E value 3.0e-21
Match length 142
% identity 26
NCBI Description Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5 protein [Homo sapiens]

Seq. No. 131399
Contig ID 56529_1.R1010
5'-most EST LIB3177-035-P1-K2-F9
Method BLASTX
NCBI GI g1916930
BLAST score 175
E value 1.0e-12
Match length 65
% identity 51
NCBI Description (U88570) CREB-binding protein homolog [Drosophila melanogaster]

Seq. No. 131400
Contig ID 56539_1.R1010
5'-most EST LIB3176-113-P2-K1-G10

Method	BLASTX
NCBI GI	g4572674
BLAST score	742
E value	1.0e-78
Match length	155
% identity	89
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	131401
Contig ID	56596_1.R1010
5'-most EST	jC-atXLIB327417P2g08a1
Method	BLASTX
NCBI GI	g4454039
BLAST score	735
E value	8.0e-78
Match length	243
% identity	59
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	131402
Contig ID	56607_1.R1010
5'-most EST	LIB3176-114-P2-K1-F1
Method	BLASTX
NCBI GI	g1773309
BLAST score	773
E value	1.0e-82
Match length	164
% identity	90
NCBI Description	(U78899) NADH dehydrogenase [Ceanothus velutinus]

Seq. No.	131403
Contig ID	56620_1.R1010
5'-most EST	LIB3176-114-P2-K1-G12
Method	BLASTX
NCBI GI	g231660
BLAST score	102
E value	2.0e-39
Match length	166
% identity	51
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	131404
Contig ID	56655_1.R1010
5'-most EST	LIB3176-115-P2-K1-B9
Method	BLASTX
NCBI GI	g3004560
BLAST score	586
E value	1.0e-60
Match length	149
% identity	81
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]

Seq. No.	131405
Contig ID	56666_1.R1010
5'-most EST	g2748857

Seq. No.	131406
Contig ID	56702_1.R1010
5'-most EST	g496400
Method	BLASTX
NCBI GI	g4581156
BLAST score	168
E value	2.0e-11
Match length	131
% identity	49
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No.	131407
Contig ID	56712_1.R1010
5'-most EST	LIB35-056-Q1-E2-B12
Method	BLASTN
NCBI GI	g2760167
BLAST score	309
E value	1.0e-173
Match length	636
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	131408
Contig ID	56717_1.R1010
5'-most EST	g453777

Seq. No.	131409
Contig ID	56752_1.R1010
5'-most EST	g2413806
Method	BLASTN
NCBI GI	g2392762
BLAST score	53
E value	1.0e-20
Match length	150
% identity	86
NCBI Description	Arabidopsis thaliana BAC T32N15 from chromsome III near 54 cM, complete sequence

Seq. No.	131410
Contig ID	56752_3.R1010
5'-most EST	LIB3176-116-P2-K1-E2

Seq. No.	131411
Contig ID	56784_1.R1010
5'-most EST	LIB3176-116-P2-K1-H2
Method	BLASTN
NCBI GI	g2961370
BLAST score	385
E value	0.0e+00
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)

Seq. No.	131412

Contig ID	56797_1.R1010
5'-most EST	jC-atXLIB327419P2g10b2
Method	BLASTX
NCBI GI	g2078350
BLAST score	144
E value	1.0e-79
Match length	204
% identity	79
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	131413
Contig ID	56799_1.R1010
5'-most EST	LIB3176-121-P2-K1-H5
Method	BLASTX
NCBI GI	g4586101
BLAST score	516
E value	1.0e-52
Match length	117
% identity	87
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	131414
Contig ID	56807_1.R1010
5'-most EST	jC-atXP92C246O15T7020d1
Method	BLASTX
NCBI GI	g4587988
BLAST score	197
E value	1.0e-14
Match length	128
% identity	37
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131415
Contig ID	56814_1.R1010
5'-most EST	g1216843
Method	BLASTN
NCBI GI	g2244829
BLAST score	483
E value	0.0e+00
Match length	523
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	131416
Contig ID	56829_1.R1010
5'-most EST	LIB3176-117-P2-K1-E1
Method	BLASTX
NCBI GI	g4454479
BLAST score	356
E value	9.0e-34
Match length	74
% identity	97
NCBI Description	(AC006234) putative riboflavin synthase alpha chain [Arabidopsis thaliana]

Seq. No. 131417

Contig ID	56845_1.R1010
5'-most EST	LIB3176-117-P2-K1-F9
Seq. No.	131418
Contig ID	56858_1.R1010
5'-most EST	LIB3176-117-P2-K1-H1
Method	BLASTN
NCBI GI	g531828
BLAST score	40
E value	7.0e-13
Match length	48
% identity	96
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	131419
Contig ID	56866_2.R1010
5'-most EST	LIB3176-117-P2-K1-H6
Method	BLASTX
NCBI GI	g549977
BLAST score	172
E value	8.0e-15
Match length	130
% identity	47
NCBI Description	(U12859) cDNA-5-encoded protein [Arabidopsis thaliana]
Seq. No.	131420
Contig ID	56914_1.R1010
5'-most EST	jC-atXP115C250H2T7085d1
Method	BLASTX
NCBI GI	g2245062
BLAST score	54
E value	2.0e-55
Match length	126
% identity	90
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	131421
Contig ID	56914_2.R1010
5'-most EST	jC-atXLIB327438P3a12a2
Method	BLASTN
NCBI GI	g2245031
BLAST score	83
E value	1.0e-38
Match length	366
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	131422
Contig ID	56918_1.R1010
5'-most EST	g2748403
Method	BLASTN
NCBI GI	g3367500
BLAST score	209
E value	1.0e-114
Match length	334
% identity	99

NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	131423
Contig ID	56920_1.R1010
5'-most EST	LIB3176-118-P2-K1-F10
Method	BLASTN
NCBI GI	g2695704
BLAST score	247
E value	1.0e-136
Match length	376
% identity	98
NCBI Description	A.thaliana constans gene

Seq. No.	131424
Contig ID	56967_1.R1010
5'-most EST	LIB3176-119-P2-K1-B6
Method	BLASTX
NCBI GI	g3785996
BLAST score	452
E value	4.0e-45
Match length	89
% identity	59
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]

Seq. No.	131425
Contig ID	56968_1.R1010
5'-most EST	LIB35-011-Q1-E1-H1
Method	BLASTX
NCBI GI	g2832649
BLAST score	521
E value	2.0e-67
Match length	135
% identity	99
NCBI Description	(AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]

Seq. No.	131426
Contig ID	56986_1.R1010
5'-most EST	jC-atXP111C125H9T7d1

Seq. No.	131427
Contig ID	57008_1.R1010
5'-most EST	LIB3176-119-P2-K1-F7
Method	BLASTX
NCBI GI	g4432859
BLAST score	251
E value	4.0e-21
Match length	86
% identity	59
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	131428
Contig ID	57020_1.R1010
5'-most EST	jC-atXP60C197M21T7027d1
Method	BLASTX
NCBI GI	g3894178

BLAST score 401
E value 7.0e-39
Match length 146
% identity 61
NCBI Description (AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No. 131429
Contig ID 57033_1.R1010
5'-most EST LIB3176-120-P2-K1-A12

Seq. No. 131430
Contig ID 57082_1.R1010
5'-most EST jC-atXLIB327423P1g09a1
Method BLASTN
NCBI GI g4753195
BLAST score 502
E value 0.0e+00
Match length 633
% identity 96
NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No. 131431
Contig ID 57085_1.R1010
5'-most EST g2576668
Method BLASTX
NCBI GI g133409
BLAST score 380
E value 8.0e-39
Match length 146
% identity 63
NCBI Description DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_66962_pir__RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi_11860_emb_CAA77376_ (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi_225228_prf__1211235BK RNA polymerase alpha [Nicotiana tabacum]

Seq. No. 131432
Contig ID 57095_1.R1010
5'-most EST g2048392

Seq. No. 131433
Contig ID 57103_1.R1010
5'-most EST jC-atXLIB327431P2f01a1
Method BLASTX
NCBI GI g2244994
BLAST score 802
E value 6.0e-86
Match length 154
% identity 98
NCBI Description (Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No. 131434
Contig ID 57103_2.R1010

5'-most EST	LIB3176-123-P2-K1-D11
Method	BLASTX
NCBI GI	g2160185
BLAST score	89
E value	7.0e-24
Match length	122
% identity	48
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	131435
Contig ID	57109_1.R1010
5'-most EST	LIB3234-049-P1-K1-B12
Method	BLASTN
NCBI GI	g4584519
BLAST score	448
E value	0.0e+00
Match length	464
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)

Seq. No.	131436
Contig ID	57113_1.R1010
5'-most EST	g397236
Method	BLASTX
NCBI GI	g2245082
BLAST score	137
E value	2.0e-27
Match length	152
% identity	46
NCBI Description	(Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No.	131437
Contig ID	57144_1.R1010
5'-most EST	LIB3177-066-P1-K1-D11
Method	BLASTN
NCBI GI	g4757414
BLAST score	39
E value	1.0e-12
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	131438
Contig ID	57150_1.R1010
5'-most EST	g1520853
Method	BLASTN
NCBI GI	g3184270
BLAST score	86
E value	2.0e-40
Match length	154
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131439
Contig ID	57154_1.R1010
5'-most EST	LIB3176-121-P2-K1-E4
Method	BLASTN
NCBI GI	g4199934
BLAST score	326
E value	0.0e+00
Match length	358
% identity	35
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	131440
Contig ID	57159_1.R1010
5'-most EST	LIB3177-064-P1-K1-B6
Method	BLASTN
NCBI GI	g4757405
BLAST score	130
E value	9.0e-67
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	131441
Contig ID	57161_1.R1010
5'-most EST	LIB3177-097-P1-K1-D11
Method	BLASTN
NCBI GI	g3228389
BLAST score	263
E value	1.0e-146
Match length	492
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	131442
Contig ID	57169_1.R1010
5'-most EST	LIB3176-121-P2-K1-G1

Seq. No.	131443
Contig ID	57180_1.R1010
5'-most EST	jC-atXP21C116G7T7d2
Method	BLASTX
NCBI GI	g2811028
BLAST score	62
E value	1.0e-50
Match length	177
% identity	79
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188 (AF007271) similar to S. cerevisiae SIK1P (PID:g984964) [Arabidopsis thaliana]

Seq. No.	131444
Contig ID	57245_1.R1010
5'-most EST	g935357
Method	BLASTN

NCBI GI	g2815404
BLAST score	135
E value	1.0e-69
Match length	619
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	131445
Contig ID	57250_1.R1010
5'-most EST	jC-atXP79C230017T7b1
Method	BLASTX
NCBI GI	g107356
BLAST score	328
E value	4.0e-30
Match length	182
% identity	29
NCBI Description	polypyrimidine tract-binding protein PTB-2 - human >gi_35770_emb_CAA46443_ (X65371) polypirimidine tract binding protein [Homo sapiens]

Seq. No.	131446
Contig ID	57250_3.R1010
5'-most EST	LIB3176-122-P2-K1-H12
Method	BLASTX
NCBI GI	g131528
BLAST score	259
E value	4.0e-22
Match length	139
% identity	42
NCBI Description	POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1) >gi_35768_emb_CAA43973_ (X62006) polypirimidine tract binding protein [Homo sapiens] >gi_35774_emb_CAA43056_ (X60648) polypyrimidine tract-binding protein (pPTB) [Homo sapiens] >gi_4096061 (AC006273) PTB_HUMAN; PTB; HETEROGENEOUS NUCLEA; HNRNP I; 57 KD RNA-BINDING PROTEIN PPTB-1 [Homo sapiens]

Seq. No.	131447
Contig ID	57253_1.R1010
5'-most EST	LIB35-034-Q1-E1-E1
Method	BLASTX
NCBI GI	g1346512
BLAST score	272
E value	7.0e-24
Match length	164
% identity	36
NCBI Description	ATP-DEPENDENT PERMEASE MDL1 >gi_1078101_pir__S51433 MDL1 protein - yeast (Saccharomyces cerevisiae) >gi_577195 (U17246) Mdl1p [Saccharomyces cerevisiae]

Seq. No.	131448
Contig ID	57277_1.R1010
5'-most EST	g1159223
Method	BLASTX
NCBI GI	g3212854

BLAST score	579
E value	1.0e-69
Match length	154
% identity	92
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	131449
Contig ID	57328_1.R1010
5'-most EST	jC-atXLIB327427P4c09b2

Seq. No.	131450
Contig ID	57338_1.R1010
5'-most EST	jC-atXLIB327426P2h08b1
Method	BLASTN
NCBI GI	g2191157
BLAST score	294
E value	1.0e-164
Match length	621
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	131451
Contig ID	57341_1.R1010
5'-most EST	g931985
Method	BLASTX
NCBI GI	g1703220
BLAST score	318
E value	4.0e-29
Match length	131
% identity	53
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	131452
Contig ID	57357_1.R1010
5'-most EST	LIB3177-002-Q1-K1-C12
Method	BLASTX
NCBI GI	g3859600
BLAST score	197
E value	2.0e-15
Match length	83
% identity	19
NCBI Description	(AF104919) T15B16.6 gene product [Arabidopsis thaliana] >gi_4558545_gb_AAD22638.1_AC007138_2 (AC007138) putative CHP-rich zinc finger protein [Arabidopsis thaliana]

Seq. No.	131453
Contig ID	57382_1.R1010
5'-most EST	g2764047
Method	BLASTN
NCBI GI	g3241924
BLAST score	218
E value	1.0e-119
Match length	353
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	131454
Contig ID	57417_1.R1010
5'-most EST	LIB3177-002-Q1-K1-H9
Method	BLASTX
NCBI GI	g3953459
BLAST score	770
E value	5.0e-82
Match length	156
% identity	99
NCBI Description	(AC002328) F20N2.4 [Arabidopsis thaliana]

Seq. No.	131455
Contig ID	57443_1.R1010
5'-most EST	LIB3177-033-P1-K1-C1
Method	BLASTX
NCBI GI	g4585882
BLAST score	302
E value	2.0e-27
Match length	134
% identity	53
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	131456
Contig ID	57480_1.R1010
5'-most EST	LIB3177-004-P1-K2-C1
Method	BLASTX
NCBI GI	g266936
BLAST score	318
E value	3.0e-29
Match length	74
% identity	80
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	131457
Contig ID	57485_1.R1010
5'-most EST	LIB3177-004-P1-K2-C7

Seq. No.	131458
Contig ID	57505_1.R1010
5'-most EST	jC-alXLIB327435P2g07a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	5.0e-26
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	131459
Contig ID	57505_2.R1010

5'-most EST	g2749393
Seq. No.	131460
Contig ID	57556_1.R1010
5'-most EST	LIB3177-012-P1-K1-D4
Method	BLASTX
NCBI GI	g4263525
BLAST score	396
E value	2.0e-38
Match length	126
% identity	66
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]
Seq. No.	131461
Contig ID	57563_1.R1010
5'-most EST	LIB3177-005-P1-K1-G7
Method	BLASTN
NCBI GI	g2656031
BLAST score	34
E value	2.0e-09
Match length	244
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
Seq. No.	131462
Contig ID	57576_1.R1010
5'-most EST	LIB3177-005-P1-K2-A5
Seq. No.	131463
Contig ID	57587_1.R1010
5'-most EST	LIB3177-005-P1-K2-B8
Method	BLASTN
NCBI GI	g4335744
BLAST score	196
E value	1.0e-106
Match length	471
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	131464
Contig ID	57590_1.R1010
5'-most EST	g2062891
Method	BLASTX
NCBI GI	g3212870
BLAST score	255
E value	9.0e-22
Match length	71
% identity	75
NCBI Description	(AC004005) putative N-myristoyltransferase [Arabidopsis thaliana]
Seq. No.	131465
Contig ID	57622_1.R1010
5'-most EST	LIB3177-020-P1-K2-H1

Method	BLASTN
NCBI GI	g2656031
BLAST score	370
E value	0.0e+00
Match length	419
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	131466
Contig ID	57634_1.R1010
5'-most EST	g398238
Method	BLASTX
NCBI GI	g2244740
BLAST score	747
E value	2.0e-79
Match length	208
% identity	66
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	131467
Contig ID	57640_1.R1010
5'-most EST	jC-atXLIB327431P3d03a1
Method	BLASTN
NCBI GI	g3046851
BLAST score	309
E value	1.0e-173
Match length	413
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	131468
Contig ID	57641_1.R1010
5'-most EST	LIB3177-016-P1-K1-D1
Method	BLASTX
NCBI GI	g115385
BLAST score	312
E value	2.0e-31
Match length	106
% identity	75
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	131469
Contig ID	57658_1.R1010
5'-most EST	LIB3177-048-P1-K1-C10
Method	BLASTX
NCBI GI	g4585935
BLAST score	96
E value	7.0e-28
Match length	125
% identity	55
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	131470
Contig ID	57720_1.R1010
5'-most EST	LIB3177-006-P1-K2-H4
Method	BLASTX
NCBI GI	g4582430
BLAST score	1205
E value	1.0e-133
Match length	233
% identity	99
NCBI Description	(AC007196) nonsense-mediated mRNA decay protein [Arabidopsis thaliana]

Seq. No.	131471
Contig ID	57750_1.R1010
5'-most EST	LIB3177-007-P1-K1-E5
Method	BLASTX
NCBI GI	g2119848
BLAST score	429
E value	2.0e-42
Match length	113
% identity	76
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	131472
Contig ID	57758_1.R1010
5'-most EST	LIB3177-050-P1-K1-B2
Method	BLASTX
NCBI GI	g2199574
BLAST score	336
E value	2.0e-31
Match length	98
% identity	65
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	131473
Contig ID	57787_1.R1010
5'-most EST	ARABL1-041-Q1-E1-A10
Method	BLASTX
NCBI GI	g4587571
BLAST score	192
E value	2.0e-14
Match length	51
% identity	69
NCBI Description	(AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]

Seq. No.	131474
Contig ID	57814_1.R1010

5'-most EST	g905699
Method	BLASTN
NCBI GI	g4056476
BLAST score	169
E value	7.0e-90
Match length	609
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131475
Contig ID	57820_1.R1010
5'-most EST	LIB3177-007-P1-K2-G2
Method	BLASTX
NCBI GI	g3287691
BLAST score	181
E value	7.0e-13
Match length	195
% identity	29
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	131476
Contig ID	57820_2.R1010
5'-most EST	LIB3234-050-P1-K1-C2
Method	BLASTX
NCBI GI	g3287691
BLAST score	165
E value	2.0e-11
Match length	65
% identity	55
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	131477
Contig ID	57842_1.R1010
5'-most EST	LIB3177-050-P1-K1-C2
Method	BLASTX
NCBI GI	g115783
BLAST score	348
E value	8.0e-33
Match length	122
% identity	61
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	131478
Contig ID	57845_1.R1010
5'-most EST	LIB3177-038-P1-K1-F7
Method	BLASTX
NCBI GI	g2506443
BLAST score	219
E value	1.0e-17
Match length	121
% identity	47

NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	131479
Contig ID	57868_1.R1010
5'-most EST	LIB3177-008-P1-K1-F1
Method	BLASTX
NCBI GI	g124224
BLAST score	365
E value	8.0e-35
Match length	114
% identity	63
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	131480
Contig ID	57905_1.R1010
5'-most EST	LIB3177-008-P1-K2-C2
Method	BLASTX
NCBI GI	g131276
BLAST score	779
E value	2.0e-83
Match length	150
% identity	98
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	131481
Contig ID	57918_1.R1010
5'-most EST	LIB3177-085-P1-K1-D8
Method	BLASTN
NCBI GI	g2564046
BLAST score	174
E value	5.0e-93
Match length	485
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	131482
Contig ID	57919_1.R1010
5'-most EST	LIB3177-013-P1-K2-H1
Method	BLASTX
NCBI GI	g3264757

BLAST score	433
E value	3.0e-67
Match length	212
% identity	63
NCBI Description	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No.	131483
Contig ID	57932_1.R1010
5'-most EST	jC-atXP76C228I24T7d1
Method	BLASTX
NCBI GI	g4585873
BLAST score	769
E value	4.0e-82
Match length	165
% identity	91
NCBI Description	(AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	131484
Contig ID	57950_1.R1010
5'-most EST	LIB3177-008-P1-K2-H9
Method	BLASTX
NCBI GI	g4538928
BLAST score	162
E value	9.0e-11
Match length	42
% identity	79
NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]

Seq. No.	131485
Contig ID	57951_1.R1010
5'-most EST	g2764055
Method	BLASTX
NCBI GI	g3702332
BLAST score	208
E value	2.0e-16
Match length	100
% identity	52
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	131486
Contig ID	57961_1.R1010
5'-most EST	LIB35-022-Q1-E1-D4

Seq. No.	131487
Contig ID	57961_4.R1010
5'-most EST	ARABL1-043-Q1-B1-F8

Seq. No.	131488
Contig ID	57983_1.R1010
5'-most EST	LIB3177-099-P1-K1-C11
Method	BLASTN
NCBI GI	g2564050
BLAST score	420
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	131489
Contig ID	57999_1.R1010
5'-most EST	LIB3177-010-P1-K1-B5

Seq. No.	131490
Contig ID	58023_1.R1010
5'-most EST	LIB3177-010-P1-K2-A11
Method	BLASTN
NCBI GI	g4406776
BLAST score	459
E value	0.0e+00
Match length	463
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131491
Contig ID	58034_1.R1010
5'-most EST	LIB3177-010-P1-K2-B3
Method	BLASTX
NCBI GI	g2190547
BLAST score	398
E value	1.0e-38
Match length	134
% identity	50
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	131492
Contig ID	58089_1.R1010
5'-most EST	LIB3177-021-P1-K1-A11
Method	BLASTX
NCBI GI	g115787
BLAST score	126
E value	2.0e-28
Match length	108
% identity	64
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-2)D (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	131493
Contig ID	58105_1.R1010
5'-most EST	LIB3177-012-P1-K1-D3

Seq. No.	131494
Contig ID	58167_1.R1010
5'-most EST	jC-atXP41C165G17T7d1
Method	BLASTX
NCBI GI	g1922244
BLAST score	689
E value	1.0e-72

Match length 147
% identity 94
NCBI Description (Y10085) putative desication related protein LEA14 [Arabidopsis thaliana] >gi_2505882_emb_CAA73311_ (Y12776) LEA protein [Arabidopsis thaliana]

Seq. No. 131495
Contig ID 58190_1.R1010
5'-most EST g1054030
Method BLASTX
NCBI GI g3894193
BLAST score 483
E value 2.0e-50
Match length 158
% identity 61
NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No. 131496
Contig ID 58253_1.R1010
5'-most EST g1520378
Method BLASTX
NCBI GI g1706130
BLAST score 271
E value 2.0e-23
Match length 76
% identity 70
NCBI Description CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]

Seq. No. 131497
Contig ID 58256_1.R1010
5'-most EST LIB3177-013-P1-K2-B1
Method BLASTN
NCBI GI g4539331
BLAST score 498
E value 0.0e+00
Match length 510
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No. 131498
Contig ID 58262_1.R1010
5'-most EST jC-atXLIB327438P1g08a1
Method BLASTN
NCBI GI g3702723
BLAST score 113
E value 2.0e-56
Match length 241
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14B20, complete sequence [Arabidopsis thaliana]

Seq. No. 131499

Contig ID	58262_2.R1010
5'-most EST	LIB3177-013-P1-K2-B8
Method	BLASTX
NCBI GI	g2827704
BLAST score	498
E value	2.0e-50
Match length	108
% identity	91
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No.	131500
Contig ID	58267_1.R1010
5'-most EST	jC-atXP29C135L1T7010d1
Method	BLASTX
NCBI GI	g119905
BLAST score	950
E value	1.0e-103
Match length	221
% identity	81
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978_ (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to 308) [Pisum sativum] >gi_226545_prf__1601517A ferredoxin NADP reductase [Arachis hypogaea]

Seq. No.	131501
Contig ID	58270_1.R1010
5'-most EST	LIB3177-075-P1-K1-C7

Seq. No.	131502
Contig ID	58275_1.R1010
5'-most EST	g3719172
Method	BLASTX
NCBI GI	g4105798
BLAST score	411
E value	4.0e-40
Match length	110
% identity	64
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	131503
Contig ID	58277_1.R1010
5'-most EST	LIB3177-013-P1-K2-E10
Method	BLASTX
NCBI GI	g132675
BLAST score	271
E value	3.0e-48
Match length	122
% identity	88
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi_71222_pir__R5NT14 ribosomal protein L14 - common tobacco chloroplast >gi_11864_emb_CAA77379_ (Z00044) ribosomal protein L14 [Nicotiana tabacum] >gi_225233_prf__1211235BQ ribosomal protein L14 [Nicotiana tabacum]

Seq. No.	131504

Contig ID 58298_1.R1010
5'-most EST LIB3177-013-P1-K2-G11

Seq. No. 131505
Contig ID 58306_1.R1010
5'-most EST g498541
Method BLASTX
NCBI GI g881615
BLAST score 204
E value 6.0e-44
Match length 162
% identity 62
NCBI Description (U29142) fatty acid elongase 1 [Arabidopsis thaliana] >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase 1 [Arabidopsis thaliana]

Seq. No. 131506
Contig ID 58321_1.R1010
5'-most EST jC-atXP107C118C20T7d1
Method BLASTX
NCBI GI g4454472
BLAST score 390
E value 2.0e-37
Match length 132
% identity 64
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 131507
Contig ID 58326_1.R1010
5'-most EST g2758904
Method BLASTX
NCBI GI g3377800
BLAST score 447
E value 1.0e-97
Match length 176
% identity 96
NCBI Description (AF075597) similar to glycosyl hydrolases family 9 (PFam:glycosyl_hydro5.hmm, score: 100.70) [Arabidopsis thaliana]

Seq. No. 131508
Contig ID 58330_1.R1010
5'-most EST LIB3177-014-P1-K2-B5
Method BLASTX
NCBI GI g2739382
BLAST score 648
E value 8.0e-68
Match length 176
% identity 77
NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No. 131509
Contig ID 58350_1.R1010
5'-most EST LIB3177-014-P1-K2-E8
Method BLASTX
NCBI GI g2244850

BLAST score 156
E value 6.0e-10
Match length 76
% identity 43
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 131510
Contig ID 58421_1.R1010
5'-most EST LIB3177-015-P1-K2-A2
Method BLASTX
NCBI GI g3522933
BLAST score 760
E value 5.0e-81
Match length 174
% identity 86
NCBI Description (AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No. 131511
Contig ID 58468_1.R1010
5'-most EST g2722220

Seq. No. 131512
Contig ID 58557_1.R1010
5'-most EST jC-atXP112C127G5T7a1
Method BLASTX
NCBI GI g4539335
BLAST score 371
E value 4.0e-35
Match length 120
% identity 53
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 131513
Contig ID 58565_1.R1010
5'-most EST g2445914

Seq. No. 131514
Contig ID 58575_1.R1010
5'-most EST jC-atXLIB327409P1b08a1
Method BLASTX
NCBI GI g393116
BLAST score 467
E value 2.0e-46
Match length 187
% identity 28
NCBI Description (L23922) P-glycoprotein 5 [Entamoeba histolytica]

Seq. No. 131515
Contig ID 58600_1.R1010
5'-most EST LIB3177-025-P1-K2-F11

Seq. No. 131516
Contig ID 58635_1.R1010
5'-most EST LIB3177-024-P1-K1-A10
Method BLASTX
NCBI GI g1363489

BLAST score 433
E value 8.0e-43
Match length 137
% identity 65
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 131517
Contig ID 58636_1.R1010
5'-most EST LIB3177-036-P1-K1-B3
Method BLASTX
NCBI GI g2119846
BLAST score 591
E value 3.0e-61
Match length 162
% identity 72
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 131518
Contig ID 58723_1.R1010
5'-most EST LIB3177-017-P1-K2-H1
Method BLASTX
NCBI GI g4506223
BLAST score 257
E value 5.0e-22
Match length 118
% identity 42
NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 >gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]

Seq. No. 131519
Contig ID 58735_1.R1010
5'-most EST LIB3177-018-P1-K1-A8
Method BLASTX
NCBI GI g543841
BLAST score 238
E value 4.0e-20
Match length 76
% identity 64
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 131520
Contig ID 58798_1.R1010
5'-most EST g3449795

Method	BLASTN
NCBI GI	g402614
BLAST score	130
E value	8.0e-67
Match length	248
% identity	86
NCBI Description	B.rapa chloroplast mRNA for ribosomal protein L32

Seq. No.	131521
Contig ID	58799_1.R1010
5'-most EST	LIB3177-018-P1-K2-D1

Seq. No.	131522
Contig ID	58800_1.R1010
5'-most EST	jC-atXP32C147N19T7d2

Seq. No.	131523
Contig ID	58870_1.R1010
5'-most EST	LIB3177-050-P1-K1-F2
Method	BLASTX
NCBI GI	g115802
BLAST score	111
E value	2.0e-21
Match length	125
% identity	43
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No.	131524
Contig ID	58901_1.R1010
5'-most EST	LIB3177-019-P1-K1-G2
Method	BLASTN
NCBI GI	g4589445
BLAST score	91
E value	2.0e-43
Match length	343
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	131525
Contig ID	58932_1.R1010
5'-most EST	LIB3177-019-P1-K2-B5
Method	BLASTX
NCBI GI	g2660671
BLAST score	592
E value	2.0e-61
Match length	116
% identity	99
NCBI Description	(AC002342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131526
Contig ID	58937_1.R1010
5'-most EST	LIB3177-019-P1-K2-C3

Method	BLASTN
NCBI GI	g4220510
BLAST score	583
E value	0.0e+00
Match length	737
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	131527
Contig ID	58967_1.R1010
5'-most EST	jC-atXLIB327410P2f08a1
Method	BLASTX
NCBI GI	g4432837
BLAST score	175
E value	2.0e-12
Match length	45
% identity	76
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131528
Contig ID	58976_1.R1010
5'-most EST	LIB3177-019-P1-K2-H1
Method	BLASTN
NCBI GI	g4586098
BLAST score	250
E value	1.0e-138
Match length	608
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	131529
Contig ID	58981_1.R1010
5'-most EST	LIB3177-019-P1-K2-H4

Seq. No.	131530
Contig ID	59005_1.R1010
5'-most EST	LIB3177-020-P1-K1-C2
Method	BLASTX
NCBI GI	g4454036
BLAST score	233
E value	2.0e-19
Match length	105
% identity	50
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	131531
Contig ID	59156_1.R1010
5'-most EST	LIB3177-021-P1-K1-F4
Method	BLASTN
NCBI GI	g2618601
BLAST score	44
E value	9.0e-16
Match length	224
% identity	80

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.	131532
Contig ID	59211_1.R1010
5'-most EST	jC-atXLIB327408P3g06a1
Seq. No.	131533
Contig ID	59236_1.R1010
5'-most EST	LIB3177-045-P1-K2-B4
Seq. No.	131534
Contig ID	59247_1.R1010
5'-most EST	jC-atXP67C212G7T7059a1
Method	BLASTX
NCBI GI	g2864615
BLAST score	338
E value	2.0e-31
Match length	85
% identity	80
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]
Seq. No.	131535
Contig ID	59264_1.R1010
5'-most EST	LIB3177-022-P1-K2-B4
Seq. No.	131536
Contig ID	59267_1.R1010
5'-most EST	g2446142
Seq. No.	131537
Contig ID	59270_1.R1010
5'-most EST	g906878
Method	BLASTX
NCBI GI	g3859599
BLAST score	406
E value	2.0e-39
Match length	143
% identity	57
NCBI Description	(AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
Seq. No.	131538
Contig ID	59274_1.R1010
5'-most EST	g2748443
Method	BLASTX
NCBI GI	g586339
BLAST score	216
E value	3.0e-17
Match length	82
% identity	46
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c [Saccharomyces cerevisiae]
Seq. No.	131539

Contig ID	59295_1.R1010
5'-most EST	LIB3177-022-P1-K2-F9
Method	BLASTX
NCBI GI	g3152618
BLAST score	404
E value	4.0e-39
Match length	113
% identity	64
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	131540
Contig ID	59297_1.R1010
5'-most EST	jC-atXP65C208D15T7014d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	131541
Contig ID	59298_1.R1010
5'-most EST	LIB3177-022-P1-K2-G12
Method	BLASTX
NCBI GI	g1363484
BLAST score	373
E value	1.0e-35
Match length	78
% identity	94
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	131542
Contig ID	59312_1.R1010
5'-most EST	LIB3177-038-P1-K1-D12
Method	BLASTX
NCBI GI	g266936
BLAST score	238
E value	5.0e-20
Match length	98
% identity	54
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	131543
Contig ID	59396_1.R1010
5'-most EST	LIB3177-024-P1-K2-D3
Method	BLASTX
NCBI GI	g3858935

BLAST score 528
E value 1.0e-53
Match length 135
% identity 72
NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No. 131544
Contig ID 59403_2.R1010
5'-most EST LIB3177-098-P1-K1-A2
Method BLASTX
NCBI GI g3335378
BLAST score 299
E value 4.0e-27
Match length 66
% identity 83
NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No. 131545
Contig ID 59410_1.R1010
5'-most EST LIB3177-024-P1-K2-F2

Seq. No. 131546
Contig ID 59446_1.R1010
5'-most EST LIB3177-064-P1-K1-F2
Method BLASTN
NCBI GI g4468801
BLAST score 329
E value 0.0e+00
Match length 463
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No. 131547
Contig ID 59460_1.R1010
5'-most EST LIB3177-025-P1-K2-G1

Seq. No. 131548
Contig ID 59469_1.R1010
5'-most EST g935342
Method BLASTX
NCBI GI g4587525
BLAST score 281
E value 9.0e-27
Match length 216
% identity 40
NCBI Description (AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No. 131549
Contig ID 59493_1.R1010

5'-most EST	LIB3177-026-P1-K2-A1
Method	BLASTX
NCBI GI	g3687887
BLAST score	373
E value	2.0e-35
Match length	179
% identity	44
NCBI Description	(AF077339) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	131550
Contig ID	59527_1.R1010
5'-most EST	LIB3177-026-P1-K2-E12
Method	BLASTX
NCBI GI	g3170230
BLAST score	185
E value	9.0e-14
Match length	75
% identity	53
NCBI Description	(AF041848) fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No.	131551
Contig ID	59541_1.R1010
5'-most EST	g3450063
Method	BLASTN
NCBI GI	g4757392
BLAST score	281
E value	1.0e-157
Match length	366
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	131552
Contig ID	59546_1.R1010
5'-most EST	g2393508
Method	BLASTX
NCBI GI	g1653516
BLAST score	226
E value	2.0e-18
Match length	77
% identity	55
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	131553
Contig ID	59546_2.R1010
5'-most EST	LIB3177-095-P1-K1-F5
Method	BLASTX
NCBI GI	g1653516
BLAST score	185
E value	1.0e-13
Match length	69
% identity	54
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No. 131554

Contig ID 59621_1.R1010
5'-most EST LIB3177-033-P1-K2-B11

Seq. No. 131555
Contig ID 59647_1.R1010
5'-most EST LIB3177-098-P1-K1-E7

Seq. No. 131556
Contig ID 59650_1.R1010
5'-most EST LIB3177-095-P1-K1-A10
Method BLASTX
NCBI GI g2129770
BLAST score 215
E value 2.0e-17
Match length 89
% identity 46
NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 131557
Contig ID 59665_1.R1010
5'-most EST g507113
Method BLASTX
NCBI GI g4680697
BLAST score 242
E value 3.0e-20
Match length 88
% identity 57
NCBI Description (AF132963) CGI-29 protein [Homo sapiens]

Seq. No. 131558
Contig ID 59672_1.R1010
5'-most EST LIB3177-067-P1-K1-G11
Method BLASTX
NCBI GI g4538903
BLAST score 139
E value 9.0e-09
Match length 72
% identity 43
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 131559
Contig ID 59679_1.R1010
5'-most EST jC-atXP50C180F14T7026d1
Method BLASTX
NCBI GI g3738329
BLAST score 882
E value 4.0e-95
Match length 174
% identity 99
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 131560
Contig ID 59730_1.R1010

5'-most EST	LIB3177-088-P1-K1-C1
Seq. No.	131561
Contig ID	59747_1.R1010
5'-most EST	jC-atXP92C246N13T7034d1
Method	BLASTX
NCBI GI	g4008008
BLAST score	282
E value	7.0e-25
Match length	85
% identity	65
NCBI Description	(AF084035) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	131562
Contig ID	59749_1.R1010
5'-most EST	LIB3177-036-P1-K2-A4
Method	BLASTX
NCBI GI	g2244780
BLAST score	356
E value	6.0e-34
Match length	101
% identity	75
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.	131563
Contig ID	59766_1.R1010
5'-most EST	LIB3177-095-P1-K1-A5
Method	BLASTX
NCBI GI	g3413714
BLAST score	156
E value	3.0e-10
Match length	162
% identity	12
NCBI Description	(AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]
Seq. No.	131564
Contig ID	59776_1.R1010
5'-most EST	LIB3177-060-P1-K1-G5
Method	BLASTX
NCBI GI	g4580527
BLAST score	1059
E value	1.0e-116
Match length	199
% identity	100
NCBI Description	(AF036307) scarecrow-like 11 [Arabidopsis thaliana]
Seq. No.	131565
Contig ID	59776_2.R1010
5'-most EST	g2047838
Method	BLASTX
NCBI GI	g4580527
BLAST score	76
E value	2.0e-32
Match length	103
% identity	74

NCBI Description (AF036307) scarecrow-like 11 [Arabidopsis thaliana]

Seq. No. 131566
Contig ID 59792_1.R1010
5'-most EST g493283
Method BLASTX
NCBI GI g2924327
BLAST score 246
E value 1.0e-20
Match length 94
% identity 60
NCBI Description (Z93766) hypothetical protein [Malus domestica]

Seq. No. 131567
Contig ID 59842_1.R1010
5'-most EST g2048391

Seq. No. 131568
Contig ID 59842_3.R1010
5'-most EST LIB3177-038-P1-K2-A4

Seq. No. 131569
Contig ID 59871_1.R1010
5'-most EST LIB3177-038-P1-K2-G1
Method BLASTX
NCBI GI g2832625
BLAST score 198
E value 3.0e-15
Match length 45
% identity 82
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 131570
Contig ID 59889_1.R1010
5'-most EST LIB3177-039-P1-K1-C4
Method BLASTN
NCBI GI g3510340
BLAST score 124
E value 3.0e-63
Match length 419
% identity 88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No. 131571
Contig ID 59935_1.R1010
5'-most EST LIB3177-039-P1-K2-G1
Method BLASTN
NCBI GI g2760316
BLAST score 290
E value 1.0e-162
Match length 372
% identity 96
NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 131572

Contig ID 59950_1.R1010
5'-most EST LIB3177-041-P1-K2-A2
Method BLASTX
NCBI GI g4539324
BLAST score 245
E value 9.0e-21
Match length 136
% identity 48
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 131573
Contig ID 59954_1.R1010
5'-most EST g1217119
Method BLASTN
NCBI GI g2584827
BLAST score 414
E value 0.0e+00
Match length 432
% identity 99
NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 131574
Contig ID 59956_1.R1010
5'-most EST g2581597
Method BLASTX
NCBI GI g4586253
BLAST score 225
E value 9.0e-22
Match length 91
% identity 64
NCBI Description (AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No. 131575
Contig ID 59973_1.R1010
5'-most EST g1520257
Method BLASTX
NCBI GI g2760322
BLAST score 431
E value 3.0e-42
Match length 107
% identity 78
NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 131576
Contig ID 59975_1.R1010
5'-most EST jC-atXLIB327433P1c12a1
Method BLASTN
NCBI GI g2290120
BLAST score 54
E value 2.0e-21
Match length 65
% identity 97
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 131577

Contig ID	60007_1.R1010
5'-most EST	jC-atXLIB327421P3f02b1
Method	BLASTX
NCBI GI	g466160
BLAST score	370
E value	3.0e-35
Match length	83
% identity	84
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	131578
Contig ID	60007_2.R1010
5'-most EST	g2446248

Seq. No.	131579
Contig ID	60007_3.R1010
5'-most EST	LIB3177-042-P1-K2-C8
Method	BLASTX
NCBI GI	g466160
BLAST score	250
E value	3.0e-21
Match length	84
% identity	61
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	131580
Contig ID	60010_1.R1010
5'-most EST	g2749528

Seq. No.	131581
Contig ID	60010_2.R1010
5'-most EST	LIB3177-042-P1-K2-D11
Method	BLASTX
NCBI GI	g2801536
BLAST score	312
E value	3.0e-28
Match length	121
% identity	51
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	131582
Contig ID	60012_1.R1010
5'-most EST	g2722164
Method	BLASTN
NCBI GI	g2864607
BLAST score	177
E value	1.0e-94
Match length	469
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	131583
Contig ID	60023_1.R1010
5'-most EST	ARABL1-04-Q1-B1-E8
Method	BLASTX
NCBI GI	g3915958
BLAST score	159
E value	5.0e-18
Match length	92
% identity	50
NCBI Description	HYPOTHETICAL HIT-LIKE PROTEIN MJ0866 >gi_2826341 (U67530) HIT family protein (hit) [Methanococcus jannaschii]

Seq. No.	131584
Contig ID	60035_1.R1010
5'-most EST	jC-atXP107C105A22T7s1
Method	BLASTN
NCBI GI	g2656028
BLAST score	406
E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	131585
Contig ID	60039_1.R1010
5'-most EST	g2048907
Method	BLASTX
NCBI GI	g3738310
BLAST score	143
E value	1.0e-08
Match length	29
% identity	100
NCBI Description	(AC005309) putative nuclear protein [Arabidopsis thaliana]

Seq. No.	131586
Contig ID	60039_2.R1010
5'-most EST	g404219
Method	BLASTN
NCBI GI	g4249393
BLAST score	268
E value	1.0e-149
Match length	399
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131587
Contig ID	60048_1.R1010
5'-most EST	LIB35-012-Q1-E1-B4

Seq. No.	131588
Contig ID	60052_1.R1010
5'-most EST	LIB3177-043-P1-K2-B6
Method	BLASTX
NCBI GI	g4507141

BLAST score 145
E value 1.0e-08
Match length 138
% identity 25
NCBI Description sorting nexin 2 >gi_3152938 (AF065482) sorting nexin 2 [Homo sapiens]

Seq. No. 131589
Contig ID 60079_1.R1010
5'-most EST LIB3177-070-P1-K1-D10

Seq. No. 131590
Contig ID 60104_1.R1010
5'-most EST LIB3177-044-P1-K2-H6
Method BLASTX
NCBI GI g99819
BLAST score 576
E value 2.0e-59
Match length 113
% identity 95
NCBI Description napin nIa - rape

Seq. No. 131591
Contig ID 60121_1.R1010
5'-most EST LIB3177-044-P1-K2-E7
Method BLASTX
NCBI GI g167136
BLAST score 570
E value 1.0e-58
Match length 124
% identity 92
NCBI Description (J05233) cruciferin precursor [Brassica napus]

Seq. No. 131592
Contig ID 60153_1.R1010
5'-most EST g936327
Method BLASTN
NCBI GI g2924651
BLAST score 368
E value 0.0e+00
Match length 423
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 131593
Contig ID 60175_1.R1010
5'-most EST LIB3177-044-P1-K2-H10
Method BLASTX
NCBI GI g4753655
BLAST score 159
E value 8.0e-22
Match length 60
% identity 87
NCBI Description (AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No.	131594
Contig ID	60208_1.R1010
5'-most EST	g2445965
Method	BLASTN
NCBI GI	g2696018
BLAST score	230
E value	1.0e-126
Match length	381
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	131595
Contig ID	60241_1.R1010
5'-most EST	LIB3177-045-P1-K2-G6
Method	BLASTN
NCBI GI	g2832667
BLAST score	260
E value	1.0e-144
Match length	381
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	131596
Contig ID	60245_1.R1010
5'-most EST	jC-atXP18C113M6T7d2
Method	BLASTN
NCBI GI	g3608126
BLAST score	240
E value	1.0e-132
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131597
Contig ID	60246_1.R1010
5'-most EST	jC-atXP3C80E11T7d1
Method	BLASTN
NCBI GI	g4539378
BLAST score	154
E value	4.0e-81
Match length	414
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	131598
Contig ID	60256_1.R1010
5'-most EST	LIB3177-046-P1-K2-A2

Seq. No.	131599
Contig ID	60261_1.R1010
5'-most EST	LIB3177-046-P1-K2-A7
Method	BLASTX
NCBI GI	g4468807

BLAST score 601
E value 1.0e-66
Match length 146
% identity 88
NCBI Description (AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No. 131600
Contig ID 60267_1.R1010
5'-most EST jC-atXP29C139L18T7070d1
Method BLASTX
NCBI GI g4646203
BLAST score 689
E value 2.0e-72
Match length 252
% identity 52
NCBI Description (AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No. 131601
Contig ID 60307_1.R1010
5'-most EST jC-atXP71C222P5T7093d1
Method BLASTN
NCBI GI g3800746
BLAST score 41
E value 4.0e-13
Match length 45
% identity 98
NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No. 131602
Contig ID 60307_2.R1010
5'-most EST jC-atXLIB327438P3e05a2

Seq. No. 131603
Contig ID 60311_1.R1010
5'-most EST jC-atXLIB327416P1h07a1
Method BLASTX
NCBI GI g4455206
BLAST score 384
E value 6.0e-37
Match length 79
% identity 85
NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No. 131604
Contig ID 60312_1.R1010
5'-most EST LIB3177-056-P1-K1-G4
Method BLASTX
NCBI GI g3036807
BLAST score 335
E value 2.0e-31
Match length 144
% identity 53
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	131605
Contig ID	60319_1.R1010
5'-most EST	LIB3177-046-P1-K2-G11
Method	BLASTN
NCBI GI	g3869065
BLAST score	276
E value	1.0e-154
Match length	458
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	131606
Contig ID	60492_1.R1010
5'-most EST	jC-atXP10C94O15T7s2
Method	BLASTN
NCBI GI	g3228389
BLAST score	389
E value	0.0e+00
Match length	516
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	131607
Contig ID	60532_1.R1010
5'-most EST	jC-atXP86CG9H8T7b1
Method	BLASTX
NCBI GI	g4559322
BLAST score	1313
E value	1.0e-145
Match length	286
% identity	93
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	131608
Contig ID	60621_1.R1010
5'-most EST	LIB3177-079-P1-K1-A4
Method	BLASTX
NCBI GI	g4454014
BLAST score	1014
E value	1.0e-110
Match length	201
% identity	100
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	131609
Contig ID	60643_1.R1010
5'-most EST	LIB3177-052-P1-K1-F5

Seq. No.	131610
Contig ID	60664_1.R1010
5'-most EST	g1565874
Method	BLASTX
NCBI GI	g3123295
BLAST score	700

E value	8.0e-74
Match length	158
% identity	89
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	131611
Contig ID	60696_1.R1010
5'-most EST	LIB3177-052-P1-K1-D3
Method	BLASTN
NCBI GI	g2264312
BLAST score	179
E value	6.0e-96
Match length	479
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	131612
Contig ID	60699_1.R1010
5'-most EST	jC-alXLIB327435P4e04a1
Method	BLASTX
NCBI GI	g2961390
BLAST score	148
E value	4.0e-09
Match length	52
% identity	60
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	131613
Contig ID	60710_1.R1010
5'-most EST	jC-atXLIB327405P2e11a1

Seq. No.	131614
Contig ID	60710_2.R1010
5'-most EST	LIB3177-073-P1-K1-B9
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	131615
Contig ID	60723_1.R1010
5'-most EST	g2047773
Method	BLASTN
NCBI GI	g3063438
BLAST score	127
E value	7.0e-65
Match length	328
% identity	94
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	131616
Contig ID	60730_1.R1010
5'-most EST	LIB3177-093-P1-K1-E2
Method	BLASTX
NCBI GI	g4309736
BLAST score	665
E value	9.0e-70
Match length	145
% identity	91
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131617
Contig ID	60734_1.R1010
5'-most EST	LIB3177-052-P1-K1-H2
Method	BLASTX
NCBI GI	g4588008
BLAST score	72
E value	1.9e+00
Match length	145
% identity	69
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131618
Contig ID	60739_1.R1010
5'-most EST	jC-atXLIB327408P3g01b1
Method	BLASTX
NCBI GI	g4138581
BLAST score	207
E value	8.0e-41
Match length	285
% identity	17
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	131619
Contig ID	60749_1.R1010
5'-most EST	LIB3177-053-P1-K1-B11
Method	BLASTN
NCBI GI	g4510360
BLAST score	351
E value	0.0e+00
Match length	896
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	131620
Contig ID	60785_1.R1010
5'-most EST	jC-atXLIB327408P1e03a1
Method	BLASTX
NCBI GI	g3786017
BLAST score	234
E value	2.0e-19
Match length	68
% identity	74
NCBI Description	(AC005499) putative non-green plastid inner envelope

membrane protein [Arabidopsis thaliana]

Seq. No.	131621
Contig ID	60816_1.R1010
5'-most EST	g315423
Method	BLASTX
NCBI GI	g2505867
BLAST score	1161
E value	1.0e-127
Match length	252
% identity	63
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131622
Contig ID	60829_1.R1010
5'-most EST	g1053921
Method	BLASTX
NCBI GI	g131162
BLAST score	451
E value	8.0e-45
Match length	81
% identity	99
NCBI Description	PHOTOSYSTEM I IRON-SULFUR CENTER 1 (PHOTOSYSTEM I SUBUNIT VII-1) (9 KD POLYPEPTIDE 1) (PSI-C-1) >gi_131163_sp_P07136_PSAC_TOBAC PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_97657_pir__S14967 photosystem I iron-sulfur protein psaC - Synechocystis sp. (PCC 6803) >gi_100391_pir__S07170 photosystem I iron-sulfur protein psaC - common tobacco chloroplast >gi_11792_emb_CAA29304_ (X05881) 9kd polypeptide (psaC gene product, AA 1 - 81) [Nicotiana tabacum] >gi_47596_emb_CAA37836_ (X53842) 8.9kDa iron-sulfur containing subunit of Photosystem I [Synechocystis sp.] >gi_2924280_emb_CAA77433_ (Z00044) PSI 9kD protein [Nicotiana tabacum]

Seq. No.	131623
Contig ID	60829_2.R1010
5'-most EST	LIB3234-050-P1-K1-F3
Method	BLASTX
NCBI GI	g131162
BLAST score	347
E value	7.0e-39
Match length	81
% identity	94
NCBI Description	PHOTOSYSTEM I IRON-SULFUR CENTER 1 (PHOTOSYSTEM I SUBUNIT VII-1) (9 KD POLYPEPTIDE 1) (PSI-C-1) >gi_131163_sp_P07136_PSAC_TOBAC PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_97657_pir__S14967 photosystem I iron-sulfur protein psaC - Synechocystis sp. (PCC 6803) >gi_100391_pir__S07170 photosystem I iron-sulfur protein psaC - common tobacco chloroplast >gi_11792_emb_CAA29304_ (X05881) 9kd polypeptide (psaC gene product, AA 1 - 81) [Nicotiana tabacum] >gi_47596_emb_CAA37836_ (X53842) 8.9kDa iron-sulfur containing subunit of Photosystem I [Synechocystis sp.] >gi_2924280_emb_CAA77433_ (Z00044) PSI

9kD protein [Nicotiana tabacum]

Seq. No.	131624
Contig ID	60835_1.R1010
5'-most EST	jC-atXLIB327427P4c05b2
Method	BLASTX
NCBI GI	g2632254
BLAST score	438
E value	3.0e-43
Match length	133
% identity	60
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	131625
Contig ID	60845_1.R1010
5'-most EST	LIB3177-055-P1-K1-E4

Seq. No.	131626
Contig ID	60856_1.R1010
5'-most EST	jC-atXP22C115P12T7d2
Method	BLASTN
NCBI GI	g3153204
BLAST score	218
E value	1.0e-119
Match length	427
% identity	98
NCBI Description	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds

Seq. No.	131627
Contig ID	60895_1.R1010
5'-most EST	jC-atXP1C66E10T7s2
Method	BLASTX
NCBI GI	g2821961
BLAST score	493
E value	1.0e-49
Match length	93
% identity	100
NCBI Description	(AB006693) spermidine synthase [Arabidopsis thaliana]

Seq. No.	131628
Contig ID	60907_1.R1010
5'-most EST	LIB3177-056-P1-K1-B9
Method	BLASTX
NCBI GI	g4678944
BLAST score	535
E value	1.0e-54
Match length	119
% identity	53
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	131629
Contig ID	60911_1.R1010
5'-most EST	LIB3177-056-P1-K1-C12

Seq. No.	131630
Contig ID	60915_1.R1010

5'-most EST	LIB3177-095-P1-K1-H2
Method	BLASTN
NCBI GI	g3249094
BLAST score	340
E value	0.0e+00
Match length	479
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131631
Contig ID	60991_1.R1010
5'-most EST	g934976
Method	BLASTN
NCBI GI	g3046854
BLAST score	21
E value	1.5e-01
Match length	656
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	131632
Contig ID	61018_1.R1010
5'-most EST	g1520915
Method	BLASTX
NCBI GI	g1363485
BLAST score	220
E value	1.0e-17
Match length	41
% identity	95
NCBI Description	IAA3 protein - Arabidopsis thaliana >gi_972911 (U18406) IAA3 [Arabidopsis thaliana] >gi_1903369_gb_AAB70452_ (AC000104) Match to Arabidopsis IAA3 (gb_U18406). EST gb_T04296 comes from this gene. [Arabidopsis thaliana]

Seq. No.	131633
Contig ID	61032_1.R1010
5'-most EST	g3868945
Method	BLASTX
NCBI GI	g3746059
BLAST score	411
E value	3.0e-40
Match length	118
% identity	64
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	131634
Contig ID	61045_1.R1010
5'-most EST	jC-atXP114C234A5T7d1
Method	BLASTX
NCBI GI	g3915665
BLAST score	469
E value	1.0e-46
Match length	186

% identity	49
NCBI Description	ELONGATION FACTOR G (EF-G) >gi_2688449 (AE001155) translation elongation factor G (fus-1) [Borrelia burgdorferi]

Seq. No.	131635
Contig ID	61045_3.R1010
5'-most EST	g2048323
Method	BLASTX
NCBI GI	g585084
BLAST score	166
E value	2.0e-11
Match length	58
% identity	59
NCBI Description	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi_543383_pir__S40780 translation elongation factor G, mitochondrial - rat >gi_310102 (L14684) elongation factor G [Rattus norvegicus]

Seq. No.	131636
Contig ID	61046_1.R1010
5'-most EST	jC-atXLIB327427P1e06a2
Method	BLASTN
NCBI GI	g403417
BLAST score	262
E value	1.0e-145
Match length	262
% identity	100
NCBI Description	Arabidopsis thaliana Columbia bZIP protein GBF4 gene, complete cds

Seq. No.	131637
Contig ID	61054_1.R1010
5'-most EST	jC-atXLIB327417P3g02b1

Seq. No.	131638
Contig ID	61067_1.R1010
5'-most EST	LIB3177-072-P1-K1-F10
Method	BLASTN
NCBI GI	g2182286
BLAST score	393
E value	0.0e+00
Match length	409
% identity	99
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	131639
Contig ID	61072_1.R1010
5'-most EST	jC-atXP112C129L3T7a1
Method	BLASTX
NCBI GI	g4522012
BLAST score	103
E value	1.0e-33
Match length	121
% identity	62
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131640
Contig ID	61080_1.R1010
5'-most EST	g1053652
Method	BLASTN
NCBI GI	g2245031
BLAST score	809
E value	0.0e+00
Match length	830
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	131641
Contig ID	61098_1.R1010
5'-most EST	g2413287
Method	BLASTX
NCBI GI	g3860315
BLAST score	48
E value	4.0e-25
Match length	70
% identity	86
NCBI Description	(AJ012684) 40S ribosomal protein S19 [Cicer arietinum]

Seq. No.	131642
Contig ID	61100_1.R1010
5'-most EST	jC-atXLIB327431P4b02a1
Method	BLASTX
NCBI GI	g2623302
BLAST score	645
E value	2.0e-67
Match length	125
% identity	100
NCBI Description	(AC002409) putative cysteine proteinase inhibitor [Arabidopsis thaliana]

Seq. No.	131643
Contig ID	61104_1.R1010
5'-most EST	jC-atXLIB327427P3g10a2
Method	BLASTN
NCBI GI	g2864607
BLAST score	408
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	131644
Contig ID	61173_1.R1010
5'-most EST	g2393266
Method	BLASTN
NCBI GI	g4678291
BLAST score	428
E value	0.0e+00
Match length	509
% identity	100

NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	131645
Contig ID	61173_2.R1010
5'-most EST	LIB3177-060-P1-K1-E1
Method	BLASTX
NCBI GI	g4678312
BLAST score	788
E value	2.0e-84
Match length	162
% identity	90
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	131646
Contig ID	61199_2.R1010
5'-most EST	LIB3177-060-P1-K1-H10
Method	BLASTN
NCBI GI	g4558521
BLAST score	92
E value	3.0e-44
Match length	291
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	131647
Contig ID	61204_1.R1010
5'-most EST	LIB3177-060-P1-K1-H5
Method	BLASTX
NCBI GI	g4455295
BLAST score	557
E value	3.0e-57
Match length	116
% identity	91
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	131648
Contig ID	61224_1.R1010
5'-most EST	LIB3234-058-P1-K1-C11
Method	BLASTX
NCBI GI	g4835234
BLAST score	466
E value	1.0e-50
Match length	124
% identity	90
NCBI Description	(AL049862) putative cold acclimation protein [Arabidopsis thaliana]

Seq. No.	131649
Contig ID	61229_1.R1010
5'-most EST	LIB3177-062-P1-K1-B9
Method	BLASTX
NCBI GI	g1652649
BLAST score	208
E value	8.0e-42

Match length 144
% identity 60
NCBI Description (D90907) hypothetical protein [Synechocystis sp.]

Seq. No. 131650
Contig ID 61254_1.R1010
5'-most EST jC-atXLIB327417P1f12a1
Method BLASTX
NCBI GI g3860613
BLAST score 166
E value 4.0e-11
Match length 79
% identity 49
NCBI Description (AJ235270) CELL DIVISION PROTEIN FTSH (ftsH) [Rickettsia prowazekii]

Seq. No. 131651
Contig ID 61254_2.R1010
5'-most EST jC-atXLIB327414P3d12a1
Method BLASTX
NCBI GI g3600100
BLAST score 271
E value 2.0e-23
Match length 112
% identity 56
NCBI Description (AF090430) ATP-dependent metalloprotease FtsH1 [Mus musculus]

Seq. No. 131652
Contig ID 61303_1.R1010
5'-most EST g2764056
Method BLASTX
NCBI GI g3892722
BLAST score 48
E value 5.0e-52
Match length 106
% identity 100
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]

Seq. No. 131653
Contig ID 61305_1.R1010
5'-most EST LIB3234-093-P1-K1-D6

Seq. No. 131654
Contig ID 61325_1.R1010
5'-most EST LIB3177-082-P1-K1-G9
Method BLASTN
NCBI GI g3046849
BLAST score 306
E value 1.0e-172
Match length 409
% identity 94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]

Seq. No. 131655
Contig ID 61345_1.R1010

5'-most EST	g2596350
Seq. No.	131656
Contig ID	61358_1.R1010
5'-most EST	g2048331
Method	BLASTN
NCBI GI	g4581084
BLAST score	266
E value	1.0e-148
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence
Seq. No.	131657
Contig ID	61389_1.R1010
5'-most EST	LIB3177-064-P1-K1-A7
Seq. No.	131658
Contig ID	61391_1.R1010
5'-most EST	jC-atXP82CG2F1T7d3
Method	BLASTN
NCBI GI	g2264307
BLAST score	380
E value	0.0e+00
Match length	547
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]
Seq. No.	131659
Contig ID	61416_1.R1010
5'-most EST	g932895
Method	BLASTX
NCBI GI	g3894186
BLAST score	478
E value	5.0e-48
Match length	94
% identity	100
NCBI Description	(AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
Seq. No.	131660
Contig ID	61441_1.R1010
5'-most EST	g1517279
Method	BLASTX
NCBI GI	g4587527
BLAST score	331
E value	1.0e-30
Match length	166
% identity	43
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238
Seq. No.	131661
Contig ID	61449_1.R1010

5'-most EST	g906076
Method	BLASTX
NCBI GI	g4455210
BLAST score	693
E value	6.0e-73
Match length	183
% identity	75
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	131662
Contig ID	61464_1.R1010
5'-most EST	LIB3177-065-P1-K1-A7
Method	BLASTX
NCBI GI	g2342684
BLAST score	708
E value	7.0e-75
Match length	172
% identity	83
NCBI Description	(AC000106) F7G19.14 [Arabidopsis thaliana]

Seq. No.	131663
Contig ID	61475_1.R1010
5'-most EST	g1268229
Method	BLASTX
NCBI GI	g3413714
BLAST score	154
E value	3.0e-12
Match length	99
% identity	26
NCBI Description	(AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	131664
Contig ID	61487_1.R1010
5'-most EST	LIB3177-079-P1-K1-G1
Method	BLASTX
NCBI GI	g4220514
BLAST score	101
E value	3.0e-52
Match length	141
% identity	71
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	131665
Contig ID	61496_1.R1010
5'-most EST	LIB3177-065-P1-K1-E1
Method	BLASTX
NCBI GI	g401153
BLAST score	83
E value	3.0e-13
Match length	100
% identity	46
NCBI Description	TABA PROTEIN >gi_281610_pir__S27649 tabA protein - Pseudomonas syringae >gi_151571 (M88485) Homology with E.coli and P.aeruginosa lysA gene; product of unknown function; putative [Pseudomonas syringae]

Seq. No.	131666
Contig ID	61496_2.R1010
5'-most EST	jC-atXL1031Q1E1F01b1
Method	BLASTX
NCBI GI	g401153
BLAST score	188
E value	4.0e-14
Match length	74
% identity	49
NCBI Description	TABA PROTEIN >gi_281610_pir__S27649 tabA protein - Pseudomonas syringae >gi_151571 (M88485) Homology with E.coli and P.aeruginosa lysA gene; product of unknown function; putative [Pseudomonas syringae]

Seq. No.	131667
Contig ID	61532_1.R1010
5'-most EST	LIB3177-065-P1-K1-H6
Method	BLASTX
NCBI GI	g3892714
BLAST score	1037
E value	1.0e-113
Match length	240
% identity	86
NCBI Description	(AL033545) trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	131668
Contig ID	61541_1.R1010
5'-most EST	LIB3177-066-P1-K1-A3
Method	BLASTX
NCBI GI	g4505823
BLAST score	96
E value	7.0e-17
Match length	89
% identity	47
NCBI Description	pirin >gi_1907076_emb_CAA69194_ (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_ (Y07868) pirin [Homo sapiens]

Seq. No.	131669
Contig ID	61550_1.R1010
5'-most EST	g931063

Seq. No.	131670
Contig ID	61556_1.R1010
5'-most EST	LIB35-026-Q1-E1-G5
Method	BLASTN
NCBI GI	g1871173
BLAST score	526
E value	0.0e+00
Match length	581
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No. 131671

Contig ID 61560_1.R1010
5'-most EST g906560

Seq. No. 131672
Contig ID 61587_1.R1010
5'-most EST jC-atXP33C148F22T7d2
Method BLASTX
NCBI GI g731284
BLAST score 258
E value 6.0e-22
Match length 243
% identity 31
NCBI Description HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION >gi_1077482_pir__S51971 probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae) >gi_595536 (U12980) Yal048cp [Saccharomyces cerevisiae]

Seq. No. 131673
Contig ID 61600_1.R1010
5'-most EST LIB3177-066-P1-K1-G4
Method BLASTX
NCBI GI g4586249
BLAST score 252
E value 2.0e-21
Match length 164
% identity 39
NCBI Description (AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No. 131674
Contig ID 61607_1.R1010
5'-most EST jC-atXP50C180I20T7077d1

Seq. No. 131675
Contig ID 61662_1.R1010
5'-most EST g2048817
Method BLASTX
NCBI GI g3805850
BLAST score 146
E value 5.0e-09
Match length 34
% identity 65
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 131676
Contig ID 61668_1.R1010
5'-most EST jC-alXLIB327435P4h09a1
Method BLASTX
NCBI GI g2501021
BLAST score 168
E value 1.0e-11
Match length 42
% identity 76
NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	131677
Contig ID	61668_2.R1010
5'-most EST	g2062922
Method	BLASTX
NCBI GI	g2501021
BLAST score	200
E value	3.0e-15
Match length	47
% identity	81
NCBI Description	LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	131678
Contig ID	61688_1.R1010
5'-most EST	g2062962
Method	BLASTN
NCBI GI	g3172156
BLAST score	351
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131679
Contig ID	61699_1.R1010
5'-most EST	LIB3177-068-P1-K1-A8
Method	BLASTX
NCBI GI	g3341479
BLAST score	157
E value	2.0e-10
Match length	88
% identity	36
NCBI Description	(AJ000513) hypothetical protein [Pseudanabaena sp.]

Seq. No.	131680
Contig ID	61750_1.R1010
5'-most EST	LIB3177-068-P1-K1-F5
Method	BLASTN
NCBI GI	g3299824
BLAST score	424
E value	0.0e+00
Match length	476
% identity	97
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	131681
Contig ID	61754_1.R1010
5'-most EST	g2393581
Method	BLASTN
NCBI GI	g4220635
BLAST score	219
E value	1.0e-120
Match length	372
% identity	94

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.	131682
Contig ID	61758_1.R1010
5'-most EST	LIB3177-068-P1-K1-G12
Method	BLASTX
NCBI GI	g4539009
BLAST score	667
E value	3.0e-70
Match length	156
% identity	77
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]
Seq. No.	131683
Contig ID	61788_1.R1010
5'-most EST	g498490
Seq. No.	131684
Contig ID	61807_1.R1010
5'-most EST	jC-atXLIB327421P3g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	7.0e-29
Match length	78
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	131685
Contig ID	61807_2.R1010
5'-most EST	g2597165
Seq. No.	131686
Contig ID	61827_1.R1010
5'-most EST	LIB3177-069-P1-K1-F10
Method	BLASTN
NCBI GI	g3046854
BLAST score	505
E value	0.0e+00
Match length	517
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.	131687
Contig ID	61851_1.R1010
5'-most EST	LIB3177-069-P1-K1-H8
Method	BLASTX
NCBI GI	g1899188
BLAST score	109
E value	1.0e-04
Match length	85
% identity	13
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	131688
Contig ID	61855_1.R1010
5'-most EST	LIB3177-070-P1-K1-A11
Method	BLASTN
NCBI GI	g4757662
BLAST score	232
E value	1.0e-127
Match length	536
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	131689
Contig ID	61892_1.R1010
5'-most EST	jC-atXLIB327431P1e08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	34
E value	3.0e-09
Match length	50
% identity	92
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	131690
Contig ID	61898_1.R1010
5'-most EST	LIB3177-070-P1-K1-E10
Method	BLASTX
NCBI GI	g4680651
BLAST score	221
E value	1.0e-17
Match length	167
% identity	36
NCBI Description	(AF132940) CGI-06 protein [Homo sapiens]

Seq. No.	131691
Contig ID	61900_1.R1010
5'-most EST	LIB3177-070-P1-K1-E12
Method	BLASTN
NCBI GI	g4199934
BLAST score	35
E value	7.0e-10
Match length	663
% identity	55
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	131692
Contig ID	61927_1.R1010
5'-most EST	LIB3177-070-P1-K1-G5
Method	BLASTN
NCBI GI	g4567237
BLAST score	404
E value	0.0e+00
Match length	478
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic

sequence, complete sequence

Seq. No.	131693
Contig ID	61938_1.R1010
5'-most EST	LIB3177-070-P1-K1-H4
Method	BLASTN
NCBI GI	g4220637
BLAST score	576
E value	0.0e+00
Match length	601
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	131694
Contig ID	61965_1.R1010
5'-most EST	LIB3177-071-P1-K1-B8
Method	BLASTX
NCBI GI	g4531434
BLAST score	312
E value	4.0e-42
Match length	137
% identity	67
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	131695
Contig ID	62031_1.R1010
5'-most EST	LIB3177-079-P1-K1-D3
Method	BLASTX
NCBI GI	g2739371
BLAST score	386
E value	2.0e-37
Match length	110
% identity	85
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	131696
Contig ID	62046_1.R1010
5'-most EST	g2757372
Method	BLASTX
NCBI GI	g3915023
BLAST score	868
E value	1.0e-93
Match length	216
% identity	79
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	131697
Contig ID	62069_1.R1010
5'-most EST	LIB3177-077-P1-K1-C3
Method	BLASTN
NCBI GI	g3985954
BLAST score	398
E value	0.0e+00

Match length	512
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No.	131698
Contig ID	62072_1.R1010
5'-most EST	jC-atXLIB327412P3f05a1
Method	BLASTX
NCBI GI	g2924515
BLAST score	295
E value	2.0e-26
Match length	57
% identity	98
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	131699
Contig ID	62081_1.R1010
5'-most EST	LIB35-016-Q1-E1-C10

Seq. No.	131700
Contig ID	62081_2.R1010
5'-most EST	jC-atXLIB327426P3d07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	2.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	131701
Contig ID	62081_3.R1010
5'-most EST	LIB35-047-Q1-E1-G4

Seq. No.	131702
Contig ID	62139_1.R1010
5'-most EST	LIB317-073-P1-K1-B10
Method	BLASTX
NCBI GI	g3218396
BLAST score	256
E value	6.0e-22
Match length	100
% identity	50
NCBI Description	(AL023860) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	131703
Contig ID	62154_1.R1010
5'-most EST	g757570
Method	BLASTX
NCBI GI	g4567269
BLAST score	764
E value	6.0e-90
Match length	178
% identity	99
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	131704
Contig ID	62158_1.R1010
5'-most EST	g507050
Method	BLASTX
NCBI GI	g3335340
BLAST score	399
E value	8.0e-39
Match length	79
% identity	85
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	131705
Contig ID	62185_1.R1010
5'-most EST	LIB3177-081-P1-K1-A7

Seq. No.	131706
Contig ID	62213_1.R1010
5'-most EST	g550256

Seq. No.	131707
Contig ID	62282_1.R1010
5'-most EST	jC-atXLIB327409P2a12a1
Method	BLASTX
NCBI GI	g2213632
BLAST score	158
E value	3.0e-10
Match length	98
% identity	43
NCBI Description	(AC000103) F21J9.24 [Arabidopsis thaliana]

Seq. No.	131708
Contig ID	62285_1.R1010
5'-most EST	LIB3177-096-P1-K1-C8
Method	BLASTN
NCBI GI	g4589440
BLAST score	394
E value	0.0e+00
Match length	442
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	131709
Contig ID	62320_1.R1010
5'-most EST	g1053557
Method	BLASTX
NCBI GI	g3319921
BLAST score	153
E value	1.0e-20
Match length	103
% identity	59
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis]

>gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	131710
Contig ID	62323_1.R1010
5'-most EST	LIB3177-075-P1-K1-E1

Seq. No.	131711
Contig ID	62372_1.R1010
5'-most EST	jC-alXLIB327435P4g06b1
Method	BLASTN
NCBI GI	g4490701
BLAST score	131
E value	5.0e-67
Match length	567
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	131712
Contig ID	62392_1.R1010
5'-most EST	LIB3177-076-P1-K1-B9
Method	BLASTX
NCBI GI	g627424
BLAST score	467
E value	2.0e-46
Match length	185
% identity	48
NCBI Description	dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50kD subunit - human >gi_2135018_pir__S66254 dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50K chain - human

Seq. No.	131713
Contig ID	62399_1.R1010
5'-most EST	LIB3177-076-P1-K1-C5
Method	BLASTN
NCBI GI	g3176694
BLAST score	275
E value	1.0e-153
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131714
Contig ID	62402_1.R1010
5'-most EST	LIB3177-076-P1-K1-C8
Method	BLASTN
NCBI GI	g4006885
BLAST score	143
E value	2.0e-74
Match length	455
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No.	131715
Contig ID	62402_2.R1010
5'-most EST	g2048345
Method	BLASTN
NCBI GI	g4006885
BLAST score	235
E value	1.0e-129
Match length	372
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	131716
Contig ID	62405_1.R1010
5'-most EST	g2596628

Seq. No.	131717
Contig ID	62438_1.R1010
5'-most EST	LIB3177-076-P1-K1-G1
Method	BLASTX
NCBI GI	g3776559
BLAST score	721
E value	2.0e-76
Match length	177
% identity	77
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	131718
Contig ID	62449_1.R1010
5'-most EST	g2580924
Method	BLASTN
NCBI GI	g2264313
BLAST score	117
E value	6.0e-59
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	131719
Contig ID	62449_2.R1010
5'-most EST	g2763434
Method	BLASTN
NCBI GI	g2264313
BLAST score	116
E value	3.0e-58
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	131720

Contig ID	62449_3.R1010
5'-most EST	g3449706
Method	BLASTN
NCBI GI	g2264313
BLAST score	361
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	131721
Contig ID	62456_1.R1010
5'-most EST	LIB35-016-Q1-E1-F2
Method	BLASTN
NCBI GI	g2351067
BLAST score	242
E value	1.0e-133
Match length	425
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	131722
Contig ID	62459_1.R1010
5'-most EST	LIB3177-076-P1-K1-H7

Seq. No.	131723
Contig ID	62478_1.R1010
5'-most EST	g757636
Method	BLASTX
NCBI GI	g3080427
BLAST score	397
E value	2.0e-38
Match length	75
% identity	100
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	131724
Contig ID	62495_1.R1010
5'-most EST	jC-atXLIB327426P2f03b1
Method	BLASTN
NCBI GI	g3449334
BLAST score	369
E value	0.0e+00
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	131725
Contig ID	62525_1.R1010
5'-most EST	jC-atXLIB327427P4b04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	1.0e-27

Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	131726
Contig ID	62525_2.R1010
5'-most EST	g2446083

Seq. No.	131727
Contig ID	62542_1.R1010
5'-most EST	LIB3177-077-P1-K1-H10

Seq. No.	131728
Contig ID	62576_1.R1010
5'-most EST	jC-atXLIB327403P3c10a2
Method	BLASTN
NCBI GI	g4468103
BLAST score	399
E value	0.0e+00
Match length	399
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	131729
Contig ID	62581_1.R1010
5'-most EST	g2762984
Method	BLASTX
NCBI GI	g3420055
BLAST score	662
E value	2.0e-69
Match length	188
% identity	74
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No.	131730
Contig ID	62581_2.R1010
5'-most EST	jC-atXLIB327414P4c11b2
Method	BLASTX
NCBI GI	g2443755
BLAST score	499
E value	2.0e-50
Match length	96
% identity	100
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	131731
Contig ID	62587_1.R1010
5'-most EST	jC-atXmonuni26Dg08a1
Method	BLASTN
NCBI GI	g4678340
BLAST score	219
E value	1.0e-120
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11

(ESSA project)

Seq. No.	131732
Contig ID	62587_2.R1010
5'-most EST	jC-atXLIB327421P3f10b1
Method	BLASTX
NCBI GI	g4678346
BLAST score	399
E value	9.0e-65
Match length	145
% identity	91
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	131733
Contig ID	62587_3.R1010
5'-most EST	LIB35-010-Q1-E1-F2
Method	BLASTX
NCBI GI	g4678346
BLAST score	740
E value	1.0e-78
Match length	185
% identity	78
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	131734
Contig ID	62590_1.R1010
5'-most EST	g947820
Method	BLASTX
NCBI GI	g2281115
BLAST score	224
E value	1.0e-160
Match length	345
% identity	87
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	131735
Contig ID	62604_1.R1010
5'-most EST	g2047916
Method	BLASTN
NCBI GI	g4733953
BLAST score	381
E value	0.0e+00
Match length	485
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	131736
Contig ID	62639_1.R1010
5'-most EST	LIB3177-078-P1-K1-H7
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	5.0e-14
Match length	42
% identity	100

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	131737
Contig ID	62650_1.R1010
5'-most EST	g2749364
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	131738
Contig ID	62650_2.R1010
5'-most EST	g937998

Seq. No.	131739
Contig ID	62656_1.R1010
5'-most EST	g2413253
Method	BLASTX
NCBI GI	g1708577
BLAST score	292
E value	4.0e-26
Match length	67
% identity	69
NCBI Description	TRYPSIN INHIBITOR 2 PRECURSOR (MTI-2) >gi_2129818_pir__S65661 trypsin inhibitor 2 - white mustard >gi_1054853_emb_CAA58994_ (X84208) trypsin inhibitor 2 [Sinapis alba] >gi_2791356_emb_CAA76116_ (Y16190) trypsin inhibitor 2 [Sinapis alba]

Seq. No.	131740
Contig ID	62666_1.R1010
5'-most EST	g2749662
Method	BLASTN
NCBI GI	g3738275
BLAST score	479
E value	0.0e+00
Match length	511
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131741
Contig ID	62676_1.R1010
5'-most EST	g931287

Seq. No.	131742
Contig ID	62700_1.R1010
5'-most EST	g1217163
Method	BLASTN
NCBI GI	g2828186
BLAST score	344
E value	0.0e+00
Match length	404
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	131743
Contig ID	62700_2.R1010
5'-most EST	g1054305
Method	BLASTN
NCBI GI	g2828186
BLAST score	334
E value	0.0e+00
Match length	648
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	131744
Contig ID	62711_1.R1010
5'-most EST	jC-atXP15C107E23T7044a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	3.0e-09
Match length	54
% identity	91
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	131745
Contig ID	62722_1.R1010
5'-most EST	LIB3177-079-P1-K1-H10
Method	BLASTX
NCBI GI	g4263791
BLAST score	491
E value	2.0e-49
Match length	93
% identity	99
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	131746
Contig ID	62729_1.R1010
5'-most EST	g315478
Method	BLASTX
NCBI GI	g3184098
BLAST score	593
E value	2.0e-61
Match length	195
% identity	60
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	131747
Contig ID	62751_1.R1010
5'-most EST	LIB35-006-Q1-E1-F11
Method	BLASTN
NCBI GI	g4691223
BLAST score	165
E value	1.0e-87

Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	131748
Contig ID	62799_1.R1010
5'-most EST	LIB3177-080-P1-K1-H12
Method	BLASTX
NCBI GI	g2914700
BLAST score	759
E value	1.0e-80
Match length	216
% identity	73
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	131749
Contig ID	62814_1.R1010
5'-most EST	g2750058
Method	BLASTN
NCBI GI	g4584387
BLAST score	374
E value	0.0e+00
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	131750
Contig ID	62814_2.R1010
5'-most EST	jC-atXLIB327414P2d03a1
Method	BLASTN
NCBI GI	g4584387
BLAST score	484
E value	0.0e+00
Match length	683
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	131751
Contig ID	62826_1.R1010
5'-most EST	LIB3177-081-P1-K1-B9
Method	BLASTN
NCBI GI	g4585952
BLAST score	490
E value	0.0e+00
Match length	671
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	131752
Contig ID	62839_1.R1010
5'-most EST	LIB3177-096-P1-K1-A6

Seq. No.	131753
Contig ID	62898_1.R1010
5'-most EST	g2576661
Method	BLASTX
NCBI GI	g2213619
BLAST score	82
E value	5.0e-25
Match length	103
% identity	62
NCBI Description	(AC000103) F21J9.14 [Arabidopsis thaliana]

Seq. No.	131754
Contig ID	62904_1.R1010
5'-most EST	LIB3177-082-P1-K1-D9
Method	BLASTN
NCBI GI	g2815519
BLAST score	360
E value	0.0e+00
Match length	428
% identity	96
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	131755
Contig ID	62974_1.R1010
5'-most EST	jC-alXLIB327436P2h05b1
Method	BLASTX
NCBI GI	g2244732
BLAST score	159
E value	1.0e-74
Match length	272
% identity	52
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	131756
Contig ID	62974_3.R1010
5'-most EST	g2748051
Method	BLASTX
NCBI GI	g4490725
BLAST score	225
E value	3.0e-18
Match length	91
% identity	47
NCBI Description	(AL035709) endo-xyloglucan transferase-like protein [Arabidopsis thaliana]

Seq. No.	131757
Contig ID	62975_1.R1010
5'-most EST	LIB3177-083-P1-K1-G1
Method	BLASTX
NCBI GI	g1617270
BLAST score	728
E value	4.0e-77
Match length	152
% identity	91
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	131758
Contig ID	63010_1.R1010
5'-most EST	jC-atXLIB327423P1a06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	131759
Contig ID	63056_1.R1010
5'-most EST	g2748828
Method	BLASTN
NCBI GI	g4314374
BLAST score	333
E value	0.0e+00
Match length	349
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131760
Contig ID	63071_1.R1010
5'-most EST	LIB3177-085-P1-K1-A1
Method	BLASTX
NCBI GI	g3128217
BLAST score	669
E value	2.0e-70
Match length	148
% identity	91
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131761
Contig ID	63076_1.R1010
5'-most EST	g2414000
Method	BLASTN
NCBI GI	g4263762
BLAST score	258
E value	1.0e-143
Match length	523
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131762
Contig ID	63076_3.R1010
5'-most EST	g948011
Method	BLASTX
NCBI GI	g4263771
BLAST score	608
E value	3.0e-63
Match length	145
% identity	90

NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	131763
Contig ID	63088_1.R1010
5'-most EST	LIB35-056-Q1-E2-E7
Method	BLASTX
NCBI GI	g4454452
BLAST score	458
E value	1.0e-45
Match length	106
% identity	83
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	131764
Contig ID	63145_1.R1010
5'-most EST	ARABL1-01-Q1-B2-E2
Method	BLASTX
NCBI GI	g1653506
BLAST score	166
E value	3.0e-11
Match length	119
% identity	34
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	131765
Contig ID	63213_1.R1010
5'-most EST	g2722935

Seq. No.	131766
Contig ID	63222_1.R1010
5'-most EST	LIB3177-086-P1-K1-F5
Method	BLASTN
NCBI GI	g3738275
BLAST score	256
E value	1.0e-142
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131767
Contig ID	63224_1.R1010
5'-most EST	LIB3177-091-P1-K1-F10
Method	BLASTX
NCBI GI	g3287695
BLAST score	407
E value	9.0e-40
Match length	111
% identity	66
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No. 131768
Contig ID 63237_1.R1010
5'-most EST jC-atXP91C247A5T7b1

Seq. No. 131769
Contig ID 63246_1.R1010
5'-most EST LIB3177-086-P1-K1-H7

Seq. No. 131770
Contig ID 63254_1.R1010
5'-most EST LIB3177-087-P1-K1-A3
Method BLASTN
NCBI GI g2760168
BLAST score 288
E value 1.0e-161
Match length 571
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 131771
Contig ID 63254_2.R1010
5'-most EST g2412939
Method BLASTX
NCBI GI g405321
BLAST score 180
E value 4.0e-13
Match length 52
% identity 56
NCBI Description (S63758) metallothionein-I gene transcription activator [mice, L cells, Peptide, 102 aa] [Mus sp.]

Seq. No. 131772
Contig ID 63268_1.R1010
5'-most EST jC-atXP83C241L21T7074d1
Method BLASTX
NCBI GI g1709205
BLAST score 562
E value 9.0e-58
Match length 138
% identity 75
NCBI Description MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL MONOPHOSPHATASE 3) >gi_1098971 (U39059) myo-inositol monophosphatase 3 [Lycopersicon esculentum]

Seq. No. 131773
Contig ID 63272_1.R1010
5'-most EST g2597549
Method BLASTX
NCBI GI g1914685
BLAST score 335
E value 2.0e-31
Match length 85
% identity 78
NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No. 131774

Contig ID	63308_1.R1010
5'-most EST	LIB3177-087-P1-K1-F6
Method	BLASTN
NCBI GI	g3399678
BLAST score	200
E value	1.0e-108
Match length	516
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131775
Contig ID	63316_1.R1010
5'-most EST	jC-atXLIB327427P4f03b2
Method	BLASTX
NCBI GI	g4678923
BLAST score	230
E value	8.0e-19
Match length	86
% identity	53
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	131776
Contig ID	63323_1.R1010
5'-most EST	jC-atXP112C132D23T7d2
Method	BLASTX
NCBI GI	g3868835
BLAST score	229
E value	2.0e-18
Match length	123
% identity	44
NCBI Description	(AB013794) CRHB4 [Ceratopteris richardii]

Seq. No.	131777
Contig ID	63346_1.R1010
5'-most EST	g1269341
Method	BLASTX
NCBI GI	g1431629
BLAST score	317
E value	7.0e-29
Match length	93
% identity	59
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	131778
Contig ID	63379_1.R1010
5'-most EST	g586968
Method	BLASTN
NCBI GI	g12219
BLAST score	73
E value	2.0e-32
Match length	194
% identity	92
NCBI Description	Mustard chloroplast trnk gene for tRNA-Lys(UUU)

Seq. No.	131779
Contig ID	63388_1.R1010

5'-most EST	LIB3177-088-P1-K1-E7
Method	BLASTX
NCBI GI	g2501435
BLAST score	181
E value	4.0e-13
Match length	70
% identity	51
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-20 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2190255_dbj_BAA20375_ (D85545) UcbP4 [Schizosaccharomyces pombe] >gi_4469325_emb_CAB38416_ (AL034564) ubiquitin conjugating enzyme [Schizosaccharomyces pombe]

Seq. No.	131780
Contig ID	63394_1.R1010
5'-most EST	jC-atXP29C138I10T7007d1
Method	BLASTN
NCBI GI	g4691223
BLAST score	253
E value	1.0e-140
Match length	509
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	131781
Contig ID	63394_3.R1010
5'-most EST	g932608
Method	BLASTN
NCBI GI	g4691223
BLAST score	117
E value	6.0e-59
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	131782
Contig ID	63400_1.R1010
5'-most EST	g2758143

Seq. No.	131783
Contig ID	63400_2.R1010
5'-most EST	g2758843

Seq. No.	131784
Contig ID	63410_2.R1010
5'-most EST	LIB3177-088-P1-K1-G5
Method	BLASTN
NCBI GI	g3510343
BLAST score	157
E value	9.0e-83
Match length	493
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	131785
Contig ID	63441_1.R1010
5'-most EST	g2722047
Method	BLASTX
NCBI GI	g2920654
BLAST score	272
E value	5.0e-37
Match length	156
% identity	58
NCBI Description	(AF047697) putative high-pI laccase [Oryza sativa]

Seq. No.	131786
Contig ID	63507_1.R1010
5'-most EST	LIB3177-097-P1-K1-H8
Method	BLASTX
NCBI GI	g4249379
BLAST score	724
E value	6.0e-77
Match length	146
% identity	68
NCBI Description	(AC005966) Strong similarity to gb_X82030 chloroplast RNA binding protein (RNP1) from Phaseolus vulgaris. [Arabidopsis thaliana]

Seq. No.	131787
Contig ID	63511_1.R1010
5'-most EST	LIB3177-089-P1-K1-H7

Seq. No.	131788
Contig ID	63519_1.R1010
5'-most EST	jC-atXLIB327431P1g02a1
Method	BLASTX
NCBI GI	g1617268
BLAST score	778
E value	4.0e-83
Match length	154
% identity	97
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]

Seq. No.	131789
Contig ID	63528_1.R1010
5'-most EST	g755114
Method	BLASTX
NCBI GI	g2213882
BLAST score	462
E value	8.0e-73
Match length	164
% identity	86
NCBI Description	(AF004165) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	131790
Contig ID	63542_1.R1010
5'-most EST	jC-atXP62C202N1T7d2
Method	BLASTX
NCBI GI	g3080371

BLAST score 811
E value 6.0e-87
Match length 149
% identity 99
NCBI Description (AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No. 131791
Contig ID 63568_1.R1010
5'-most EST LIB3177-090-P1-K1-E7
Method BLASTX
NCBI GI g4510389
BLAST score 72
E value 2.0e-62
Match length 184
% identity 69
NCBI Description (AC007017) putative solute carrier protein [Arabidopsis thaliana]

Seq. No. 131792
Contig ID 63586_1.R1010
5'-most EST LIB3177-090-P1-K1-G3
Method BLASTN
NCBI GI g4159706
BLAST score 347
E value 0.0e+00
Match length 470
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No. 131793
Contig ID 63633_1.R1010
5'-most EST g410352
Method BLASTN
NCBI GI g3763915
BLAST score 657
E value 0.0e+00
Match length 1049
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 131794
Contig ID 63653_2.R1010
5'-most EST LIB3177-091-P1-K1-E5
Method BLASTX
NCBI GI g1871181
BLAST score 285
E value 4.0e-25
Match length 137
% identity 54
NCBI Description (U90439) ring zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 131795
Contig ID 63709_1.R1010

5'-most EST	LIB3234-041-P1-K1-E5
Method	BLASTN
NCBI GI	g2337888
BLAST score	228
E value	1.0e-125
Match length	561
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	131796
Contig ID	63734_1.R1010
5'-most EST	g1520806

Seq. No.	131797
Contig ID	63747_1.R1010
5'-most EST	LIB3177-092-P1-K1-F3
Method	BLASTX
NCBI GI	g3036805
BLAST score	152
E value	2.0e-58
Match length	128
% identity	93
NCBI Description	(AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	131798
Contig ID	63784_1.R1010
5'-most EST	jC-atXLIB327417P1a12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	38
E value	1.0e-11
Match length	46
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	131799
Contig ID	63784_2.R1010
5'-most EST	g2393472

Seq. No.	131800
Contig ID	63802_1.R1010
5'-most EST	LIB3177-093-P1-K1-C3

Seq. No.	131801
Contig ID	63806_1.R1010
5'-most EST	jC-atXP40C163B24T7095a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	2.0e-29
Match length	68
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 131802
Contig ID 63806_2.R1010
5'-most EST jC-atXP112C127P22T7a1

Seq. No. 131803
Contig ID 63806_3.R1010
5'-most EST jC-atXP60C198G3T7046d1

Seq. No. 131804
Contig ID 63812_1.R1010
5'-most EST jC-atXP3C82C10T7049a1
Method BLASTX
NCBI GI g3850823
BLAST score 186
E value 2.0e-36
Match length 143
% identity 62
NCBI Description (Y18351) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]

Seq. No. 131805
Contig ID 63812_2.R1010
5'-most EST jC-atXP82CG2B4T7b1
Method BLASTX
NCBI GI g4006898
BLAST score 356
E value 2.0e-33
Match length 139
% identity 99
NCBI Description (Z99708) splicing factor-like protein [Arabidopsis thaliana]

Seq. No. 131806
Contig ID 63812_3.R1010
5'-most EST g2748127
Method BLASTX
NCBI GI g4006898
BLAST score 232
E value 5.0e-19
Match length 54
% identity 83
NCBI Description (Z99708) splicing factor-like protein [Arabidopsis thaliana]

Seq. No. 131807
Contig ID 63812_4.R1010
5'-most EST jC-atXP3C83E8T7066a1
Method BLASTX
NCBI GI g4006898
BLAST score 240
E value 6.0e-20
Match length 126
% identity 54
NCBI Description (Z99708) splicing factor-like protein [Arabidopsis thaliana]

Seq. No. 131808

Contig ID	63855_1.R1010
5'-most EST	LIB3234-017-P1-K1-B6
Method	BLASTX
NCBI GI	g1931655
BLAST score	351
E value	3.0e-33
Match length	70
% identity	100
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	131809
Contig ID	63870_1.R1010
5'-most EST	LIB3234-088-Q1-K1-C11
Method	BLASTX
NCBI GI	g4538923
BLAST score	175
E value	1.0e-12
Match length	48
% identity	71
NCBI Description	(AL049483) predicted protein destination factor [Arabidopsis thaliana]

Seq. No.	131810
Contig ID	63876_1.R1010
5'-most EST	LIB3177-094-P1-K1-A9
Method	BLASTN
NCBI GI	g3643588
BLAST score	577
E value	0.0e+00
Match length	605
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131811
Contig ID	63890_1.R1010
5'-most EST	jC-atX25021Q1E1E06b1
Method	BLASTX
NCBI GI	g2393775
BLAST score	286
E value	2.0e-25
Match length	58
% identity	81
NCBI Description	(U82230) prolamin box binding factor [Zea mays]

Seq. No.	131812
Contig ID	63913_1.R1010
5'-most EST	ARABLI-033-Q1-B1-G8
Method	BLASTX
NCBI GI	g3776578
BLAST score	146
E value	1.0e-22
Match length	134
% identity	45
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	131813
Contig ID	63916_1.R1010
5'-most EST	jC-alXLIB327435P1h08a1
Method	BLASTN
NCBI GI	g4581103
BLAST score	247
E value	1.0e-136
Match length	251
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	131814
Contig ID	63944_1.R1010
5'-most EST	LIB3177-094-P1-K1-G7
Method	BLASTX
NCBI GI	g2244990
BLAST score	320
E value	3.0e-99
Match length	250
% identity	81
NCBI Description	(Z97340) similarity to LIM homeobox protein - Caenorhabditis [Arabidopsis thaliana]

Seq. No.	131815
Contig ID	63974_1.R1010
5'-most EST	g315551

Seq. No.	131816
Contig ID	63975_1.R1010
5'-most EST	LIB3177-095-P1-K1-B8
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	4.0e-11
Match length	65
% identity	89
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	131817
Contig ID	63978_1.R1010
5'-most EST	LIB3177-095-P1-K1-C10
Method	BLASTN
NCBI GI	g3510340
BLAST score	293
E value	1.0e-164
Match length	354
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	131818
Contig ID	63985_1.R1010
5'-most EST	LIB3234-025-P1-K1-D1

Seq. No.	131819
Contig ID	64027_1.R1010

5'-most EST	g2722405
Method	BLASTX
NCBI GI	g4455315
BLAST score	161
E value	2.0e-41
Match length	102
% identity	91
NCBI Description	(AL035528) RNA-binding protein like [Arabidopsis thaliana]

Seq. No.	131820
Contig ID	64053_1.R1010
5'-most EST	LIB3177-096-P1-K1-B2

Seq. No.	131821
Contig ID	64057_1.R1010
5'-most EST	LIB3177-096-P1-K1-B6
Method	BLASTX
NCBI GI	g4097549
BLAST score	305
E value	9.0e-28
Match length	119
% identity	61
NCBI Description	(U64907) ATFP4 [Arabidopsis thaliana]

Seq. No.	131822
Contig ID	64057_2.R1010
5'-most EST	jC-atXP18C115B7T7d2

Seq. No.	131823
Contig ID	64072_1.R1010
5'-most EST	ARABL1-025-Q1-B1-B1
Method	BLASTX
NCBI GI	g4587513
BLAST score	251
E value	2.0e-21
Match length	146
% identity	40
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	131824
Contig ID	64073_1.R1010
5'-most EST	g1215971
Method	BLASTX
NCBI GI	g3892048
BLAST score	388
E value	7.0e-94
Match length	185
% identity	98
NCBI Description	(AC002330) putative tryptophan synthase alpha 1-like protein [Arabidopsis thaliana]

Seq. No.	131825
Contig ID	64090_1.R1010
5'-most EST	g2749683
Method	BLASTX
NCBI GI	g4585995

BLAST score	286
E value	2.0e-25
Match length	85
% identity	73
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	131826
Contig ID	64106_1.R1010
5'-most EST	g1149444
Method	BLASTN
NCBI GI	g246255
BLAST score	65
E value	6.0e-28
Match length	158
% identity	90
NCBI Description	Bcg4-4=acyl carrier protein [Brassica rapa, Genomic, 3898 nt]

Seq. No.	131827
Contig ID	64121_1.R1010
5'-most EST	LIB3177-096-P1-K1-H2
Method	BLASTX
NCBI GI	g1176658
BLAST score	244
E value	3.0e-20
Match length	76
% identity	63
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	131828
Contig ID	64140_1.R1010
5'-most EST	g2723199
Method	BLASTN
NCBI GI	g3510336
BLAST score	325
E value	0.0e+00
Match length	451
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	131829
Contig ID	64143_1.R1010
5'-most EST	g1158840
Method	BLASTN
NCBI GI	g4756963
BLAST score	134
E value	4.0e-69
Match length	472
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	131830
Contig ID	64172_1.R1010

5'-most EST	LIB3177-097-P1-K1-D9
Method	BLASTX
NCBI GI	g4467137
BLAST score	352
E value	9.0e-39
Match length	157
% identity	49
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	131831
Contig ID	64192_1.R1010
5'-most EST	g1041250
Method	BLASTX
NCBI GI	g3980383
BLAST score	440
E value	1.0e-43
Match length	83
% identity	100
NCBI Description	(AC004561) unknown protein [Arabidopsis thaliana]

Seq. No.	131832
Contig ID	64211_1.R1010
5'-most EST	g2749521
Method	BLASTX
NCBI GI	g4455336
BLAST score	170
E value	7.0e-12
Match length	96
% identity	39
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	131833
Contig ID	64211_2.R1010
5'-most EST	jC-atXP50C179D9T7011d1
Method	BLASTX
NCBI GI	g4455336
BLAST score	759
E value	7.0e-81
Match length	163
% identity	91
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	131834
Contig ID	64214_1.R1010
5'-most EST	jC-atXP41C164P13T7d1
Method	BLASTX
NCBI GI	g3560243
BLAST score	254
E value	1.0e-21
Match length	169
% identity	41
NCBI Description	(AL031532) putative hydrolase [Schizosaccharomyces pombe]

Seq. No.	131835
Contig ID	64232_1.R1010

5'-most EST	LIB3177-098-P1-K1-B2
Method	BLASTX
NCBI GI	g4106388
BLAST score	183
E value	1.0e-22
Match length	162
% identity	51
NCBI Description	(AF074849) unknown [Arabidopsis thaliana]

Seq. No.	131836
Contig ID	64233_1.R1010
5'-most EST	jC-atXP35C151L14T7d1

Seq. No.	131837
Contig ID	64241_1.R1010
5'-most EST	LIB3177-098-P1-K1-C11
Method	BLASTX
NCBI GI	g3482975
BLAST score	549
E value	3.0e-56
Match length	147
% identity	79
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	131838
Contig ID	64246_1.R1010
5'-most EST	jC-atXP62C203D16T7d2
Method	BLASTX
NCBI GI	g2244800
BLAST score	639
E value	1.0e-118
Match length	238
% identity	93
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No.	131839
Contig ID	64263_1.R1010
5'-most EST	jC-atXP73CF3A12T7d2
Method	BLASTX
NCBI GI	g629592
BLAST score	516
E value	1.0e-113
Match length	319
% identity	65
NCBI Description	hypothetical protein - rape

Seq. No.	131840
Contig ID	64314_1.R1010
5'-most EST	jC-atXP108C175L24T7085d1

Seq. No.	131841
Contig ID	64314_2.R1010
5'-most EST	g2762614

Seq. No.	131842
Contig ID	64338_1.R1010
5'-most EST	LIB3177-099-P1-K1-C6

Method	BLASTN
NCBI GI	g2088638
BLAST score	410
E value	0.0e+00
Match length	459
% identity	36
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131843
Contig ID	64341_1.R1010
5'-most EST	g2393166
Method	BLASTN
NCBI GI	g2828182
BLAST score	392
E value	0.0e+00
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	131844
Contig ID	64353_1.R1010
5'-most EST	LIB3177-099-P1-K1-E1
Method	BLASTX
NCBI GI	g4164539
BLAST score	202
E value	1.0e-20
Match length	106
% identity	55
NCBI Description	(AF079170) phloem protein [Cucurbita maxima]

Seq. No.	131845
Contig ID	64356_1.R1010
5'-most EST	jC-atXLIB327425P3f09a1
Method	BLASTN
NCBI GI	g3510347
BLAST score	39
E value	2.0e-12
Match length	177
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	131846
Contig ID	64381_1.R1010
5'-most EST	jC-atXLIB327402P1d04a1

Seq. No.	131847
Contig ID	64412_1.R1010
5'-most EST	jC-atXP40C161L14T7d1
Method	BLASTX
NCBI GI	g3914002
BLAST score	65
E value	4.0e-87
Match length	193
% identity	90

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No. 131848
Contig ID 64428_1.R1010
5'-most EST LIB3234-001-P1-K1-D11

Seq. No. 131849
Contig ID 64429_1.R1010
5'-most EST LIB3234-001-P1-K1-D12
Method BLASTX
NCBI GI g2062164
BLAST score 333
E value 6.0e-31
Match length 125
% identity 27
NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No. 131850
Contig ID 64454_1.R1010
5'-most EST jC-atXLIB327406P2b08b1
Method BLASTN
NCBI GI g3047100
BLAST score 438
E value 0.0e+00
Match length 490
% identity 97
NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 131851
Contig ID 64468_1.R1010
5'-most EST LIB3234-001-P1-K1-G8
Method BLASTX
NCBI GI g1931639
BLAST score 185
E value 1.0e-13
Match length 62
% identity 58
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 131852
Contig ID 64495_1.R1010
5'-most EST g17175

Seq. No. 131853
Contig ID 64501_1.R1010
5'-most EST LIB3234-020-P1-K1-G12
Method BLASTN
NCBI GI g12218
BLAST score 258
E value 1.0e-143
Match length 414
% identity 90
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly

Seq. No. 131854

Contig ID	64511_1.R1010
5'-most EST	LIB3234-003-P1-K1-D9
Method	BLASTX
NCBI GI	g4678285
BLAST score	266
E value	6.0e-23
Match length	148
% identity	43
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	131855
Contig ID	64576_1.R1010
5'-most EST	LIB3234-004-P1-K1-C7
Method	BLASTN
NCBI GI	g3128142
BLAST score	392
E value	0.0e+00
Match length	479
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	131856
Contig ID	64603_1.R1010
5'-most EST	LIB3234-004-P1-K1-G3
Method	BLASTN
NCBI GI	g4586098
BLAST score	471
E value	0.0e+00
Match length	706
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	131857
Contig ID	64670_1.R1010
5'-most EST	LIB3234-006-P1-K1-F1
Method	BLASTN
NCBI GI	g3449326
BLAST score	34
E value	1.0e-09
Match length	54
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	131858
Contig ID	64680_1.R1010
5'-most EST	g905815
Method	BLASTX
NCBI GI	g3417425
BLAST score	315
E value	8.0e-29
Match length	102
% identity	58
NCBI Description	(AL031261) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	131859
Contig ID	64712_1.R1010
5'-most EST	g1216060
Method	BLASTN
NCBI GI	g3241916
BLAST score	581
E value	0.0e+00
Match length	593
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	131860
Contig ID	64756_1.R1010
5'-most EST	g735935
Method	BLASTX
NCBI GI	g140551
BLAST score	706
E value	9.0e-75
Match length	151
% identity	90
NCBI Description	HYPOTHETICAL 250 KD PROTEIN (ORF 2131) >gi_81505_pir__S01446 hypothetical protein 2131 - spinach chloroplast >gi_12246_emb_CAA30743_ (X07908) ORF 2131 (AA 1-2131) [Spinacia oleracea]

Seq. No.	131861
Contig ID	64757_1.R1010
5'-most EST	LIB3234-008-P1-K1-F12
Method	BLASTX
NCBI GI	g3063706
BLAST score	345
E value	1.0e-32
Match length	79
% identity	81
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	131862
Contig ID	64758_1.R1010
5'-most EST	LIB3234-008-P1-K1-F2

Seq. No.	131863
Contig ID	64791_1.R1010
5'-most EST	g1268612

Seq. No.	131864
Contig ID	64793_1.R1010
5'-most EST	jC-atXP24C123M4T7047a1
Method	BLASTX
NCBI GI	g4567203
BLAST score	625
E value	4.0e-65
Match length	139
% identity	86
NCBI Description	(AC007168) putative beta-hydroxyacyl-ACP dehydratase [Arabidopsis thaliana]

Seq. No.	131865
Contig ID	64798_1.R1010
5'-most EST	LIB3234-009-P1-K1-B10

Seq. No.	131866
Contig ID	64821_1.R1010
5'-most EST	jC-atXLIB327402P1a06b1
Method	BLASTX
NCBI GI	g3687224
BLAST score	222
E value	5.0e-18
Match length	121
% identity	76
NCBI Description	(AC005169) putative N-acetyl-gamma-glutamyl-phosphate reductase [Arabidopsis thaliana]

Seq. No.	131867
Contig ID	64837_1.R1010
5'-most EST	g406796
Method	BLASTX
NCBI GI	g2245019
BLAST score	642
E value	4.0e-67
Match length	125
% identity	98
NCBI Description	(Z97341) proteinase homolog [Arabidopsis thaliana]

Seq. No.	131868
Contig ID	64862_1.R1010
5'-most EST	LIB3234-010-P1-K1-A12
Method	BLASTX
NCBI GI	g4558556
BLAST score	697
E value	0.0e+00
Match length	454
% identity	100
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	131869
Contig ID	64869_1.R1010
5'-most EST	LIB3234-041-P1-K1-B6
Method	BLASTN
NCBI GI	g3985950
BLAST score	435
E value	0.0e+00
Match length	865
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]

Seq. No.	131870
Contig ID	64891_1.R1010
5'-most EST	LIB3234-010-P1-K1-D12
Method	BLASTX
NCBI GI	g2583111

BLAST score 960
E value 1.0e-104
Match length 189
% identity 97
NCBI Description (AC002387) putative dihydrodipicolinate synthase [Arabidopsis thaliana]

Seq. No. 131871
Contig ID 64900_1.R1010
5'-most EST LIB3234-010-P1-K1-E10
Method BLASTX
NCBI GI g4588001
BLAST score 403
E value 5.0e-39
Match length 163
% identity 57
NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No. 131872
Contig ID 64903_1.R1010
5'-most EST jC-atXLIB327439P3a03b2
Method BLASTN
NCBI GI g1279629
BLAST score 344
E value 0.0e+00
Match length 473
% identity 96
NCBI Description O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA genes

Seq. No. 131873
Contig ID 64911_1.R1010
5'-most EST g2763073
Method BLASTX
NCBI GI g3980412
BLAST score 1190
E value 1.0e-131
Match length 252
% identity 36
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 131874
Contig ID 64928_1.R1010
5'-most EST LIB3234-039-P1-K1-D7
Method BLASTX
NCBI GI g4586053
BLAST score 387
E value 2.0e-37
Match length 170
% identity 49
NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana]

Seq. No. 131875
Contig ID 64961_1.R1010
5'-most EST g1054100
Method BLASTX

NCBI GI	g4505499
BLAST score	311
E value	2.0e-28
Match length	163
% identity	10
NCBI Description	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) >gi_2266994 (U77413) O-linked GlcNAc transferase [Homo sapiens]

Seq. No.	131876
Contig ID	64961_2.R1010
5'-most EST	LIB3234-011-P1-K1-D2
Method	BLASTX
NCBI GI	g2266992
BLAST score	138
E value	4.0e-08
Match length	105
% identity	9
NCBI Description	(U77412) O-linked GlcNAc transferase [Caenorhabditis elegans]

Seq. No.	131877
Contig ID	64966_1.R1010
5'-most EST	g934996
Method	BLASTN
NCBI GI	g2351068
BLAST score	246
E value	1.0e-136
Match length	361
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	131878
Contig ID	64969_1.R1010
5'-most EST	LIB3234-011-P1-K1-E1

Seq. No.	131879
Contig ID	64969_2.R1010
5'-most EST	jC-atXLIB327408P2e04b1

Seq. No.	131880
Contig ID	64970_1.R1010
5'-most EST	g957744
Method	BLASTN
NCBI GI	g2583106
BLAST score	303
E value	1.0e-170
Match length	388
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131881
Contig ID	64983_1.R1010
5'-most EST	jC-atXP118C142N15T7042d2

Method	BLASTX
NCBI GI	g4337195
BLAST score	1104
E value	1.0e-121
Match length	242
% identity	89
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	131882
Contig ID	64983_2.R1010
5'-most EST	g906201
Method	BLASTX
NCBI GI	g4337195
BLAST score	1058
E value	1.0e-115
Match length	205
% identity	100
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	131883
Contig ID	64983_3.R1010
5'-most EST	g2722933
Method	BLASTN
NCBI GI	g4337186
BLAST score	121
E value	2.0e-61
Match length	259
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131884
Contig ID	64984_1.R1010
5'-most EST	LIB3234-011-P1-K1-F6
Method	BLASTX
NCBI GI	g2160144
BLAST score	151
E value	6.0e-10
Match length	63
% identity	43
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	131885
Contig ID	64987_1.R1010
5'-most EST	jC-atXP115C124E17T7048d1
Method	BLASTX
NCBI GI	g4544473
BLAST score	1243
E value	1.0e-137
Match length	267
% identity	87
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	131886
Contig ID	65003_1.R1010
5'-most EST	LIB3234-011-P1-K1-H5

Method	BLASTN
NCBI GI	g2618683
BLAST score	317
E value	1.0e-178
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131887
Contig ID	65026_1.R1010
5'-most EST	LIB3234-015-P1-K1-D5
Method	BLASTN
NCBI GI	g2564049
BLAST score	63
E value	7.0e-27
Match length	131
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	131888
Contig ID	65040_1.R1010
5'-most EST	jC-atXP82CG2E12T7d3
Method	BLASTX
NCBI GI	g3608412
BLAST score	531
E value	5.0e-54
Match length	131
% identity	75
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	131889
Contig ID	65069_1.R1010
5'-most EST	LIB3234-026-Q1-K1-G1

Seq. No.	131890
Contig ID	65099_1.R1010
5'-most EST	g1269066

Seq. No.	131891
Contig ID	65100_1.R1010
5'-most EST	LIB3234-013-P1-K1-B1
Method	BLASTN
NCBI GI	g4678315
BLAST score	398
E value	0.0e+00
Match length	430
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	131892
Contig ID	65110_1.R1010
5'-most EST	LIB3234-013-P1-K1-C1
Method	BLASTN

NCBI GI	g2924257
BLAST score	35
E value	4.0e-10
Match length	55
% identity	91
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	131893
Contig ID	65112_1.R1010
5'-most EST	LIB3234-013-P1-K1-C11
Method	BLASTN
NCBI GI	g3241917
BLAST score	309
E value	1.0e-173
Match length	369
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	131894
Contig ID	65153_1.R1010
5'-most EST	g907251
Method	BLASTN
NCBI GI	g2894591
BLAST score	207
E value	1.0e-112
Match length	583
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	131895
Contig ID	65164_1.R1010
5'-most EST	LIB3234-013-P1-K1-H12
Method	BLASTN
NCBI GI	g166913
BLAST score	192
E value	1.0e-103
Match length	221
% identity	100
NCBI Description	Arabidopsis thaliana alpha-2 tubulin (TUA2) gene, exon and 5' end

Seq. No.	131896
Contig ID	65210_1.R1010
5'-most EST	ARABLI-039-Q1-B1-D6
Method	BLASTX
NCBI GI	g2462931
BLAST score	908
E value	3.0e-98
Match length	179
% identity	94
NCBI Description	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]

Seq. No.	131897
Contig ID	65236_1.R1010

5'-most EST	LIB3234-015-P1-K1-H6
Method	BLASTX
NCBI GI	g3033386
BLAST score	373
E value	7.0e-36
Match length	124
% identity	65
NCBI Description	(AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No.	131898
Contig ID	65250_1.R1010
5'-most EST	LIB3234-016-P1-K1-A5
Method	BLASTX
NCBI GI	g4455342
BLAST score	143
E value	6.0e-09
Match length	29
% identity	100
NCBI Description	(AL035522) O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	131899
Contig ID	65252_1.R1010
5'-most EST	LIB3234-041-P1-K1-B3
Method	BLASTX
NCBI GI	g3249107
BLAST score	484
E value	7.0e-49
Match length	101
% identity	92
NCBI Description	(AC003114) Contains similarity to phloem-specific lectin PP2 gb_Z17331 from Cucubita maxima. [Arabidopsis thaliana]

Seq. No.	131900
Contig ID	65256_1.R1010
5'-most EST	LIB3234-016-P1-K1-B9
Method	BLASTX
NCBI GI	g4056485
BLAST score	150
E value	9.0e-10
Match length	89
% identity	10
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131901
Contig ID	65265_1.R1010
5'-most EST	ARABLI-032-Q1-B1-B2
Method	BLASTX
NCBI GI	g1711513
BLAST score	408
E value	5.0e-40
Match length	85
% identity	99
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54) >gi_515681 (U12127) signal recognition particle 54 kDa subunit [Arabidopsis thaliana]

Seq. No.	131902
Contig ID	65268_1.R1010
5'-most EST	LIB3234-016-P1-K1-C12

Seq. No.	131903
Contig ID	65278_1.R1010
5'-most EST	LIB3234-016-P1-K1-D6

Seq. No.	131904
Contig ID	65291_1.R1010
5'-most EST	g2393702
Method	BLASTX
NCBI GI	g3763932
BLAST score	187
E value	9.0e-14
Match length	67
% identity	61
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	131905
Contig ID	65291_2.R1010
5'-most EST	g905559
Method	BLASTX
NCBI GI	g3763932
BLAST score	612
E value	1.0e-63
Match length	136
% identity	87
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	131906
Contig ID	65300_1.R1010
5'-most EST	LIB3234-043-P1-K1-A1
Method	BLASTN
NCBI GI	g2088638
BLAST score	238
E value	1.0e-131
Match length	648
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131907
Contig ID	65331_1.R1010
5'-most EST	jC-atXP19C111K14T7090a1
Method	BLASTX
NCBI GI	g2801448
BLAST score	542
E value	3.0e-55
Match length	97
% identity	100
NCBI Description	(AF028341) ubiquitin-conjugating enzyme 18 [Arabidopsis thaliana]

Seq. No.	131908
Contig ID	65333_1.R1010
5'-most EST	jC-atXP65C206016T7066d1

Method	BLASTX
NCBI GI	g2244807
BLAST score	612
E value	2.0e-63
Match length	281
% identity	33
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131909
Contig ID	65342_1.R1010
5'-most EST	LIB3234-017-P1-K1-C10

Seq. No.	131910
Contig ID	65366_1.R1010
5'-most EST	LIB3234-075-P1-K1-D11
Method	BLASTN
NCBI GI	g2656026
BLAST score	380
E value	0.0e+00
Match length	526
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	131911
Contig ID	65369_1.R1010
5'-most EST	LIB3234-017-P1-K1-E7
Method	BLASTX
NCBI GI	g4581155
BLAST score	211
E value	6.0e-17
Match length	112
% identity	41
NCBI Description	(AC006919) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	131912
Contig ID	65373_1.R1010
5'-most EST	g93551 4
Method	BLASTN
NCBI GI	g1469227
BLAST score	96
E value	2.0e-46
Match length	224
% identity	86
NCBI Description	B.oleracea mRNA for hypothetical protein

Seq. No.	131913
Contig ID	65374_1.R1010
5'-most EST	LIB3234-043-P1-K1-G8
Method	BLASTN
NCBI GI	g3985955
BLAST score	329
E value	0.0e+00
Match length	396
% identity	78
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	131914
Contig ID	65428_1.R1010
5'-most EST	g2596867
Method	BLASTX
NCBI GI	g3834307
BLAST score	590
E value	4.0e-79
Match length	148
% identity	99
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	131915
Contig ID	65485_1.R1010
5'-most EST	LIB3234-019-P1-K1-H8
Method	BLASTX
NCBI GI	g4539348
BLAST score	291
E value	5.0e-52
Match length	138
% identity	83
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	131916
Contig ID	65486_1.R1010
5'-most EST	jC-alXLIB327434P4d09a1
Method	BLASTX
NCBI GI	g4204263
BLAST score	350
E value	7.0e-33
Match length	105
% identity	68
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	131917
Contig ID	65499_1.R1010
5'-most EST	LIB3234-078-P1-K1-B10
Method	BLASTX
NCBI GI	g2832707
BLAST score	479
E value	3.0e-48
Match length	96
% identity	99
NCBI Description	(AL021713) translation initiation factor eIF-2 gamma chain-like protein [Arabidopsis thaliana]

Seq. No.	131918
Contig ID	65504_1.R1010
5'-most EST	LIB3234-020-P1-K1-D10

Seq. No.	131919
Contig ID	65509_1.R1010
5'-most EST	LIB3234-020-P1-K1-D12
Method	BLASTN

NCBI GI g4580745
BLAST score 114
E value 4.0e-57
Match length 490
% identity 96
NCBI Description Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No. 131920
Contig ID 65510_1.R1010
5'-most EST LIB3234-020-P1-K1-D2
Method BLASTX
NCBI GI g631291
BLAST score 383
E value 5.0e-37
Match length 91
% identity 87
NCBI Description MAP kinase-activated protein kinase 2 - human >gi_407075_emb_CAA53094_ (X75346) MAP kinase activated protein kinase-2 [Homo sapiens]

Seq. No. 131921
Contig ID 65551_1.R1010
5'-most EST LIB3234-021-P1-K1-C11
Method BLASTX
NCBI GI g4510348
BLAST score 446
E value 3.0e-44
Match length 160
% identity 54
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 131922
Contig ID 65573_1.R1010
5'-most EST LIB3234-021-P1-K1-F6
Method BLASTN
NCBI GI g4580745
BLAST score 912
E value 0.0e+00
Match length 933
% identity 99
NCBI Description Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No. 131923
Contig ID 65576_1.R1010
5'-most EST g2757817

Seq. No. 131924
Contig ID 65592_1.R1010
5'-most EST jC-atXLIB327432P4f08a1
Method BLASTX
NCBI GI g4587680
BLAST score 237
E value 1.0e-29
Match length 107
% identity 64

NCBI Description	(AC007197) putative cytochrome p450 [Arabidopsis thaliana]
Seq. No.	131925
Contig ID	65602_1.R1010
5'-most EST	LIB3234-022-P1-K1-C11
Method	BLASTN
NCBI GI	g4589434
BLAST score	441
E value	0.0e+00
Match length	503
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence
Seq. No.	131926
Contig ID	65616_1.R1010
5'-most EST	jC-alX25046Q1E1D10b1
Seq. No.	131927
Contig ID	65631_1.R1010
5'-most EST	jC-atXP43C170D10T7045d1
Method	BLASTN
NCBI GI	g4760411
BLAST score	408
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence
Seq. No.	131928
Contig ID	65631_2.R1010
5'-most EST	jC-atXL1041Q1E1B01b1
Method	BLASTX
NCBI GI	g3367524
BLAST score	93
E value	2.0e-26
Match length	129
% identity	62
NCBI Description	(AC004392) F8K4.12 [Arabidopsis thaliana]
Seq. No.	131929
Contig ID	65637_1.R1010
5'-most EST	LIB3234-025-P1-K1-A11
Seq. No.	131930
Contig ID	65641_1.R1010
5'-most EST	LIB3234-025-P1-K1-A4
Method	BLASTX
NCBI GI	g4468813
BLAST score	281
E value	1.0e-24
Match length	111
% identity	51
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]
Seq. No.	131931

Contig ID	65661_1.R1010
5'-most EST	jC-atXLIB327405P1e04a2
Method	BLASTX
NCBI GI	g3522950
BLAST score	222
E value	5.0e-18
Match length	41
% identity	98
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	131932
Contig ID	65716_1.R1010
5'-most EST	LIB3234-026-Q1-K1-A2
Method	BLASTX
NCBI GI	g112305
BLAST score	67
E value	4.0e-13
Match length	136
% identity	38
NCBI Description	small nuclear ribonucleoprotein-associated protein N - rat >gi_206694 (J05497) snRNP-associated polypeptide N [Rattus norvegicus]

Seq. No.	131933
Contig ID	65720_1.R1010
5'-most EST	jC-atXLIB327413P2g01a1

Seq. No.	131934
Contig ID	65755_1.R1010
5'-most EST	LIB3234-055-P1-K1-E3
Method	BLASTX
NCBI GI	g2493910
BLAST score	713
E value	3.0e-75
Match length	217
% identity	65
NCBI Description	CULLIN HOMOLOG 4B (CUL-4B) >gi_1381150 (U58091) Hs-CUL-4B [Homo sapiens]

Seq. No.	131935
Contig ID	65764_1.R1010
5'-most EST	g755113
Method	BLASTX
NCBI GI	g3894168
BLAST score	146
E value	8.0e-09
Match length	77
% identity	39
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	131936
Contig ID	65789_1.R1010
5'-most EST	LIB3234-030-P1-K1-C7

Seq. No.	131937
Contig ID	65797_1.R1010

5'-most EST	g2758323
Method	BLASTX
NCBI GI	g2342724
BLAST score	592
E value	2.0e-61
Match length	158
% identity	82
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	131938
Contig ID	65821_1.R1010
5'-most EST	g1517319
Method	BLASTX
NCBI GI	g3831463
BLAST score	202
E value	1.0e-15
Match length	50
% identity	84
NCBI Description	(AC005700) unknown protein [Arabidopsis thaliana]

Seq. No.	131939
Contig ID	65821_2.R1010
5'-most EST	g315421
Method	BLASTX
NCBI GI	g3831463
BLAST score	997
E value	1.0e-108
Match length	190
% identity	99
NCBI Description	(AC005700) unknown protein [Arabidopsis thaliana]

Seq. No.	131940
Contig ID	65824_1.R1010
5'-most EST	LIB3234-033-P1-K1-F10

Seq. No.	131941
Contig ID	65856_1.R1010
5'-most EST	g398650
Method	BLASTX
NCBI GI	g2914703
BLAST score	204
E value	8.0e-16
Match length	193
% identity	64
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	131942
Contig ID	65857_1.R1010
5'-most EST	jC-atXLIB327408P2g08a1

Seq. No.	131943
Contig ID	65906_1.R1010
5'-most EST	g931124
Method	BLASTN
NCBI GI	g4467094
BLAST score	403
E value	0.0e+00

Match length 427
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No. 131944
Contig ID 65906_2.R1010
5'-most EST g2762709
Method BLASTN
NCBI GI g4467094
BLAST score 487
E value 0.0e+00
Match length 507
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No. 131945
Contig ID 65911_1.R1010
5'-most EST LIB3234-038-P1-K1-C3
Method BLASTX
NCBI GI g4507857
BLAST score 137
E value 5.0e-21
Match length 281
% identity 32
NCBI Description Herpes virus-associated ubiquitin-specific protease >gi_2501460_sp_Q93009_UBPH_HUMAN PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952_emb_CAA96580_ (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]

Seq. No. 131946
Contig ID 65911_2.R1010
5'-most EST g3983l0

Seq. No. 131947
Contig ID 65913_1.R1010
5'-most EST LIB3234-038-P1-K1-C6

Seq. No. 131948
Contig ID 65921_1.R1010
5'-most EST g9580l3
Method BLASTX
NCBI GI g4467132
BLAST score 928
E value 1.0e-100
Match length 219
% identity 82
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 131949
Contig ID 65927_1.R1010
5'-most EST g906040

Seq. No. 131950
Contig ID 65943_1.R1010
5'-most EST LIB3234-038-P1-K1-G1

Seq. No. 131951
Contig ID 65956_1.R1010
5'-most EST jC-a1X25048Q1E1C03a1
Method BLASTX
NCBI GI g3980417
BLAST score 68
E value 2.9e+00
Match length 52
% identity 11
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 131952
Contig ID 65985_1.R1010
5'-most EST LIB3234-039-P1-K1-C8
Method BLASTN
NCBI GI g4559375
BLAST score 279
E value 1.0e-156
Match length 346
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No. 131953
Contig ID 65995_1.R1010
5'-most EST jC-atXLIB327413P2d08a1
Method BLASTX
NCBI GI g3142294
BLAST score 528
E value 8.0e-54
Match length 110
% identity 96
NCBI Description (AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No. 131954
Contig ID 66014_1.R1010
5'-most EST g2445932
Method BLASTX
NCBI GI g485514
BLAST score 369
E value 5.0e-35
Match length 85
% identity 75
NCBI Description ADR11-2 protein - soybean (fragment) >gi_296443_emb_CAA49341_ (X69640) auxin down regulated [Glycine max]

Seq. No. 131955
Contig ID 66027_1.R1010
5'-most EST g935352

Method	BLASTX
NCBI GI	g3776559
BLAST score	308
E value	2.0e-33
Match length	131
% identity	60
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	131956
Contig ID	66050_1.R1010
5'-most EST	LIB3234-059-P1-K1-B9

Seq. No.	131957
Contig ID	66089_1.R1010
5'-most EST	jC-atXP118C155K3T7024d2

Seq. No.	131958
Contig ID	66120_1.R1010
5'-most EST	LIB3234-041-P1-K1-A9
Method	BLASTX
NCBI GI	g3738288
BLAST score	802
E value	5.0e-86
Match length	158
% identity	95
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	131959
Contig ID	66121_1.R1010
5'-most EST	g2748821

Seq. No.	131960
Contig ID	66138_1.R1010
5'-most EST	jC-atXP11C97F18T7009d1
Method	BLASTX
NCBI GI	g585922
BLAST score	614
E value	9.0e-64
Match length	175
% identity	67
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

Seq. No.	131961
Contig ID	66138_2.R1010
5'-most EST	g2048891
Method	BLASTX
NCBI GI	g2924258
BLAST score	547
E value	5.0e-56
Match length	135
% identity	73
NCBI Description	(Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No.	131962
Contig ID	66170_1.R1010
5'-most EST	LIB3234-041-P1-K1-G11
Method	BLASTN
NCBI GI	g4220510
BLAST score	331
E value	0.0e+00
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	131963
Contig ID	66185_1.R1010
5'-most EST	jC-atX35023Q1E1F11b1
Method	BLASTN
NCBI GI	g4079614
BLAST score	406
E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131964
Contig ID	66186_1.R1010
5'-most EST	g905867
Method	BLASTX
NCBI GI	g3522943
BLAST score	418
E value	5.0e-41
Match length	127
% identity	31
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	131965
Contig ID	66194_1.R1010
5'-most EST	LIB3234-043-P1-K1-A6

Seq. No.	131966
Contig ID	66239_1.R1010
5'-most EST	LIB3234-055-P1-K1-C9
Method	BLASTN
NCBI GI	g4309747
BLAST score	372
E value	0.0e+00
Match length	392
% identity	40
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131967
Contig ID	66246_1.R1010
5'-most EST	g958164
Method	BLASTX
NCBI GI	g3785999
BLAST score	405

E value	2.0e-39
Match length	93
% identity	82
NCBI Description	(AC005499) putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	131968
Contig ID	66256_1.R1010
5'-most EST	g870889
Method	BLASTX
NCBI GI	g1814424
BLAST score	167
E value	1.0e-11
Match length	44
% identity	66
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No.	131969
Contig ID	66263_2.R1010
5'-most EST	LIB3234-046-P1-K1-B3

Seq. No.	131970
Contig ID	66276_1.R1010
5'-most EST	g416446

Seq. No.	131971
Contig ID	66323_1.R1010
5'-most EST	LIB3234-046-P1-K1-G7
Method	BLASTN
NCBI GI	g3659491
BLAST score	422
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	131972
Contig ID	66328_1.R1010
5'-most EST	LIB3234-046-P1-K1-H11
Method	BLASTN
NCBI GI	g3449327
BLAST score	335
E value	0.0e+00
Match length	454
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	131973
Contig ID	66335_1.R1010
5'-most EST	LIB3234-046-P1-K1-H7

Seq. No.	131974
Contig ID	66361_1.R1010
5'-most EST	LIB3234-047-P1-K1-C10
Method	BLASTX

NCBI GI	g1216389
BLAST score	140
E value	2.0e-58
Match length	114
% identity	99
NCBI Description	(U39289) myrosinase-associated protein [Brassica napus] >gi_1589009_prf__2209432A myrosinase-associated protein:ISOTYPE=5 [Brassica napus]

Seq. No.	131975
Contig ID	66363_1.R1010
5'-most EST	LIB3234-048-P1-K1-G3
Method	BLASTX
NCBI GI	g167134
BLAST score	581
E value	7.0e-60
Match length	230
% identity	49
NCBI Description	(M16860) cruciferin precursor [Brassica napus]

Seq. No.	131976
Contig ID	66440_1.R1010
5'-most EST	LIB3234-048-P1-K1-E6
Method	BLASTX
NCBI GI	g266693
BLAST score	669
E value	3.0e-70
Match length	175
% identity	79
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	131977
Contig ID	66462_1.R1010
5'-most EST	LIB3234-048-P1-K1-D6
Method	BLASTN
NCBI GI	g4558674
BLAST score	166
E value	4.0e-88
Match length	401
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7B19 genomic sequence, complete sequence

Seq. No.	131978
Contig ID	66487_1.R1010
5'-most EST	g936609
Method	BLASTN
NCBI GI	g2564044
BLAST score	139
E value	4.0e-72
Match length	390
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	131979
Contig ID	66520_1.R1010
5'-most EST	LIB3234-049-P1-K1-A9
Method	BLASTN
NCBI GI	g12235
BLAST score	46
E value	1.0e-16
Match length	74
% identity	91
NCBI Description	S.cereale chloroplast ribosomal protein S15 (rpS15) gene in inverted repeat I (IR-I), complete cds

Seq. No.	131980
Contig ID	66524_1.R1010
5'-most EST	g2757936
Method	BLASTX
NCBI GI	g2583131
BLAST score	161
E value	2.0e-24
Match length	176
% identity	44
NCBI Description	(AC002387) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	131981
Contig ID	66562_1.R1010
5'-most EST	g410354

Seq. No.	131982
Contig ID	66570_1.R1010
5'-most EST	LIB3234-053-P1-K1-G9
Method	BLASTN
NCBI GI	g2914688
BLAST score	351
E value	0.0e+00
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131983
Contig ID	66576_1.R1010
5'-most EST	LIB3234-049-P1-K1-G4
Method	BLASTX
NCBI GI	g3445207
BLAST score	678
E value	2.0e-71
Match length	150
% identity	85
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	131984
Contig ID	66580_1.R1010
5'-most EST	g453899
Method	BLASTX
NCBI GI	g3335169
BLAST score	340

E value	6.0e-32
Match length	65
% identity	95
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	131985
Contig ID	66583_1.R1010
5'-most EST	g2048725

Seq. No.	131986
Contig ID	66599_1.R1010
5'-most EST	LIB3234-050-P1-K1-A9
Method	BLASTX
NCBI GI	g3123209
BLAST score	554
E value	1.0e-67
Match length	233
% identity	58
NCBI Description	ELONGATION FACTOR G, MITOCHONDRIAL 1 PRECURSOR (MEF-G-1) >gi_2119928_pir__S61642 translation elongation factor G, mitochondrial - yeast (Saccharomyces cerevisiae) >gi_1181289_emb_CAA64315_ (X94607) Mef1 protein [Saccharomyces cerevisiae] >gi_1360422_emb_CAA97626_ (Z73241) ORF YLR069c [Saccharomyces cerevisiae]

Seq. No.	131987
Contig ID	66617_1.R1010
5'-most EST	LIB3234-050-P1-K1-D1
Method	BLASTN
NCBI GI	g4455348
BLAST score	437
E value	0.0e+00
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	131988
Contig ID	66632_1.R1010
5'-most EST	jC-atXLIB327415P4c02a1
Method	BLASTX
NCBI GI	g4539321
BLAST score	156
E value	4.0e-10
Match length	57
% identity	46
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	131989
Contig ID	66638_1.R1010
5'-most EST	g905918

Seq. No.	131990
Contig ID	66690_1.R1010
5'-most EST	jC-atXLIB327410P1a08a1

Method	BLASTX
NCBI GI	g3176709
BLAST score	187
E value	1.0e-13
Match length	72
% identity	44
NCBI Description	(AC002392) putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana]

Seq. No.	131991
Contig ID	66696_1.R1010
5'-most EST	jC-atXLIB327422P4e11a1
Method	BLASTX
NCBI GI	g2160138
BLAST score	717
E value	9.0e-76
Match length	151
% identity	49
NCBI Description	(AC000375) No definition line found [Arabidopsis thaliana]

Seq. No.	131992
Contig ID	66699_1.R1010
5'-most EST	LIB3234-076-P1-K1-G9

Seq. No.	131993
Contig ID	66725_1.R1010
5'-most EST	LIB3234-052-P1-K1-F11
Method	BLASTX
NCBI GI	g3377517
BLAST score	225
E value	2.0e-18
Match length	90
% identity	43
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	131994
Contig ID	66730_1.R1010
5'-most EST	jC-atXP86CG9F12T7b1
Method	BLASTN
NCBI GI	g4454447
BLAST score	191
E value	1.0e-103
Match length	609
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	131995
Contig ID	66744_1.R1010
5'-most EST	g204864 3

Seq. No.	131996
Contig ID	66799_1.R1010
5'-most EST	g638612

Seq. No.	131997

Contig ID	66808_1.R1010
5'-most EST	LIB3234-053-P1-K1-F2
Method	BLASTX
NCBI GI	g4758634
BLAST score	158
E value	3.0e-26
Match length	146
% identity	39
NCBI Description	Sec24p, S. Cerevisiae, homolog of >gi_1723050_sp_P53992_YO79_HUMAN HYPOTHETICAL PROTEIN KIAA0079 (HA3543) >gi_559717_dbj_BAA07558_ (D38555) The ha3543 gene product is related to S.cerevisiae protein encoded in chromosome VIII. [Homo sapiens] >gi_4741921_gb_AAD28756.1_ (AF130464) sec24D protein [Homo sapiens]

Seq. No.	131998
Contig ID	66822_1.R1010
5'-most EST	jC-atXP5C90D5T7086a1

Seq. No.	131999
Contig ID	66829_1.R1010
5'-most EST	jC-atXP82CG2C10T7d3

Seq. No.	132000
Contig ID	66843_1.R1010
5'-most EST	g936008
Method	BLASTX
NCBI GI	g4468806
BLAST score	453
E value	6.0e-45
Match length	115
% identity	78
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No.	132001
Contig ID	66867_1.R1010
5'-most EST	LIB3234-054-P1-K1-C7
Method	BLASTN
NCBI GI	g3292807
BLAST score	329
E value	0.0e+00
Match length	377
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	132002
Contig ID	66887_1.R1010
5'-most EST	LIB3234-054-P1-K1-E5
Method	BLASTN
NCBI GI	g3695372
BLAST score	278
E value	1.0e-155
Match length	439
% identity	96

NCBI Description	Arabidopsis thaliana BAC F1104
Seq. No.	132003
Contig ID	66895_1.R1010
5'-most EST	jC-atXP71CF1A7T7094d1
Method	BLASTX
NCBI GI	g3925363
BLAST score	304
E value	1.0e-49
Match length	184
% identity	63
NCBI Description	(AF067961) homeodomain protein [Malus domestica]
Seq. No.	132004
Contig ID	66905_1.R1010
5'-most EST	g937506
Seq. No.	132005
Contig ID	66909_1.R1010
5'-most EST	g2747511
Method	BLASTX
NCBI GI	g4033735
BLAST score	176
E value	2.0e-12
Match length	112
% identity	33
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]
Seq. No.	132006
Contig ID	66923_2.R1010
5'-most EST	jC-atXLIB327402P4c02a1
Method	BLASTX
NCBI GI	g4586582
BLAST score	187
E value	5.0e-14
Match length	44
% identity	82
NCBI Description	(AB024995) rab-type small GTP-binding protein [Cicer arietinum]
Seq. No.	132007
Contig ID	66932_1.R1010
5'-most EST	LIB3234-055-P1-K1-A7
Seq. No.	132008
Contig ID	66940_1.R1010
5'-most EST	LIB3234-055-P1-K1-B4
Method	BLASTN
NCBI GI	g4662609
BLAST score	254
E value	1.0e-141
Match length	287
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence
Seq. No.	132009

Contig ID	66961_1.R1010
5'-most EST	jC-atXP53C185C18T7015d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	41
E value	2.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	132010
Contig ID	67007_1.R1010
5'-most EST	LIB3234-056-P1-K1-A3
Method	BLASTN
NCBI GI	g2760164
BLAST score	386
E value	0.0e+00
Match length	394
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	132011
Contig ID	67015_1.R1010
5'-most EST	LIB3234-056-P1-K1-B10
Method	BLASTX
NCBI GI	g3819099
BLAST score	268
E value	1.0e-23
Match length	129
% identity	46
NCBI Description	(AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No.	132012
Contig ID	67029_1.R1010
5'-most EST	LIB3234-056-P1-K1-C12
Method	BLASTN
NCBI GI	g3406034
BLAST score	240
E value	1.0e-132
Match length	682
% identity	96
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	132013
Contig ID	67067_1.R1010
5'-most EST	g507032
Method	BLASTX
NCBI GI	g3080400
BLAST score	796
E value	5.0e-85
Match length	177
% identity	89
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No.	132014
Contig ID	67079_1.R1010
5'-most EST	g1158926
Method	BLASTX
NCBI GI	g4415934
BLAST score	231
E value	2.0e-19
Match length	115
% identity	55
NCBI Description	(AC006418) putative auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	132015
Contig ID	67105_1.R1010
5'-most EST	LIB3234-057-P1-K1-B7
Method	BLASTN
NCBI GI	g4314374
BLAST score	316
E value	1.0e-178
Match length	403
% identity	26
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132016
Contig ID	67123_1.R1010
5'-most EST	LIB3234-057-P1-K1-D4
Method	BLASTX
NCBI GI	g4582446
BLAST score	362
E value	2.0e-34
Match length	124
% identity	65
NCBI Description	(AC007071) putative RING finger protein [Arabidopsis thaliana]

Seq. No.	132017
Contig ID	67133_1.R1010
5'-most EST	g2749407
Method	BLASTX
NCBI GI	g2623303
BLAST score	470
E value	5.0e-47
Match length	92
% identity	95
NCBI Description	(AC002409) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	132018
Contig ID	67133_2.R1010
5'-most EST	g2597798
Method	BLASTX
NCBI GI	g2623303
BLAST score	253
E value	2.0e-21
Match length	230

% identity	67
NCBI Description	(AC002409) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	132019
Contig ID	67240_1.R1010
5'-most EST	LIB3234-058-P1-K1-G2
Method	BLASTN
NCBI GI	g4376087
BLAST score	440
E value	0.0e+00
Match length	824
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	132020
Contig ID	67242_1.R1010
5'-most EST	LIB3234-058-P1-K1-G4
Method	BLASTX
NCBI GI	g3548815
BLAST score	1142
E value	1.0e-125
Match length	245
% identity	90
NCBI Description	(AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No.	132021
Contig ID	67258_1.R1010
5'-most EST	g509434
Method	BLASTX
NCBI GI	g3915961
BLAST score	407
E value	2.0e-39
Match length	244
% identity	78
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	132022
Contig ID	67266_1.R1010
5'-most EST	ARABL1-047-Q1-B1-D3
Method	BLASTX
NCBI GI	g2102691
BLAST score	382
E value	1.0e-36
Match length	127
% identity	62
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	132023
Contig ID	67273_1.R1010
5'-most EST	jC-atXP62C203G5T7d2

Seq. No.	132024

Contig ID	67281_1.R1010
5'-most EST	LIB3234-059-P1-K1-C10
Method	BLASTN
NCBI GI	g2264318
BLAST score	374
E value	0.0e+00
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	132025
Contig ID	67296_1.R1010
5'-most EST	jC-atXP121C131M8T7019d1
Method	BLASTX
NCBI GI	g2781348
BLAST score	937
E value	1.0e-101
Match length	198
% identity	93
NCBI Description	(AC003113) F24O1.4 [Arabidopsis thaliana]

Seq. No.	132026
Contig ID	67342_1.R1010
5'-most EST	LIB3234-060-P1-K1-A3
Method	BLASTN
NCBI GI	g3985949
BLAST score	267
E value	1.0e-148
Match length	493
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	132027
Contig ID	67355_1.R1010
5'-most EST	LIB3234-060-P1-K1-C1
Method	BLASTX
NCBI GI	g3128176
BLAST score	281
E value	1.0e-24
Match length	145
% identity	36
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	132028
Contig ID	67366_1.R1010
5'-most EST	LIB3234-060-P1-K1-D10
Method	BLASTN
NCBI GI	g3241923
BLAST score	51
E value	2.0e-19
Match length	88
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	132029
Contig ID	67470_1.R1010
5'-most EST	jC-atXLIB327401P4a02b1
Method	BLASTX
NCBI GI	g3292817
BLAST score	358
E value	8.0e-34
Match length	130
% identity	63
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132030
Contig ID	67470_2.R1010
5'-most EST	LIB3234-065-P1-K1-H10

Seq. No.	132031
Contig ID	67514_1.R1010
5'-most EST	jC-atXLIB327422P3c06b2
Method	BLASTX
NCBI GI	g3548808
BLAST score	672
E value	9.0e-71
Match length	134
% identity	99
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	132032
Contig ID	67522_1.R1010
5'-most EST	jC-atXP52C182O16T7d2
Method	BLASTX
NCBI GI	g3184283
BLAST score	719
E value	4.0e-76
Match length	141
% identity	99
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	132033
Contig ID	67527_1.R1010
5'-most EST	LIB3234-070-P1-K1-G11

Seq. No.	132034
Contig ID	67531_1.R1010
5'-most EST	jC-atXP95CG12G2T7005b1
Method	BLASTN
NCBI GI	g2980787
BLAST score	195
E value	1.0e-105
Match length	478
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	132035
Contig ID	67563_1.R1010
5'-most EST	jC-atXP82CG2E11T7b1

Method	BLASTX
NCBI GI	g3819164
BLAST score	537
E value	1.0e-54
Match length	112
% identity	96
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	132036
Contig ID	67563_2.R1010
5'-most EST	jC-atXLIB327402P1g07a1

Seq. No.	132037
Contig ID	67582_1.R1010
5'-most EST	LIB3234-071-P1-K1-E8

Seq. No.	132038
Contig ID	67588_1.R1010
5'-most EST	jC-atX22081Q1E2D09a1
Method	BLASTX
NCBI GI	g4507131
BLAST score	183
E value	2.0e-13
Match length	41
% identity	80
NCBI Description	small nuclear ribonucleoprotein polypeptide F >gi_1085384_pir__S55053 Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm protein F [Homo sapiens]

Seq. No.	132039
Contig ID	67598_1.R1010
5'-most EST	LIB3234-072-P1-K1-H6
Method	BLASTN
NCBI GI	g4753195
BLAST score	327
E value	0.0e+00
Match length	379
% identity	90
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	132040
Contig ID	67628_1.R1010
5'-most EST	jC-atXLIB327423P1a08a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132041
Contig ID	67631_1.R1010
5'-most EST	LIB3234-072-P1-K1-E11

Method	BLASTX
NCBI GI	g4263722
BLAST score	184
E value	9.0e-29
Match length	78
% identity	87
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	132042
Contig ID	67672_1.R1010
5'-most EST	LIB3234-087-Q1-K1-E1
Method	BLASTX
NCBI GI	g3445209
BLAST score	406
E value	1.0e-39
Match length	101
% identity	71
NCBI Description	(AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	132043
Contig ID	67677_1.R1010
5'-most EST	LIB3234-074-P1-K1-B9
Method	BLASTN
NCBI GI	g3169169
BLAST score	63
E value	7.0e-27
Match length	160
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132044
Contig ID	67682_1.R1010
5'-most EST	g937139
Method	BLASTN
NCBI GI	g2828185
BLAST score	447
E value	0.0e+00
Match length	690
% identity	53
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	132045
Contig ID	67694_1.R1010
5'-most EST	LIB3234-074-P1-K1-D10
Method	BLASTN
NCBI GI	g4220645
BLAST score	352
E value	0.0e+00
Match length	376
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 132046

Contig ID 67712_1.R1010
5'-most EST LIB3234-074-P1-K1-F11
Method BLASTX
NCBI GI g3643595
BLAST score 364
E value 5.0e-35
Match length 100
% identity 76
NCBI Description (AC005395) putative oleosin protein [Arabidopsis thaliana]

Seq. No. 132047
Contig ID 67781_1.R1010
5'-most EST LIB3234-075-P1-K1-E10

Seq. No. 132048
Contig ID 67796_1.R1010
5'-most EST LIB3234-075-P1-K1-F6
Method BLASTX
NCBI GI g3128172
BLAST score 526
E value 8.0e-54
Match length 112
% identity 95
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 132049
Contig ID 67804_1.R1010
5'-most EST g1269392
Method BLASTX
NCBI GI g2062169
BLAST score 630
E value 1.0e-65
Match length 153
% identity 36
NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No. 132050
Contig ID 67841_1.R1010
5'-most EST LIB3234-076-P1-K1-E4

Seq. No. 132051
Contig ID 67889_1.R1010
5'-most EST ARABL1-031-Q1-B1-F5
Method BLASTX
NCBI GI g2829918
BLAST score 641
E value 3.0e-67
Match length 127
% identity 98
NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 132052
Contig ID 67894_1.R1010
5'-most EST LIB3234-077-P1-K1-B11

Seq. No.	132053
Contig ID	67921_1.R1010
5'-most EST	LIB3234-077-P1-K1-D8
Method	BLASTN
NCBI GI	g2564047
BLAST score	344
E value	0.0e+00
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	132054
Contig ID	67948_1.R1010
5'-most EST	LIB3234-077-P1-K1-G3

Seq. No.	132055
Contig ID	68003_1.R1010
5'-most EST	LIB3234-078-P1-K1-E2

Seq. No.	132056
Contig ID	68030_1.R1010
5'-most EST	LIB3234-078-P1-K1-H1
Method	BLASTX
NCBI GI	g2244905
BLAST score	503
E value	4.0e-51
Match length	128
% identity	75
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	132057
Contig ID	68031_1.R1010
5'-most EST	LIB3234-078-P1-K1-H5
Method	BLASTN
NCBI GI	g1707006
BLAST score	171
E value	2.0e-91
Match length	248
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132058
Contig ID	68111_1.R1010
5'-most EST	jC-atXLIB327427P3g12a2
Method	BLASTN
NCBI GI	g4756963
BLAST score	505
E value	0.0e+00
Match length	1086
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No. 132059

Contig ID	68120_1.R1010
5'-most EST	LIB3234-080-P1-K1-B3
Method	BLASTN
NCBI GI	g3445196
BLAST score	187
E value	1.0e-101
Match length	291
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132060
Contig ID	68127_1.R1010
5'-most EST	LIB3234-080-P1-K1-B1
Method	BLASTN
NCBI GI	g2564047
BLAST score	82
E value	3.0e-38
Match length	358
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	132061
Contig ID	68131_1.R1010
5'-most EST	jC-atX25003Q1E1A09a1
Method	BLASTX
NCBI GI	g3540196
BLAST score	628
E value	1.0e-65
Match length	125
% identity	99
NCBI Description	(AC004260) Putative amp-binding protein [Arabidopsis thaliana]

Seq. No.	132062
Contig ID	68144_1.R1010
5'-most EST	LIB3234-080-P1-K1-C4
Method	BLASTN
NCBI GI	g4572664
BLAST score	201
E value	1.0e-109
Match length	362
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	132063
Contig ID	68194_1.R1010
5'-most EST	LIB3234-080-P1-K1-H5

Seq. No.	132064
Contig ID	68239_1.R1010
5'-most EST	g935296

Seq. No.	132065
Contig ID	68242_1.R1010

5'-most EST	jC-atXP110CG3H6T7038a1
Method	BLASTX
NCBI GI	g3885328
BLAST score	250
E value	5.0e-21
Match length	78
% identity	63
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	132066
Contig ID	68245_1.R1010
5'-most EST	LIB3234-081-Q1-K1-E5

Seq. No.	132067
Contig ID	68264_1.R1010
5'-most EST	LIB3234-081-Q1-K1-G9
Method	BLASTX
NCBI GI	g3805845
BLAST score	1242
E value	1.0e-167
Match length	327
% identity	93
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	132068
Contig ID	68384_2.R1010
5'-most EST	LIB3234-083-Q1-K1-E12
Method	BLASTX
NCBI GI	g2323410
BLAST score	367
E value	1.0e-34
Match length	137
% identity	49
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	132069
Contig ID	68406_1.R1010
5'-most EST	g406805
Method	BLASTN
NCBI GI	g2264312
BLAST score	274
E value	1.0e-152
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	132070
Contig ID	68437_1.R1010
5'-most EST	LIB3234-084-Q1-K1-D10
Method	BLASTX
NCBI GI	g2494121
BLAST score	538
E value	4.0e-55
Match length	118
% identity	86

NCBI Description	(AC002376) Strong similarity to Triticum ABA induced membrane protein (gb_U80037). EST gb_Z27032 comes from this gene. [Arabidopsis thaliana]

Seq. No.	132071
Contig ID	68449_1.R1010
5'-most EST	g16839
Method	BLASTX
NCBI GI	g2618686
BLAST score	257
E value	8.0e-22
Match length	101
% identity	46
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132072
Contig ID	68491_1.R1010
5'-most EST	jC-atXLIB327431P2d06a1
Method	BLASTX
NCBI GI	g4580471
BLAST score	240
E value	5.0e-20
Match length	160
% identity	35
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	132073
Contig ID	68493_1.R1010
5'-most EST	LIB3234-085-Q1-K1-B1
Method	BLASTX
NCBI GI	g2447107
BLAST score	215
E value	3.0e-17
Match length	119
% identity	37
NCBI Description	(U42580) A638R [Paramecium bursaria Chlorella virus 1]

Seq. No.	132074
Contig ID	68508_1.R1010
5'-most EST	LIB3234-085-Q1-K1-C12
Method	BLASTN
NCBI GI	g4678371
BLAST score	334
E value	0.0e+00
Match length	372
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	132075
Contig ID	68522_1.R1010
5'-most EST	g2733950
Method	BLASTX
NCBI GI	g1171577
BLAST score	196
E value	4.0e-15
Match length	121

% identity	33
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	132076
Contig ID	68537_1.R1010
5'-most EST	jC-atXLIB327410P3g07a1
Method	BLASTX
NCBI GI	g1931640
BLAST score	381
E value	1.0e-36
Match length	82
% identity	85
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	132077
Contig ID	68544_1.R1010
5'-most EST	jC-atXP119C155P4T7025a1

Seq. No.	132078
Contig ID	68544_2.R1010
5'-most EST	jC-atXP119C156I16T7073a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	6.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132079
Contig ID	68544_3.R1010
5'-most EST	jC-atXLIB327414P3d11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	5.0e-11
Match length	45
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132080
Contig ID	68549_1.R1010
5'-most EST	g2048594

Seq. No.	132081
Contig ID	68549_2.R1010
5'-most EST	g934834
Method	BLASTX
NCBI GI	g4507183
BLAST score	197
E value	7.0e-15
Match length	121
% identity	36
NCBI Description	speckle-type POZ protein >gi_2695708_emb_CAA04199_ (AJ000644) SPOP [Homo sapiens]

Seq. No. 132082
Contig ID 68555_1.R1010
5'-most EST LIB3234-085-Q1-K1-H11

Seq. No. 132083
Contig ID 68562_1.R1010
5'-most EST jC-atXP59C193H24T7d1
Method BLASTX
NCBI GI g2160182
BLAST score 269
E value 3.0e-23
Match length 163
% identity 39
NCBI Description (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No. 132084
Contig ID 68562_2.R1010
5'-most EST LIB3234-086-Q1-K1-A11

Seq. No. 132085
Contig ID 68605_1.R1010
5'-most EST jC-atXLIB327402P1g09a1
Method BLASTN
NCBI GI g2462264
BLAST score 43
E value 9.0e-15
Match length 62
% identity 92
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 132086
Contig ID 68605_2.R1010
5'-most EST g2048419

Seq. No. 132087
Contig ID 68647_1.R1010
5'-most EST LIB3234-091-P1-K1-E8
Method BLASTN
NCBI GI g2358139
BLAST score 359
E value 0.0e+00
Match length 367
% identity 99
NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No. 132088
Contig ID 68656_1.R1010
5'-most EST g1053709

Seq. No. 132089
Contig ID 68662_1.R1010
5'-most EST LIB3234-087-Q1-K1-B7

Seq. No. 132090
Contig ID 68732_1.R1010

5'-most EST	jC-atXLIB327431P4g05a1
Method	BLASTN
NCBI GI	g3172156
BLAST score	536
E value	0.0e+00
Match length	603
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132091
Contig ID	68741_1.R1010
5'-most EST	LIB3234-088-Q1-K1-G12
Method	BLASTX
NCBI GI	g3935152
BLAST score	493
E value	6.0e-50
Match length	112
% identity	76
NCBI Description	(AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No.	132092
Contig ID	68744_1.R1010
5'-most EST	LIB3234-088-Q1-K1-B10

Seq. No.	132093
Contig ID	68796_1.R1010
5'-most EST	LIB3234-088-Q1-K1-G4
Method	BLASTN
NCBI GI	g3449327
BLAST score	143
E value	2.0e-74
Match length	442
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	132094
Contig ID	68832_1.R1010
5'-most EST	ARABL1-042-Q1-B1-H4
Method	BLASTX
NCBI GI	g3913794
BLAST score	628
E value	2.0e-65
Match length	166
% identity	67
NCBI Description	GLUTATHIONE PEROXIDASE 1 >gi_2326453_emb_CAA74775_ (Y14429) glutathione peroxidase [Helianthus annuus]

Seq. No.	132095
Contig ID	68843_1.R1010
5'-most EST	jC-atXL1025Q1B1H10b1
Method	BLASTX
NCBI GI	g12282
BLAST score	291
E value	6.0e-26
Match length	71

% identity	80
NCBI Description	(X01724) unidentified reading frame [Spinacia oleracea] >gi_473512 (M27308) unknown protein [Spinacia oleracea]

Seq. No.	132096
Contig ID	68881_1.R1010
5'-most EST	LIB3234-089-P1-K1-G4
Method	BLASTN
NCBI GI	g3063438
BLAST score	336
E value	0.0e+00
Match length	364
% identity	77
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	132097
Contig ID	68931_1.R1010
5'-most EST	jC-atXP112C132G2T7d2
Method	BLASTX
NCBI GI	g4454480
BLAST score	405
E value	4.0e-39
Match length	121
% identity	59
NCBI Description	(AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No.	132098
Contig ID	68939_1.R1010
5'-most EST	LIB3234-096-P1-K1-A12
Method	BLASTN
NCBI GI	g4699904
BLAST score	132
E value	2.0e-68
Match length	136
% identity	64
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	132099
Contig ID	68940_1.R1010
5'-most EST	LIB3234-090-P1-K1-D8

Seq. No.	132100
Contig ID	68950_1.R1010
5'-most EST	LIB3234-090-P1-K1-E7
Method	BLASTX
NCBI GI	g3643602
BLAST score	477
E value	6.0e-48
Match length	88
% identity	100
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 132101

Contig ID	68978_1.R1010
5'-most EST	LIB3234-090-P1-K1-H7
Method	BLASTX
NCBI GI	g4580521
BLAST score	586
E value	2.0e-60
Match length	112
% identity	100
NCBI Description	(AF036304) scarecrow-like 7 [Arabidopsis thaliana]

Seq. No.	132102
Contig ID	68995_1.R1010
5'-most EST	g2723125
Method	BLASTN
NCBI GI	g2656030
BLAST score	299
E value	1.0e-167
Match length	750
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	132103
Contig ID	69015_1.R1010
5'-most EST	LIB3234-091-P1-K1-D4
Method	BLASTN
NCBI GI	g4127298
BLAST score	37
E value	2.0e-11
Match length	80
% identity	88
NCBI Description	Allium altaicum chloroplast psaA-trnS intergenic spacer, partial sequence (cultivar TAX2760)

Seq. No.	132104
Contig ID	69018_1.R1010
5'-most EST	LIB3234-091-P1-K1-D7
Method	BLASTN
NCBI GI	g2264321
BLAST score	279
E value	1.0e-156
Match length	379
% identity	43
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	132105
Contig ID	69078_1.R1010
5'-most EST	LIB3234-092-P1-K1-B5
Method	BLASTX
NCBI GI	g2244793
BLAST score	245
E value	3.0e-20
Match length	242
% identity	29
NCBI Description	(Z97336) TMV resistance protein homolog [Arabidopsis thaliana]

Seq. No.	132106
Contig ID	69117_1.R1010
5'-most EST	LIB3234-092-P1-K1-F5
Method	BLASTX
NCBI GI	g118926
BLAST score	151
E value	7.0e-10
Match length	61
% identity	52
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	132107
Contig ID	69125_1.R1010
5'-most EST	g2393460
Method	BLASTN
NCBI GI	g4249393
BLAST score	233
E value	1.0e-128
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132108
Contig ID	69144_1.R1010
5'-most EST	LIB3234-096-P1-K1-F6
Method	BLASTN
NCBI GI	g3047088
BLAST score	324
E value	0.0e+00
Match length	637
% identity	100
NCBI Description	Arabidopsis thaliana BAC T26D22

Seq. No.	132109
Contig ID	69163_1.R1010
5'-most EST	jC-atXLIB327431P2b04b1
Method	BLASTN
NCBI GI	g3894156
BLAST score	401
E value	0.0e+00
Match length	433
% identity	65
NCBI Description	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132110
Contig ID	69165_1.R1010
5'-most EST	jC-atXP112C127M10T7d2
Method	BLASTN
NCBI GI	g3269280

BLAST score 256
E value 1.0e-141
Match length 682
% identity 81
NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No. 132111
Contig ID 69226_1.R1010
5'-most EST LIB3234-094-P1-K1-A11

Seq. No. 132112
Contig ID 69275_1.R1010
5'-most EST LIB3234-094-P1-K1-F7
Method BLASTX
NCBI GI g3150415
BLAST score 140
E value 2.0e-49
Match length 122
% identity 80
NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No. 132113
Contig ID 69319_1.R1010
5'-most EST LIB3234-096-P1-K1-C12

Seq. No. 132114
Contig ID 69353_1.R1010
5'-most EST LIB3234-095-P1-K1-F12
Method BLASTX
NCBI GI g4455313
BLAST score 675
E value 4.0e-71
Match length 160
% identity 86
NCBI Description (AL035528) fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]

Seq. No. 132115
Contig ID 69410_2.R1010
5'-most EST LIB3234-096-P1-K1-C5
Method BLASTX
NCBI GI g4580467
BLAST score 418
E value 9.0e-41
Match length 116
% identity 65
NCBI Description (AC006081) putative protein phosphatase; similar to protein phosphatase 2C from Mesembryanthemum [Arabidopsis thaliana]

Seq. No. 132116
Contig ID 69464_1.R1010
5'-most EST g2446181

Seq. No. 132117

Contig ID	69477_1.R1010
5'-most EST	jC-atXLIB327427P3c06b2
Method	BLASTX
NCBI GI	g3860272
BLAST score	1184
E value	1.0e-130
Match length	229
% identity	99
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	132118
Contig ID	69520_1.R1010
5'-most EST	jC-alXLIB327434P1d02a1

Seq. No.	132119
Contig ID	69521_1.R1010
5'-most EST	LIB3234-097-P1-K1-G1
Method	BLASTX
NCBI GI	g4510348
BLAST score	47
E value	6.0e-94
Match length	187
% identity	87
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	132120
Contig ID	69548_1.R1010
5'-most EST	LIB3234-098-P1-K1-A9
Method	BLASTX
NCBI GI	g462147
BLAST score	79
E value	2.0e-64
Match length	136
% identity	92
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase (EC 5.3.1.9) - Arabidopsis thaliana >gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	132121
Contig ID	69563_1.R1010
5'-most EST	LIB3234-098-P1-K1-C4
Method	BLASTN
NCBI GI	g2618600
BLAST score	77
E value	4.0e-35
Match length	406
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	132122
Contig ID	69646_1.R1010

5'-most EST	jC-atXP121C96P23T7053d1
Method	BLASTX
NCBI GI	g3980413
BLAST score	383
E value	1.0e-36
Match length	81
% identity	39
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	132123
Contig ID	69648_1.R1010
5'-most EST	g1223586
Method	BLASTN
NCBI GI	g3449322
BLAST score	453
E value	0.0e+00
Match length	518
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	132124
Contig ID	69670_1.R1010
5'-most EST	jC-atXLIB327426P3b11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	7.0e-19
Match length	73
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132125
Contig ID	69679_1.R1010
5'-most EST	jC-atXLIB327426P2c03b1
Method	BLASTX
NCBI GI	g3150402
BLAST score	731
E value	2.0e-77
Match length	194
% identity	79
NCBI Description	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]

Seq. No.	132126
Contig ID	69687_1.R1010
5'-most EST	jC-atXmonuni26Bc04b1

Seq. No.	132127
Contig ID	69688_1.R1010
5'-most EST	jC-atXLIB327431P4b05a1
Method	BLASTX
NCBI GI	g4417287
BLAST score	1083
E value	1.0e-119
Match length	214

% identity 94
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 132128
Contig ID 69693_1.R1010
5'-most EST LIB35-043-Q1-E1-H7

Seq. No. 132129
Contig ID 69697_1.R1010
5'-most EST g1520448

Seq. No. 132130
Contig ID 69697_2.R1010
5'-most EST jC-atXP102CE6A5T7b1
Method BLASTN
NCBI GI g2645198
BLAST score 75
E value 1.0e-33
Match length 274
% identity 90
NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 132131
Contig ID 69700_1.R1010
5'-most EST jC-atXmonuni26Cc04b1
Method BLASTN
NCBI GI g3510347
BLAST score 221
E value 1.0e-121
Match length 565
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 132132
Contig ID 69723_1.R1010
5'-most EST jC-atXmonuni26Ad04b1
Method BLASTN
NCBI GI g4263694
BLAST score 216
E value 1.0e-118
Match length 413
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 132133
Contig ID 69724_1.R1010
5'-most EST jC-alX24006Q1E1D01b1
Method BLASTX
NCBI GI g2507198
BLAST score 189
E value 5.0e-14
Match length 156
% identity 35
NCBI Description PROTEIN KINASE CEK1 >gi_1853976_dbj_BAA06551_ (D31773)

protein kinase [Schizosaccharomyces pombe]

Seq. No.	132134
Contig ID	69743_1.R1010
5'-most EST	LIB35-002-Q1-E1-C9

Seq. No.	132135
Contig ID	69751_1.R1010
5'-most EST	jC-atXmonuni26Dc03b1
Method	BLASTN
NCBI GI	g3337347
BLAST score	109
E value	2.0e-54
Match length	258
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132136
Contig ID	69769_1.R1010
5'-most EST	g2758243

Seq. No.	132137
Contig ID	69775_1.R1010
5'-most EST	jC-atXLIB327426P2d04b1
Method	BLASTX
NCBI GI	g4455172
BLAST score	553
E value	2.0e-59
Match length	140
% identity	87
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	132138
Contig ID	69779_1.R1010
5'-most EST	jC-atXLIB327423P1f12b1
Method	BLASTX
NCBI GI	g4585908
BLAST score	788
E value	4.0e-84
Match length	178
% identity	87
NCBI Description	(AC006298) putative lysosomal acid lipase [Arabidopsis thaliana]

Seq. No.	132139
Contig ID	69798_1.R1010
5'-most EST	jC-atX35003Q1E1B09b1
Method	BLASTN
NCBI GI	g3738313
BLAST score	186
E value	1.0e-100
Match length	341
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132140
Contig ID	69802_1.R1010
5'-most EST	LIB35-049-Q1-E1-G9
Method	BLASTN
NCBI GI	g4589412
BLAST score	408
E value	0.0e+00
Match length	598
% identity	50
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	132141
Contig ID	69812_1.R1010
5'-most EST	jC-atXmonuni26Bc07b1
Method	BLASTN
NCBI GI	g2098816
BLAST score	310
E value	1.0e-174
Match length	505
% identity	88
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	132142
Contig ID	69818_1.R1010
5'-most EST	jC-atXP44C168O18T7011a1
Method	BLASTX
NCBI GI	g586099
BLAST score	235
E value	3.0e-19
Match length	115
% identity	40
NCBI Description	THIOREDOXIN H-TYPE 2 (TRX-H2) >gi_486690_pir__S34812 thioredoxin h2 - common tobacco >gi_297519_emb_CAA77847_ (Z11803) THIOREDOXIN [Nicotiana tabacum] >gi_447151_prf__1913431A thioredoxin [Nicotiana tabacum]

Seq. No.	132143
Contig ID	69825_1.R1010
5'-most EST	g2749707
Method	BLASTX
NCBI GI	g1170601
BLAST score	142
E value	1.0e-08
Match length	96
% identity	34
NCBI Description	FRUIT PROTEIN PKIWI502 >gi_1085869_pir__S48036 hypothetical protein - kiwi fruit >gi_450237 (L27809) pKIWI502 [Actinidia deliciosa]

Seq. No.	132144
Contig ID	69841_1.R1010
5'-most EST	jC-atX35003Q1E1G01b1
Method	BLASTX
NCBI GI	g3687244
BLAST score	490
E value	3.0e-49

Match length	118
% identity	85
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	132145
Contig ID	69843_1.R1010
5'-most EST	jC-atXmonuni26Dc09b1
Method	BLASTX
NCBI GI	g4587989
BLAST score	414
E value	3.0e-40
Match length	143
% identity	62
NCBI Description	(AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No.	132146
Contig ID	69843_2.R1010
5'-most EST	jC-atXmonuni26Dc09a1
Method	BLASTN
NCBI GI	g540252
BLAST score	50
E value	6.0e-19
Match length	58
% identity	97
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	132147
Contig ID	69867_1.R1010
5'-most EST	jC-atXLIB327426P4b10a1
Method	BLASTN
NCBI GI	g4006885
BLAST score	194
E value	1.0e-105
Match length	346
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	132148
Contig ID	69867_2.R1010
5'-most EST	jC-atXLIB327426P3b10b1
Method	BLASTN
NCBI GI	g4006885
BLAST score	405
E value	0.0e+00
Match length	542
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	132149
Contig ID	69875_1.R1010
5'-most EST	g2763782
Method	BLASTX
NCBI GI	g1362065

BLAST score 294
E value 2.0e-26
Match length 69
% identity 83
NCBI Description small GTP-binding protein - garden pea
>gi_871506_emb_CAA90081_ (Z49901) small GTP-binding protein
[Pisum sativum]

Seq. No. 132150
Contig ID 69877_1.R1010
5'-most EST jC-atXLIB327426P2c08b1

Seq. No. 132151
Contig ID 69878_1.R1010
5'-most EST jC-atXLIB327426P2c05b1
Method BLASTX
NCBI GI g3289002
BLAST score 171
E value 7.0e-12
Match length 162
% identity 4
NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 132152
Contig ID 69881_1.R1010
5'-most EST jC-atXLIB327430P4b08b1
Method BLASTX
NCBI GI g4581163
BLAST score 630
E value 1.0e-65
Match length 124
% identity 100
NCBI Description (AC006220) unknown protein [Arabidopsis thaliana]

Seq. No. 132153
Contig ID 69884_1.R1010
5'-most EST g2048195
Method BLASTN
NCBI GI g531828
BLAST score 52
E value 4.0e-20
Match length 52
% identity 100
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 132154
Contig ID 69884_2.R1010
5'-most EST jC-atXLIB327426P2c10b1

Seq. No. 132155
Contig ID 69888_1.R1010
5'-most EST LIB35-011-Q1-E1-G6
Method BLASTN
NCBI GI g3241916
BLAST score 354
E value 0.0e+00
Match length 374

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	132156
Contig ID	69893_1.R1010
5'-most EST	LIB35-023-Q1-E1-G3
Method	BLASTN
NCBI GI	g4105695
BLAST score	561
E value	0.0e+00
Match length	625
% identity	98
NCBI Description	Arabidopsis thaliana beta tubulin 1, thaumatin-like protein (TL1), small hydrophobic protein, receptor kinase (CLAVATA1), and antifungal protein (PDF1.1) genes, complete cds

Seq. No.	132157
Contig ID	69902_1.R1010
5'-most EST	LIB35-004-Q1-E1-G6

Seq. No.	132158
Contig ID	69904_1.R1010
5'-most EST	jC-atX35004Q1E1G08b1
Method	BLASTN
NCBI GI	g4757393
BLAST score	228
E value	1.0e-125
Match length	257
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E14, complete sequence

Seq. No.	132159
Contig ID	69916_1.R1010
5'-most EST	jC-atXLIB327426P2d10b1
Method	BLASTN
NCBI GI	g2749918
BLAST score	237
E value	1.0e-130
Match length	516
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132160
Contig ID	69916_2.R1010
5'-most EST	jC-atXmonuni26Bd10a1
Method	BLASTN
NCBI GI	g2749918
BLAST score	327
E value	0.0e+00
Match length	356
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132161
Contig ID	69923_1.R1010
5'-most EST	jC-atXmonuni26Ad09b1
Method	BLASTX
NCBI GI	g4835244
BLAST score	802
E value	1.0e-85
Match length	192
% identity	84
NCBI Description	(AL049862) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	132162
Contig ID	69923_2.R1010
5'-most EST	jC-atXLIB327426P1d09b1
Method	BLASTX
NCBI GI	g4835244
BLAST score	460
E value	1.0e-45
Match length	149
% identity	66
NCBI Description	(AL049862) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	132163
Contig ID	69929_1.R1010
5'-most EST	LIB35-043-Q1-E1-A4
Method	BLASTX
NCBI GI	g2660677
BLAST score	407
E value	8.0e-40
Match length	116
% identity	62
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	132164
Contig ID	69937_1.R1010
5'-most EST	jC-atXmonuni26Cd10b1
Method	BLASTN
NCBI GI	g4582444
BLAST score	310
E value	1.0e-174
Match length	735
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	132165
Contig ID	69944_1.R1010
5'-most EST	jC-atXLIB327426P3d02b1
Method	BLASTN
NCBI GI	g2980757
BLAST score	235
E value	1.0e-129
Match length	414
% identity	98

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)
Seq. No.	132166
Contig ID	69945_1.R1010
5'-most EST	jC-atXLIB327426P2e11b1
Method	BLASTX
NCBI GI	g4469025
BLAST score	292
E value	6.0e-26
Match length	97
% identity	53
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	132167
Contig ID	69949_1.R1010
5'-most EST	g1158956
Seq. No.	132168
Contig ID	69952_1.R1010
5'-most EST	jC-atXLIB327426P2e02b1
Method	BLASTX
NCBI GI	g4204271
BLAST score	768
E value	9.0e-82
Match length	191
% identity	77
NCBI Description	(AC005223) Unknown protein [Arabidopsis thaliana]
Seq. No.	132169
Contig ID	69974_1.R1010
5'-most EST	LIB35-031-Q1-E1-B12
Method	BLASTX
NCBI GI	g3885327
BLAST score	518
E value	7.0e-53
Match length	99
% identity	100
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.	132170
Contig ID	69976_1.R1010
5'-most EST	jC-atXmonuni26Bg08b1
Method	BLASTX
NCBI GI	g3169059
BLAST score	464
E value	2.0e-46
Match length	146
% identity	62
NCBI Description	(AL023704) weak similarity to B.subtilis spore outgrowth factor B [Schizosaccharomyces pombe]
Seq. No.	132171
Contig ID	69993_1.R1010
5'-most EST	jC-atXLIB327426P3d09b1
Method	BLASTN
NCBI GI	g4106527

BLAST score	67
E value	5.0e-29
Match length	128
% identity	54
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	132172
Contig ID	70006_1.R1010
5'-most EST	jC-atXmonuni26De07b1
Method	BLASTX
NCBI GI	g3901294
BLAST score	291
E value	3.0e-26
Match length	105
% identity	51
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	132173
Contig ID	70016_1.R1010
5'-most EST	jC-atXLIB327426P2d08b1
Method	BLASTX
NCBI GI	g2982243
BLAST score	327
E value	4.0e-30
Match length	125
% identity	54
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	132174
Contig ID	70017_1.R1010
5'-most EST	jC-atXLIB327426P2d05b1
Method	BLASTX
NCBI GI	g2499087
BLAST score	655
E value	1.0e-68
Match length	205
% identity	58
NCBI Description	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein glucosyltransferase - fruit fly (Drosophila sp.) >gi_790585 (U20554) UDP-glucose:glycoprotein glucosyltransferase precursor [Drosophila melanogaster]

Seq. No.	132175
Contig ID	70024_1.R1010
5'-most EST	jC-atXLIB327426P2d12b1
Method	BLASTN
NCBI GI	g4218109
BLAST score	131
E value	4.0e-67
Match length	493
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	132176
Contig ID	70024_2.R1010

5'-most EST	jC-atXmonuni26Bd12a1
Method	BLASTN
NCBI GI	g4218109
BLAST score	140
E value	1.0e-72
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	132177
Contig ID	70039_1.R1010
5'-most EST	LIB35-047-Q1-E1-A4
Method	BLASTX
NCBI GI	g132908
BLAST score	144
E value	1.0e-08
Match length	41
% identity	68
NCBI Description	50S RIBOSOMAL PROTEIN L34 >gi_79021_pir__JQ0732 ribosomal protein L34 - Proteus mirabilis >gi_150877 (M58352) ribosomal protein L34 [Proteus mirabilis]

Seq. No.	132178
Contig ID	70040_1.R1010
5'-most EST	jC-atXLIB327426P3d12b1
Method	BLASTX
NCBI GI	g2160185
BLAST score	434
E value	7.0e-43
Match length	121
% identity	59
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	132179
Contig ID	70049_1.R1010
5'-most EST	jC-atXmonuni26Be05b1
Method	BLASTN
NCBI GI	g4218109
BLAST score	255
E value	1.0e-141
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	132180
Contig ID	70059_1.R1010
5'-most EST	LIB35-017-Q1-E1-E10
Method	BLASTX
NCBI GI	g3298546
BLAST score	383
E value	8.0e-37
Match length	116
% identity	67
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 132181
Contig ID 70061_1.R1010
5'-most EST LIB35-053-Q1-E1-H5

Seq. No. 132182
Contig ID 70084_2.R1010
5'-most EST g2445961
Method BLASTX
NCBI GI g4337001
BLAST score 377
E value 4.0e-36
Match length 87
% identity 69
NCBI Description (AF118129) Tsi1-interacting protein TSIP1 [Nicotiana tabacum]

Seq. No. 132183
Contig ID 70084_3.R1010
5'-most EST g957583
Method BLASTN
NCBI GI g4559344
BLAST score 200
E value 1.0e-108
Match length 394
% identity 65
NCBI Description Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No. 132184
Contig ID 70089_1.R1010
5'-most EST jC-atXLIB327426P2d07b1
Method BLASTN
NCBI GI g2337888
BLAST score 181
E value 4.0e-97
Match length 412
% identity 50
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No. 132185
Contig ID 70096_1.R1010
5'-most EST LIB35-008-Q1-E1-B10
Method BLASTX
NCBI GI g3834319
BLAST score 717
E value 4.0e-76
Match length 140
% identity 98
NCBI Description (AC005679) Similar to gi_2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No. 132186
Contig ID 70108_1.R1010
5'-most EST jC-atX35008Q1E1C06b1

Seq. No.	132187
Contig ID	70115_1.R1010
5'-most EST	jC-atXP57C190F24T7004a1
Method	BLASTX
NCBI GI	g3269287
BLAST score	400
E value	7.0e-39
Match length	74
% identity	100
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	132188
Contig ID	70115_2.R1010
5'-most EST	jC-alXLIB327435P1g05b1
Method	BLASTX
NCBI GI	g3269287
BLAST score	386
E value	3.0e-37
Match length	83
% identity	86
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	132189
Contig ID	70124_1.R1010
5'-most EST	LIB35-008-Q1-E1-E5
Method	BLASTX
NCBI GI	g2739385
BLAST score	707
E value	5.0e-75
Match length	134
% identity	99
NCBI Description	(AC002505) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	132190
Contig ID	70128_1.R1010
5'-most EST	jC-atXmonuni26Ae05b1
Method	BLASTX
NCBI GI	g1438881
BLAST score	177
E value	1.0e-26
Match length	123
% identity	50
NCBI Description	(U43839) GmCK2p [Glycine max]

Seq. No.	132191
Contig ID	70136_1.R1010
5'-most EST	jC-atXLIB327426P2e10b1

Seq. No.	132192
Contig ID	70136_2.R1010
5'-most EST	jC-atXmonuni26Be10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21

Match length	66
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132193
Contig ID	70140_1.R1010
5'-most EST	LIB35-008-Q1-E1-G1
Method	BLASTN
NCBI GI	g2924728
BLAST score	315
E value	1.0e-177
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	132194
Contig ID	70158_1.R1010
5'-most EST	LIB35-008-Q1-E1-H6
Method	BLASTN
NCBI GI	g532646
BLAST score	63
E value	9.0e-27
Match length	67
% identity	99
NCBI Description	Santalum album 18S ribosomal RNA gene, partial sequence

Seq. No.	132195
Contig ID	70159_1.R1010
5'-most EST	g2062834
Method	BLASTX
NCBI GI	g3135261
BLAST score	498
E value	3.0e-50
Match length	131
% identity	76
NCBI Description	(AC003058) putative 18.5 KDa class I heat shock protein [Arabidopsis thaliana]

Seq. No.	132196
Contig ID	70159_2.R1010
5'-most EST	LIB35-044-Q1-E1-A4
Method	BLASTX
NCBI GI	g3135261
BLAST score	669
E value	2.0e-70
Match length	125
% identity	100
NCBI Description	(AC003058) putative 18.5 KDa class I heat shock protein [Arabidopsis thaliana]

Seq. No.	132197
Contig ID	70162_1.R1010
5'-most EST	LIB35-009-Q1-E1-A11
Method	BLASTX
NCBI GI	g2245005
BLAST score	371

E value	3.0e-35
Match length	91
% identity	52
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132198
Contig ID	70168_1.R1010
5'-most EST	LIB35-009-Q1-E1-A8
Method	BLASTX
NCBI GI	g3219937
BLAST score	315
E value	1.0e-28
Match length	139
% identity	50
NCBI Description	HYPOTHETICAL 35.1 KD PROTEIN C57A10.07 IN CHROMOSOME I >gi_2058374_emb_CAB08170_ (Z94864) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	132199
Contig ID	70174_1.R1010
5'-most EST	jC-atXLIB327426P3f01b1
Method	BLASTX
NCBI GI	g2347192
BLAST score	431
E value	3.0e-42
Match length	186
% identity	48
NCBI Description	(AC002338) spliceosomal protein U2B isolog [Arabidopsis thaliana]

Seq. No.	132200
Contig ID	70194_1.R1010
5'-most EST	g2733107
Method	BLASTN
NCBI GI	g2182287
BLAST score	42
E value	5.0e-14
Match length	82
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	132201
Contig ID	70196_1.R1010
5'-most EST	g906708

Seq. No.	132202
Contig ID	70197_1.R1010
5'-most EST	jC-atXLIB327426P1g05b1
Method	BLASTN
NCBI GI	g2760169
BLAST score	396
E value	0.0e+00
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	132203
Contig ID	70207_1.R1010
5'-most EST	jC-atXP82CG1H9T7b1

Seq. No.	132204
Contig ID	70221_1.R1010
5'-most EST	g860744
Method	BLASTN
NCBI GI	g3249094
BLAST score	235
E value	1.0e-129
Match length	494
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132205
Contig ID	70224_1.R1010
5'-most EST	jC-atXLIB327426P1h02b1
Method	BLASTX
NCBI GI	g2809233
BLAST score	541
E value	2.0e-55
Match length	132
% identity	85
NCBI Description	(AC002560) F21B7.2 [Arabidopsis thaliana]

Seq. No.	132206
Contig ID	70224_2.R1010
5'-most EST	jC-atXP54C187A5T7045d1
Method	BLASTX
NCBI GI	g4263047
BLAST score	142
E value	4.0e-20
Match length	116
% identity	51
NCBI Description	(AC005142) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132207
Contig ID	70240_1.R1010
5'-most EST	jC-atXLIB327426P2f06b1
Method	BLASTN
NCBI GI	g2477521
BLAST score	256
E value	1.0e-142
Match length	386
% identity	84
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132208
Contig ID	70242_1.R1010
5'-most EST	LIB35-026-Q1-E1-G6

Seq. No.	132209
Contig ID	70247_1.R1010

5'-most EST	LIB35-010-Q1-E1-B8
Method	BLASTN
NCBI GI	g4753645
BLAST score	196
E value	1.0e-106
Match length	377
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)

Seq. No.	132210
Contig ID	70249_1.R1010
5'-most EST	jC-atXLIB327426P3f09b1
Method	BLASTN
NCBI GI	g2244991
BLAST score	373
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132211
Contig ID	70250_1.R1010
5'-most EST	jC-atXmonuni26Cf10b1

Seq. No.	132212
Contig ID	70257_1.R1010
5'-most EST	jC-atXLIB327426P1g04b1
Method	BLASTN
NCBI GI	g4206059
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens map 20q13.3; 51cR from D20S173 repeat region, complete sequence

Seq. No.	132213
Contig ID	70268_1.R1010
5'-most EST	jC-atX35010Q1E1F04b1
Method	BLASTN
NCBI GI	g2815404
BLAST score	608
E value	0.0e+00
Match length	688
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	132214
Contig ID	70272_1.R1010
5'-most EST	g3450095

Seq. No.	132215
Contig ID	70272_2.R1010
5'-most EST	jC-atXLIB327426P1h03b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	6.0e-16
Match length	57
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132216
Contig ID	70273_1.R1010
5'-most EST	jC-atXLIB327426P2h03b1
Method	BLASTX
NCBI GI	g3859570
BLAST score	182
E value	5.0e-13
Match length	48
% identity	73
NCBI Description	(AF098753) unknown [Oryza sativa]

Seq. No.	132217
Contig ID	70280_1.R1010
5'-most EST	jC-atXmonuni26Dh01b1

Seq. No.	132218
Contig ID	70284_1.R1010
5'-most EST	LIB35-010-Q1-E1-H8
Method	BLASTX
NCBI GI	g543565
BLAST score	245
E value	1.0e-20
Match length	67
% identity	63
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903_(U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	132219
Contig ID	70284_2.R1010
5'-most EST	g2757322
Method	BLASTX
NCBI GI	g498036
BLAST score	200
E value	2.0e-15
Match length	48
% identity	60
NCBI Description	(L33791) lipid transfer protein [Senecio odorus]

Seq. No.	132220
Contig ID	70285_1.R1010
5'-most EST	jC-atXLIB327426P2f02b1
Method	BLASTX
NCBI GI	g3287861
BLAST score	384
E value	7.0e-37
Match length	90

% identity	81
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01O24.26 PRECURSOR >gi_2288995 (AC002335) trypsin inhibitor isolog [Arabidopsis thaliana]

Seq. No.	132221
Contig ID	70293_1.R1010
5'-most EST	jC-atXLIB327426P1f03b1
Method	BLASTX
NCBI GI	g4115937
BLAST score	713
E value	1.0e-75
Match length	143
% identity	93
NCBI Description	(AF118223) contains similarity to human PCF11p homolog (GB:AF046935) [Arabidopsis thaliana]

Seq. No.	132222
Contig ID	70309_1.R1010
5'-most EST	jC-atXLIB327438P1e10a1
Method	BLASTX
NCBI GI	g549060
BLAST score	570
E value	1.0e-58
Match length	210
% identity	55
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	132223
Contig ID	70309_2.R1010
5'-most EST	jC-atX22072Q1E1G07b1
Method	BLASTX
NCBI GI	g3041738
BLAST score	95
E value	2.0e-50
Match length	199
% identity	56
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]

Seq. No.	132224
Contig ID	70323_1.R1010
5'-most EST	jC-atXLIB327402P1b07b1
Method	BLASTX
NCBI GI	g4584526
BLAST score	628
E value	2.0e-65
Match length	125
% identity	99
NCBI Description	(AL049607) glutathione peroxidase-like protein [Arabidopsis thaliana]

Seq. No.	132225

Contig ID	70353_1.R1010
5'-most EST	jC-atXLIB327423P3e12b1
Method	BLASTX
NCBI GI	g3413721
BLAST score	338
E value	2.0e-31
Match length	80
% identity	76
NCBI Description	(AC004747) putative antifungal protein [Arabidopsis thaliana]

Seq. No.	132226
Contig ID	70354_1.R1010
5'-most EST	jC-atXmonuni26Bh07b1
Method	BLASTX
NCBI GI	g2981439
BLAST score	160
E value	8.0e-11
Match length	108
% identity	38
NCBI Description	(AF051853) t-SNARE SED5 [Arabidopsis thaliana]

Seq. No.	132227
Contig ID	70358_1.R1010
5'-most EST	g2597149
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	9.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132228
Contig ID	70373_1.R1010
5'-most EST	g2748440
Method	BLASTN
NCBI GI	g3046851
BLAST score	268
E value	1.0e-149
Match length	535
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	132229
Contig ID	70396_1.R1010
5'-most EST	LIB35-012-Q1-E1-D8
Method	BLASTN
NCBI GI	g3869065
BLAST score	373
E value	0.0e+00
Match length	384
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	132230
Contig ID	70441_1.R1010
5'-most EST	LIB35-040-Q1-E1-D7
Method	BLASTX
NCBI GI	g3378491
BLAST score	254
E value	1.0e-21
Match length	83
% identity	59
NCBI Description	(AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.	132231
Contig ID	70442_1.R1010
5'-most EST	jC-atXLIB327427P1a03b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132232
Contig ID	70442_2.R1010
5'-most EST	g2747790

Seq. No.	132233
Contig ID	70443_1.R1010
5'-most EST	LIB35-013-Q1-E1-C3
Method	BLASTX
NCBI GI	g2827536
BLAST score	240
E value	9.0e-20
Match length	94
% identity	47
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132234
Contig ID	70445_1.R1010
5'-most EST	jC-atXLIB327427P2a03b1
Method	BLASTN
NCBI GI	g4519195
BLAST score	512
E value	0.0e+00
Match length	520
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	132235
Contig ID	70452_1.R1010
5'-most EST	jC-atXP118C155D24T7023d2
Method	BLASTN
NCBI GI	g3399678
BLAST score	224
E value	1.0e-122
Match length	713

% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132236
Contig ID	70471_1.R1010
5'-most EST	jC-atXLIB327427P2b06b1
Method	BLASTX
NCBI GI	g2829889
BLAST score	222
E value	8.0e-18
Match length	85
% identity	52
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	132237
Contig ID	70471_2.R1010
5'-most EST	jC-atXP58C192F17T7s3
Method	BLASTX
NCBI GI	g2829889
BLAST score	208
E value	3.0e-16
Match length	59
% identity	76
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	132238
Contig ID	70473_1.R1010
5'-most EST	jC-atXLIB327427P2b04b1
Method	BLASTN
NCBI GI	g2351072
BLAST score	275
E value	1.0e-153
Match length	446
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence [Arabidopsis thaliana]

Seq. No.	132239
Contig ID	70475_1.R1010
5'-most EST	jC-atXmonuni27Bb05b1
Method	BLASTN
NCBI GI	g2656031
BLAST score	402
E value	0.0e+00
Match length	602
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	132240
Contig ID	70486_1.R1010
5'-most EST	LIB35-014-Q1-E1-B1
Method	BLASTX
NCBI GI	g2911058
BLAST score	111
E value	6.0e-21

Match length	132
% identity	48
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	132241
Contig ID	70489_1.R1010
5'-most EST	jC-atXLIB327426P3h10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132242
Contig ID	70508_1.R1010
5'-most EST	g2722931
Method	BLASTN
NCBI GI	g3128143
BLAST score	244
E value	1.0e-134
Match length	383
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	132243
Contig ID	70509_1.R1010
5'-most EST	g2047778

Seq. No.	132244
Contig ID	70512_1.R1010
5'-most EST	jC-atXP124C121J13T7d1
Method	BLASTN
NCBI GI	g4589437
BLAST score	198
E value	1.0e-107
Match length	877
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	132245
Contig ID	70527_1.R1010
5'-most EST	jC-atXLIB327427P4a11b2
Method	BLASTN
NCBI GI	g4106527
BLAST score	78
E value	2.0e-35
Match length	82
% identity	51
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	132246
Contig ID	70528_1.R1010

5'-most EST	jC-atXLIB327427P3a11b2
Method	BLASTX
NCBI GI	g1749492
BLAST score	165
E value	3.0e-11
Match length	73
% identity	47
NCBI Description	(D89142) unnamed protein product [Schizosaccharomyces pombe]

Seq. No.	132247
Contig ID	70556_1.R1010
5'-most EST	LIB35-015-Q1-E1-B11

Seq. No.	132248
Contig ID	70575_1.R1010
5'-most EST	jC-atXLIB327420P1c04a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	51
E value	2.0e-19
Match length	246
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	132249
Contig ID	70592_1.R1010
5'-most EST	LIB35-015-Q1-E1-F2
Method	BLASTX
NCBI GI	g3033377
BLAST score	727
E value	2.0e-77
Match length	134
% identity	99
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	132250
Contig ID	70594_1.R1010
5'-most EST	g2749663
Method	BLASTN
NCBI GI	g2924733
BLAST score	296
E value	1.0e-166
Match length	381
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	132251
Contig ID	70594_2.R1010
5'-most EST	LIB35-015-Q1-E1-F5
Method	BLASTN
NCBI GI	g2924733
BLAST score	425
E value	0.0e+00

Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	132252
Contig ID	70596_1.R1010
5'-most EST	jC-atXLIB327427P3a01b2
Method	BLASTX
NCBI GI	g4376873
BLAST score	228
E value	2.0e-18
Match length	121
% identity	45
NCBI Description	(AE001642) Pseudouridylate Synthase I [Chlamydia pneumoniae]

Seq. No.	132253
Contig ID	70629_1.R1010
5'-most EST	jC-atXLIB327429P3h08a2
Method	BLASTN
NCBI GI	g1871173
BLAST score	225
E value	1.0e-123
Match length	632
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	132254
Contig ID	70633_1.R1010
5'-most EST	LIB35-022-Q1-E1-B9
Method	BLASTX
NCBI GI	g2980793
BLAST score	204
E value	6.0e-16
Match length	82
% identity	46
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	132255
Contig ID	70646_1.R1010
5'-most EST	jC-atXLIB327421P1f03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132256
Contig ID	70655_1.R1010
5'-most EST	g860772
Method	BLASTX
NCBI GI	g3128168

BLAST score	760
E value	4.0e-81
Match length	146
% identity	95
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	132257
Contig ID	70670_1.R1010
5'-most EST	LIB35-016-Q1-E1-G1
Method	BLASTN
NCBI GI	g4582444
BLAST score	261
E value	1.0e-145
Match length	490
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	132258
Contig ID	70681_1.R1010
5'-most EST	jC-atXLIB327427P2b02b1
Method	BLASTX
NCBI GI	g3096928
BLAST score	153
E value	1.0e-09
Match length	125
% identity	36
NCBI Description	(AL023094) bZIP transcription factor ATB2 [Arabidopsis thaliana]

Seq. No.	132259
Contig ID	70687_1.R1010
5'-most EST	jC-atXLIB327427P1b02b1
Method	BLASTN
NCBI GI	g3859590
BLAST score	279
E value	1.0e-155
Match length	578
% identity	100
NCBI Description	Arabidopsis thaliana BAC T15B16

Seq. No.	132260
Contig ID	70692_1.R1010
5'-most EST	jC-atXmonuni27Ab12b1
Method	BLASTN
NCBI GI	g4521999
BLAST score	276
E value	1.0e-154
Match length	491
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	132261
Contig ID	70699_1.R1010
5'-most EST	jC-atXLIB327423P3e10b1

Method	BLASTX
NCBI GI	g267124
BLAST score	279
E value	2.0e-24
Match length	110
% identity	42
NCBI Description	THIOREDOXIN H-TYPE 1 (TRX-H1) >gi_100387_pir__S16590 thioredoxin h1 - common tobacco >gi_20047_emb_CAA41415_ (X58527) thioredoxin [Nicotiana tabacum]

Seq. No.	132262
Contig ID	70701_1.R1010
5'-most EST	jC-atXLIB327427P3b05b2
Method	BLASTN
NCBI GI	g4455262
BLAST score	380
E value	0.0e+00
Match length	478
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	132263
Contig ID	70701_2.R1010
5'-most EST	g936457
Method	BLASTX
NCBI GI	g4038034
BLAST score	341
E value	6.0e-32
Match length	87
% identity	71
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	132264
Contig ID	70705_1.R1010
5'-most EST	jC-atXmonuni27Cb08b1
Method	BLASTX
NCBI GI	g2213600
BLAST score	260
E value	2.0e-22
Match length	93
% identity	57
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	132265
Contig ID	70706_1.R1010
5'-most EST	jC-atXLIB327427P3b04b2
Method	BLASTX
NCBI GI	g2995953
BLAST score	344
E value	6.0e-32
Match length	95
% identity	71
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	132266
Contig ID	70711_1.R1010

5'-most EST	LIB35-017-Q1-E1-C3
Method	BLASTX
NCBI GI	g3150416
BLAST score	1314
E value	1.0e-145
Match length	283
% identity	89
NCBI Description	(AC004165) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No.	132267
Contig ID	70723_1.R1010
5'-most EST	jC-atXLIB327427P1c05b1
Method	BLASTX
NCBI GI	g4544454
BLAST score	294
E value	2.0e-26
Match length	58
% identity	98
NCBI Description	(AC006592) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	132268
Contig ID	70733_2.R1010
5'-most EST	jC-atXLIB327427P4c08b2
Method	BLASTX
NCBI GI	g3935150
BLAST score	550
E value	4.0e-56
Match length	149
% identity	81
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No.	132269
Contig ID	70736_1.R1010
5'-most EST	jC-atXLIB327427P4c12b2
Method	BLASTN
NCBI GI	g2264312
BLAST score	296
E value	1.0e-165
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	132270
Contig ID	70753_1.R1010
5'-most EST	jC-atXLIB327427P2e04b1
Method	BLASTN
NCBI GI	g4567259
BLAST score	587
E value	0.0e+00
Match length	683
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No. 132271

Contig ID	70754_1.R1010
5'-most EST	jC-atXLIB327427P2b11b1
Method	BLASTX
NCBI GI	g4581150
BLAST score	285
E value	3.0e-25
Match length	101
% identity	28
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132272
Contig ID	70762_1.R1010
5'-most EST	jC-atXmonuni27Cb05b1
Method	BLASTX
NCBI GI	g3024028
BLAST score	192
E value	2.0e-14
Match length	64
% identity	62
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA)

Seq. No.	132273
Contig ID	70764_1.R1010
5'-most EST	jC-atXLIB327427P4b06b2
Method	BLASTX
NCBI GI	g2501555
BLAST score	393
E value	8.0e-38
Match length	107
% identity	65
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	132274
Contig ID	70766_1.R1010
5'-most EST	jC-atXLIB327427P3b07b2

Seq. No.	132275
Contig ID	70771_1.R1010
5'-most EST	jC-atXmonuni27Cb12b1
Method	BLASTX
NCBI GI	g4587988
BLAST score	984
E value	1.0e-107
Match length	193
% identity	100
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132276
Contig ID	70775_1.R1010
5'-most EST	jC-atXLIB327427P2c01b1
Method	BLASTX
NCBI GI	g1097877
BLAST score	625
E value	6.0e-65
Match length	128

% identity	94
NCBI Description	aminolevulinate dehydratase [Lycopersicon esculentum]

Seq. No.	132277
Contig ID	70779_1.R1010
5'-most EST	LIB35-018-Q1-E1-C8

Seq. No.	132278
Contig ID	70794_1.R1010
5'-most EST	jC-atXLIB327427P2c12b1
Method	BLASTN
NCBI GI	g3449331
BLAST score	92
E value	5.0e-44
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	132279
Contig ID	70801_1.R1010
5'-most EST	jC-atXLIB327427P3c07b2
Method	BLASTX
NCBI GI	g2739362
BLAST score	524
E value	3.0e-53
Match length	124
% identity	85
NCBI Description	(AC002505) similar to peroxisomal Ca-dependent solute carrier [Arabidopsis thaliana]

Seq. No.	132280
Contig ID	70816_1.R1010
5'-most EST	jC-atXP85CG8A2T7b1
Method	BLASTX
NCBI GI	g115530
BLAST score	92
E value	1.6e-02
Match length	126
% identity	24
NCBI Description	CALMODULIN >gi_71679_pir__MCUTG calmodulin - Trypanosoma brucei gambiense >gi_539401_pir__A48111 calmodulin C - Trypanosoma brucei >gi_10386_emb_CAA39861_ (X56511) calmodulin [Trypanosoma brucei]

Seq. No.	132281
Contig ID	70816_2.R1010
5'-most EST	jC-atXLIB327427P3c12b2
Method	BLASTX
NCBI GI	g115531
BLAST score	91
E value	2.5e-02
Match length	149
% identity	20
NCBI Description	CALMODULIN >gi_71680_pir__MCUTC calmodulin - Trypanosoma cruzi >gi_10604_emb_CAA36316_ (X52096) calmodulin (AA 1-149) [Trypanosoma cruzi]

Seq. No.	132282
Contig ID	70836_1.R1010
5'-most EST	jC-atXLIB327427P3b03b2
Method	BLASTX
NCBI GI	g4678349
BLAST score	711
E value	7.0e-87
Match length	197
% identity	38
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	132283
Contig ID	70848_1.R1010
5'-most EST	jC-atXLIB327427P4b11b2
Method	BLASTX
NCBI GI	g4587562
BLAST score	799
E value	3.0e-85
Match length	174
% identity	95
NCBI Description	(AC006550) Belongs to PF_00583 Acetyltransfersase (GNAT) family. [Arabidopsis thaliana]

Seq. No.	132284
Contig ID	70871_1.R1010
5'-most EST	jC-atXLIB327427P4c06b2
Method	BLASTX
NCBI GI	g2880049
BLAST score	451
E value	9.0e-45
Match length	136
% identity	67
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132285
Contig ID	70877_1.R1010
5'-most EST	jC-atXLIB327427P3c03b2

Seq. No.	132286
Contig ID	70885_1.R1010
5'-most EST	LIB35-019-Q1-E1-G7
Method	BLASTN
NCBI GI	g3201608
BLAST score	129
E value	3.0e-66
Match length	345
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132287
Contig ID	70904_1.R1010
5'-most EST	jC-atXP63C206C10T7d2
Method	BLASTX
NCBI GI	g3980377
BLAST score	778

E value	5.0e-83
Match length	156
% identity	99
NCBI Description	(AC004561) unknown protein [Arabidopsis thaliana]

Seq. No.	132288
Contig ID	70910_1.R1010
5'-most EST	jC-atX35020Q1E1B02b1
Method	BLASTX
NCBI GI	g3702331
BLAST score	529
E value	4.0e-54
Match length	137
% identity	77
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132289
Contig ID	70917_1.R1010
5'-most EST	jC-atXLIB327427P3b09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	3.0e-30
Match length	73
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132290
Contig ID	70921_1.R1010
5'-most EST	jC-atXLIB327427P4b09b2
Method	BLASTN
NCBI GI	g3738088
BLAST score	410
E value	0.0e+00
Match length	445
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132291
Contig ID	70935_1.R1010
5'-most EST	LIB35-052-Q1-E1-H12
Method	BLASTX
NCBI GI	g2827663
BLAST score	146
E value	4.0e-09
Match length	141
% identity	3
NCBI Description	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]

Seq. No.	132292
Contig ID	70948_1.R1010
5'-most EST	jC-alXLIB327435P2h02a1
Method	BLASTX
NCBI GI	g2258336

BLAST score	206
E value	4.0e-16
Match length	100
% identity	45
NCBI Description	(AF007261) component involved in Haem biosynthesis [Reclinomonas americana]

Seq. No.	132293
Contig ID	70955_1.R1010
5'-most EST	jC-atXLIB327427P3c11b2
Method	BLASTX
NCBI GI	g1652892
BLAST score	236
E value	2.0e-19
Match length	74
% identity	31
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	132294
Contig ID	70962_1.R1010
5'-most EST	LIB35-020-Q1-E1-H4
Method	BLASTX
NCBI GI	g3063473
BLAST score	430
E value	2.0e-42
Match length	144
% identity	65
NCBI Description	(AC003981) F22O13.35 [Arabidopsis thaliana]

Seq. No.	132295
Contig ID	70963_1.R1010
5'-most EST	jC-atXLIB327427P2d05b1
Method	BLASTX
NCBI GI	g2104536
BLAST score	272
E value	1.0e-23
Match length	51
% identity	88
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	132296
Contig ID	70967_1.R1010
5'-most EST	jC-atXLIB327427P2d09b1

Seq. No.	132297
Contig ID	70978_1.R1010
5'-most EST	jC-atXP46C173L7T7014a1
Method	BLASTN
NCBI GI	g3873174
BLAST score	548
E value	0.0e+00
Match length	573
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	132298
Contig ID	70987_1.R1010
5'-most EST	LIB35-021-Q1-E1-C4
Method	BLASTN
NCBI GI	g4519183
BLAST score	37
E value	3.0e-11
Match length	414
% identity	72
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	132299
Contig ID	71014_1.R1010
5'-most EST	jC-atXmonuni27Be10b1
Method	BLASTN
NCBI GI	g16181
BLAST score	136
E value	4.0e-70
Match length	152
% identity	97
NCBI Description	A.thaliana gene for tonoplast intrinsic protein alpha-TIP(Ara) >gi_166622_gb_M84343_ATHATIP Arabidopsis thaliana tonoplast intrinsic protein (alpha-TIP) gene, complete cds

Seq. No.	132300
Contig ID	71019_1.R1010
5'-most EST	LIB35-021-Q1-E1-G12
Method	BLASTN
NCBI GI	g2252848
BLAST score	305
E value	1.0e-171
Match length	633
% identity	96
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	132301
Contig ID	71040_1.R1010
5'-most EST	jC-atXmonuni27Bd09b1

Seq. No.	132302
Contig ID	71051_1.R1010
5'-most EST	jC-atXmonuni27Cd05b1
Method	BLASTX
NCBI GI	g4006853
BLAST score	871
E value	4.0e-94
Match length	167
% identity	100
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	132303
Contig ID	71056_1.R1010
5'-most EST	jC-atXLIB327427P4d09b2
Method	BLASTN

NCBI GI g1402874
BLAST score 805
E value 0.0e+00
Match length 825
% identity 99
NCBI Description A.thaliana 81kb genomic sequence

Seq. No. 132304
Contig ID 71056_2.R1010
5'-most EST g933381
Method BLASTN
NCBI GI g1402874
BLAST score 124
E value 4.0e-63
Match length 363
% identity 98
NCBI Description A.thaliana 81kb genomic sequence

Seq. No. 132305
Contig ID 71072_1.R1010
5'-most EST jC-atXmonuni27Be09a1

Seq. No. 132306
Contig ID 71083_1.R1010
5'-most EST jC-atXLIB327427P2e12b1

Seq. No. 132307
Contig ID 71122_1.R1010
5'-most EST jC-atXLIB327427P3d07b2
Method BLASTN
NCBI GI g2582640
BLAST score 44
E value 4.0e-15
Match length 68
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 132308
Contig ID 71136_1.R1010
5'-most EST jC-atXLIB327427P4d11b2

Seq. No. 132309
Contig ID 71145_1.R1010
5'-most EST jC-atXLIB327427P1e07b1
Method BLASTN
NCBI GI g4063730
BLAST score 409
E value 0.0e+00
Match length 475
% identity 53
NCBI Description Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 132310
Contig ID 71154_1.R1010

5'-most EST	jC-atXLIB327427P1e11b1
Method	BLASTX
NCBI GI	g4581162
BLAST score	351
E value	8.0e-33
Match length	115
% identity	55
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	132311
Contig ID	71163_1.R1010
5'-most EST	jC-atXLIB327427P3e04b2

Seq. No.	132312
Contig ID	71169_1.R1010
5'-most EST	jC-atXLIB327427P1d07b1
Method	BLASTX
NCBI GI	g4454015
BLAST score	175
E value	4.0e-12
Match length	161
% identity	23
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	132313
Contig ID	71176_1.R1010
5'-most EST	jC-atXLIB327427P2d07b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	75
E value	8.0e-34
Match length	79
% identity	50
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	132314
Contig ID	71176_2.R1010
5'-most EST	jC-atXLIB327427P2d07a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	1.0e-20
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132315
Contig ID	71176_3.R1010
5'-most EST	jC-atXP22C114N10T7050a1
Method	BLASTX
NCBI GI	g1304599
BLAST score	206
E value	7.0e-16
Match length	70
% identity	50
NCBI Description	(U41315) ZNF127-Xp [Homo sapiens]

Seq. No.	132316
Contig ID	71177_1.R1010
5'-most EST	jC-atXLIB327427P2d11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	2.0e-23
Match length	77
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132317
Contig ID	71180_1.R1010
5'-most EST	jC-atXLIB327427P2d12b1
Method	BLASTX
NCBI GI	g1066499
BLAST score	547
E value	4.0e-56
Match length	133
% identity	80
NCBI Description	(L37606) NADH-dependent glutamate synthase [Medicago sativa]

Seq. No.	132318
Contig ID	71186_1.R1010
5'-most EST	jC-atX35024Q1E1C10b1
Method	BLASTX
NCBI GI	g3461817
BLAST score	183
E value	1.0e-13
Match length	71
% identity	55
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	132319
Contig ID	71194_1.R1010
5'-most EST	g2723054
Method	BLASTN
NCBI GI	g3128136
BLAST score	207
E value	1.0e-112
Match length	330
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	132320
Contig ID	71204_1.R1010
5'-most EST	jC-atXmonuni27Cd12b1
Method	BLASTX
NCBI GI	g3041738
BLAST score	300
E value	6.0e-27
Match length	83
% identity	70

NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]

Seq. No.	132321
Contig ID	71210_1.R1010
5'-most EST	jC-atXLIB327427P3d10b2
Method	BLASTN
NCBI GI	g4713943
BLAST score	388
E value	0.0e+00
Match length	588
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	132322
Contig ID	71214_1.R1010
5'-most EST	jC-atXLIB327402P1b01b1
Method	BLASTX
NCBI GI	g4469025
BLAST score	661
E value	3.0e-69
Match length	137
% identity	77
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	132323
Contig ID	71244_1.R1010
5'-most EST	LIB35-025-Q1-E1-B12
Method	BLASTN
NCBI GI	g4262221
BLAST score	153
E value	1.0e-80
Match length	262
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132324
Contig ID	71246_1.R1010
5'-most EST	jC-alXLIB327435P4g08b1
Method	BLASTX
NCBI GI	g1076294
BLAST score	144
E value	1.0e-08
Match length	67
% identity	63
NCBI Description	ATAF2 protein - Arabidopsis thaliana

Seq. No.	132325
Contig ID	71271_1.R1010
5'-most EST	g2749159
Method	BLASTN
NCBI GI	g2244788
BLAST score	64

E value	3.0e-27
Match length	136
% identity	69
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132326
Contig ID	71271_2.R1010
5'-most EST	LIB35-025-Q1-E1-E11
Method	BLASTX
NCBI GI	g4006854
BLAST score	442
E value	2.0e-43
Match length	136
% identity	62
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	132327
Contig ID	71276_1.R1010
5'-most EST	LIB35-034-Q1-E1-H1
Method	BLASTN
NCBI GI	g4376087
BLAST score	205
E value	1.0e-111
Match length	383
% identity	69
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	132328
Contig ID	71277_1.R1010
5'-most EST	jC-atXLIB327423P2e12b1
Method	BLASTX
NCBI GI	g3789911
BLAST score	271
E value	1.0e-23
Match length	76
% identity	62
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	132329
Contig ID	71299_1.R1010
5'-most EST	g2749714
Method	BLASTN
NCBI GI	g4567193
BLAST score	287
E value	1.0e-160
Match length	331
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	132330
Contig ID	71369_1.R1010
5'-most EST	jC-atXLIB327413P2e03b1
Method	BLASTX

NCBI GI	g4204268
BLAST score	47
E value	7.0e-58
Match length	136
% identity	90
NCBI Description	(AC005223) 62134 [Arabidopsis thaliana]

Seq. No.	132331
Contig ID	71382_1.R1010
5'-most EST	g2762558

Seq. No.	132332
Contig ID	71394_1.R1010
5'-most EST	jC-atXLIB327427P4a05a2
Method	BLASTN
NCBI GI	g3785992
BLAST score	402
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132333
Contig ID	71407_1.R1010
5'-most EST	LIB35-046-Q1-E1-E3
Method	BLASTX
NCBI GI	g2129687
BLAST score	267
E value	3.0e-23
Match length	54
% identity	98
NCBI Description	protein kinase AK19 - Arabidopsis thaliana (fragment) >gi_2146756_pir__S66332 protein kinase AK19 - Arabidopsis thaliana (fragment) >gi_928904_emb_CAA60527_ (X86964) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]

Seq. No.	132334
Contig ID	71445_1.R1010
5'-most EST	LIB35-027-Q1-E1-H4

Seq. No.	132335
Contig ID	71452_1.R1010
5'-most EST	g1158648
Method	BLASTX
NCBI GI	g123178
BLAST score	729
E value	3.0e-77
Match length	156
% identity	94
NCBI Description	HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi_99844_pir__A39358 histidinol dehydrogenase (EC 1.1.1.23) precursor, chloroplast - cabbage >gi_167142 (M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No. 132336

Contig ID	71466_1.R1010
5'-most EST	LIB35-044-Q1-E1-F1
Method	BLASTX
NCBI GI	g2894607
BLAST score	248
E value	2.0e-21
Match length	90
% identity	51
NCBI Description	(AL021889) NAM (no apical meristem) - like protein [Arabidopsis thaliana]

Seq. No.	132337
Contig ID	71559_1.R1010
5'-most EST	jC-atXLIB327423P2e11b1
Method	BLASTX
NCBI GI	g3687245
BLAST score	183
E value	3.0e-13
Match length	132
% identity	25
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	132338
Contig ID	71559_2.R1010
5'-most EST	LIB35-029-Q1-E1-E4
Method	BLASTX
NCBI GI	g3687245
BLAST score	422
E value	1.0e-41
Match length	110
% identity	73
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	132339
Contig ID	71650_1.R1010
5'-most EST	LIB35-030-Q1-E1-G7
Method	BLASTX
NCBI GI	g4455260
BLAST score	695
E value	2.0e-73
Match length	132
% identity	97
NCBI Description	(AL035353) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	132340
Contig ID	71658_1.R1010
5'-most EST	jC-atXLIB327402P2d02a1
Method	BLASTN
NCBI GI	g4512656
BLAST score	261
E value	1.0e-145
Match length	451
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No.	132341
Contig ID	71658_2.R1010
5'-most EST	jC-atXLIB327423P4e11b1
Method	BLASTN
NCBI GI	g4512656
BLAST score	308
E value	1.0e-173
Match length	383
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	132342
Contig ID	71697_1.R1010
5'-most EST	LIB35-031-Q1-E1-E2
Method	BLASTN
NCBI GI	g4558521
BLAST score	161
E value	2.0e-85
Match length	359
% identity	51
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	132343
Contig ID	71715_1.R1010
5'-most EST	jC-atXLIB327423P4e10b1
Method	BLASTX
NCBI GI	g3738315
BLAST score	195
E value	1.0e-14
Match length	76
% identity	55
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	132344
Contig ID	71741_1.R1010
5'-most EST	jC-atXLIB327423P4d02b1
Method	BLASTX
NCBI GI	g4803711
BLAST score	214
E value	8.0e-37
Match length	87
% identity	85
NCBI Description	(AJ012374) iron sulfur subunit of succinate dehydrogenase [Zea mays]

Seq. No.	132345
Contig ID	71748_1.R1010
5'-most EST	LIB35-046-Q1-E1-B2

Seq. No.	132346
Contig ID	71760_1.R1010
5'-most EST	jC-alX35032Q1E1C07b1
Method	BLASTX

NCBI GI g2500376
BLAST score 461
E value 4.0e-46
Match length 95
% identity 93
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]

Seq. No. 132347
Contig ID 71764_1.R1010
5'-most EST jC-atXLIB327423P2e02b1
Method BLASTX
NCBI GI g2281088
BLAST score 334
E value 4.0e-31
Match length 132
% identity 49
NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No. 132348
Contig ID 71769_1.R1010
5'-most EST jC-atXP18C111E24T7d2
Method BLASTN
NCBI GI g3869067
BLAST score 433
E value 0.0e+00
Match length 1081
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No. 132349
Contig ID 71792_1.R1010
5'-most EST jC-alX35034Q1E1E12b1

Seq. No. 132350
Contig ID 71820_1.R1010
5'-most EST jC-atXLIB327423P1f07b1
Method BLASTN
NCBI GI g4757405
BLAST score 171
E value 6.0e-91
Match length 586
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No. 132351
Contig ID 71853_1.R1010
5'-most EST jC-atXLIB327423P4f08b1
Method BLASTX
NCBI GI g3860271
BLAST score 471
E value 6.0e-47
Match length 177
% identity 50

NCBI Description	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]

Seq. No.	132352
Contig ID	71861_2.R1010
5'-most EST	LIB35-033-Q1-E1-F3
Method	BLASTX
NCBI GI	g4572665
BLAST score	230
E value	5.0e-19
Match length	122
% identity	15
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	132353
Contig ID	71889_1.R1010
5'-most EST	jC-atXLIB327423P1f08b1
Method	BLASTX
NCBI GI	g4758520
BLAST score	158
E value	3.0e-10
Match length	152
% identity	4
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	132354
Contig ID	71895_1.R1010
5'-most EST	jC-atXP8C92J6T7s1
Method	BLASTX
NCBI GI	g3164140
BLAST score	742
E value	1.0e-78
Match length	215
% identity	62
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	132355
Contig ID	71895_3.R1010
5'-most EST	jC-atXLIB327423P2f06b1
Method	BLASTX
NCBI GI	g3164140
BLAST score	147
E value	6.0e-69
Match length	193
% identity	62
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	132356
Contig ID	71895_4.R1010
5'-most EST	jC-atXP60C198F7T7022d1
Method	BLASTX
NCBI GI	g3164140
BLAST score	498
E value	5.0e-50

Match length	222
% identity	46
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	132357
Contig ID	71919_1.R1010
5'-most EST	jC-atXLIB327423P4f06b1
Method	BLASTX
NCBI GI	g4325369
BLAST score	331
E value	1.0e-30
Match length	170
% identity	40
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	132358
Contig ID	71919_2.R1010
5'-most EST	jC-atX24041Q1E1E05a1
Method	BLASTX
NCBI GI	g4325369
BLAST score	315
E value	6.0e-29
Match length	127
% identity	53
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	132359
Contig ID	71926_1.R1010
5'-most EST	jC-atXLIB327423P3f08b1
Method	BLASTN
NCBI GI	g4699904
BLAST score	153
E value	3.0e-80
Match length	422
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	132360
Contig ID	71928_1.R1010
5'-most EST	ARABLI-06-Q1-B1-D9
Method	BLASTX
NCBI GI	g3080414
BLAST score	609
E value	2.0e-63
Match length	140
% identity	88
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	132361
Contig ID	72027_1.R1010
5'-most EST	LIB35-036-Q1-E2-E1
Method	BLASTX
NCBI GI	g2501766
BLAST score	176
E value	8.0e-13

Match length	62
% identity	63
NCBI Description	(U69174) calmodulin-like domain protein kinase isoenzyme gamma [Glycine max]

Seq. No.	132362
Contig ID	72033_1.R1010
5'-most EST	LIB35-036-Q1-E2-F3
Method	BLASTX
NCBI GI	g3461835
BLAST score	341
E value	2.0e-32
Match length	80
% identity	82
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	132363
Contig ID	72040_1.R1010
5'-most EST	LIB35-036-Q1-E2-G5

Seq. No.	132364
Contig ID	72042_1.R1010
5'-most EST	jC-alXLIB327435P4g10b1
Method	BLASTX
NCBI GI	g130696
BLAST score	207
E value	6.0e-16
Match length	105
% identity	40
NCBI Description	PLACENTAL PROTEIN 11 PRECURSOR (PP11) >gi_107308_pir__A34614 placental protein 11 precursor - human >gi_190211 (M32402) placental protein 11 (PP11) precursor [Homo sapiens] >gi_190213 (M36109) placental protein 11 [Homo sapiens]

Seq. No.	132365
Contig ID	72045_1.R1010
5'-most EST	jC-alXLIB327435P2h03a1
Method	BLASTN
NCBI GI	g3046856
BLAST score	455
E value	0.0e+00
Match length	516
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	132366
Contig ID	72093_1.R1010
5'-most EST	LIB35-036-Q1-E2-F10
Method	BLASTX
NCBI GI	g4512018
BLAST score	383
E value	5.0e-37
Match length	84

% identity	85
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	132367
Contig ID	72111_1.R1010
5'-most EST	LIB35-036-Q1-E2-H12
Method	BLASTN
NCBI GI	g2182286
BLAST score	173
E value	2.0e-92
Match length	409
% identity	100
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	132368
Contig ID	72125_1.R1010
5'-most EST	jC-alXLIB327435P4f12b1
Method	BLASTN
NCBI GI	g3337347
BLAST score	176
E value	6.0e-94
Match length	603
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132369
Contig ID	72195_1.R1010
5'-most EST	jC-alXLIB327435P2g01a1
Method	BLASTX
NCBI GI	g3980393
BLAST score	1165
E value	1.0e-128
Match length	227
% identity	100
NCBI Description	(AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	132370
Contig ID	72202_1.R1010
5'-most EST	g2048552
Method	BLASTN
NCBI GI	g4691223
BLAST score	241
E value	1.0e-133
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	132371
Contig ID	72202_2.R1010
5'-most EST	LIB35-038-Q1-E1-B2
Method	BLASTN
NCBI GI	g4691223

BLAST score 229
E value 1.0e-126
Match length 386
% identity 96
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No. 132372
Contig ID 72202_3.R1010
5'-most EST g2757574
Method BLASTX
NCBI GI g4678935
BLAST score 397
E value 2.0e-38
Match length 76
% identity 99
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 132373
Contig ID 72217_1.R1010
5'-most EST jC-alXLIB327435P2g10a1
Method BLASTN
NCBI GI g2351072
BLAST score 374
E value 0.0e+00
Match length 390
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence [Arabidopsis thaliana]

Seq. No. 132374
Contig ID 72220_1.R1010
5'-most EST jC-alXLIB327436P1g10b1
Method BLASTN
NCBI GI g4106527
BLAST score 67
E value 5.0e-29
Match length 71
% identity 47
NCBI Description Mus musculus Pontin52 mRNA, complete cds

Seq. No. 132375
Contig ID 72275_1.R1010
5'-most EST g396609
Method BLASTX
NCBI GI g3894191
BLAST score 282
E value 7.0e-25
Match length 92
% identity 58
NCBI Description (AC005662) unknown protein [Arabidopsis thaliana]

Seq. No. 132376
Contig ID 72286_1.R1010
5'-most EST LIB35-039-Q1-E1-C4
Method BLASTX
NCBI GI g3164134

BLAST score 429
E value 2.0e-42
Match length 105
% identity 77
NCBI Description (D78602) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No. 132377
Contig ID 72298_1.R1010
5'-most EST g2763664

Seq. No. 132378
Contig ID 72356_1.R1010
5'-most EST jC-atXP65C208H9T7007d1
Method BLASTX
NCBI GI g2464879
BLAST score 764
E value 4.0e-87
Match length 167
% identity 98
NCBI Description (Z99707) caltractin-like protein [Arabidopsis thaliana]

Seq. No. 132379
Contig ID 72356_3.R1010
5'-most EST g2759114
Method BLASTX
NCBI GI g2464879
BLAST score 455
E value 1.0e-46
Match length 104
% identity 97
NCBI Description (Z99707) caltractin-like protein [Arabidopsis thaliana]

Seq. No. 132380
Contig ID 72357_1.R1010
5'-most EST LIB35-040-Q1-E1-C8
Method BLASTN
NCBI GI g3869069
BLAST score 273
E value 1.0e-152
Match length 405
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 132381
Contig ID 72374_1.R1010
5'-most EST LIB35-040-Q1-E1-E7
Method BLASTN
NCBI GI g2462264
BLAST score 46
E value 2.0e-16
Match length 46
% identity 100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 132382

Contig ID	72377_1.R1010
5'-most EST	g2758289
Method	BLASTN
NCBI GI	g4220468
BLAST score	663
E value	0.0e+00
Match length	731
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132383
Contig ID	72404_1.R1010
5'-most EST	LIB35-041-Q1-E1-C12
Method	BLASTX
NCBI GI	g4150963
BLAST score	308
E value	4.0e-28
Match length	89
% identity	63
NCBI Description	(Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No.	132384
Contig ID	72405_1.R1010
5'-most EST	LIB35-052-Q1-E1-D6
Method	BLASTX
NCBI GI	g4733959
BLAST score	563
E value	4.0e-58
Match length	133
% identity	85
NCBI Description	(AC007294) putative glucose inhibited division protein A [Arabidopsis thaliana]

Seq. No.	132385
Contig ID	72424_1.R1010
5'-most EST	jC-atXLIB327402P1b10b1
Method	BLASTX
NCBI GI	g4469020
BLAST score	657
E value	6.0e-69
Match length	152
% identity	88
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	132386
Contig ID	72424_2.R1010
5'-most EST	ARABL1-028-Q1-B1-D5
Method	BLASTX
NCBI GI	g4469020
BLAST score	436
E value	1.0e-49
Match length	130
% identity	81
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	132387
Contig ID	72425_1.R1010
5'-most EST	LIB35-041-Q1-E1-F9
Method	BLASTN
NCBI GI	g2182287
BLAST score	429
E value	0.0e+00
Match length	815
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	132388
Contig ID	72444_1.R1010
5'-most EST	LIB35-042-Q1-E1-B3
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	3.0e-21
Match length	62
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132389
Contig ID	72459_1.R1010
5'-most EST	LIB35-042-Q1-E1-D2
Method	BLASTN
NCBI GI	g2264314
BLAST score	103
E value	1.0e-50
Match length	350
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	132390
Contig ID	72470_1.R1010
5'-most EST	LIB35-042-Q1-E1-E7
Method	BLASTN
NCBI GI	g4038029
BLAST score	475
E value	0.0e+00
Match length	539
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132391
Contig ID	72479_1.R1010
5'-most EST	jC-atXLIB327402P1b08b1
Method	BLASTX
NCBI GI	g3879119
BLAST score	259
E value	3.0e-22
Match length	135

% identity	46
NCBI Description	(Z70310) similar to Glutathione S-transferases. [Caenorhabditis elegans]

Seq. No.	132392
Contig ID	72495_1.R1010
5'-most EST	jC-atXLIB327402P4b12b1

Seq. No.	132393
Contig ID	72535_1.R1010
5'-most EST	jC-atXLIB327421P2e10b1
Method	BLASTX
NCBI GI	g3386604
BLAST score	187
E value	7.0e-14
Match length	131
% identity	38
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	132394
Contig ID	72557_1.R1010
5'-most EST	jC-atXLIB327421P3e07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132395
Contig ID	72558_1.R1010
5'-most EST	jC-atXP7C91J9T7d1
Method	BLASTX
NCBI GI	g1613878
BLAST score	918
E value	1.0e-117
Match length	301
% identity	63
NCBI Description	(U72236) ModA [Dictyostelium discoideum]

Seq. No.	132396
Contig ID	72578_1.R1010
5'-most EST	jC-atXP5C89B11T7023a1
Method	BLASTX
NCBI GI	g4071212
BLAST score	325
E value	2.0e-46
Match length	148
% identity	62
NCBI Description	(AF047478) GDP-mannose dehydratase; Gmd [Brucella melitensis]

Seq. No.	132397
Contig ID	72578_2.R1010
5'-most EST	jC-atXP104CE10D10T7b1

Method	BLASTN
NCBI GI	g4159700
BLAST score	136
E value	4.0e-70
Match length	591
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	132398
Contig ID	72578_3.R1010
5'-most EST	g1159353
Method	BLASTN
NCBI GI	g4159700
BLAST score	694
E value	0.0e+00
Match length	1023
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	132399
Contig ID	72636_1.R1010
5'-most EST	LIB35-044-Q1-E1-G9
Method	BLASTN
NCBI GI	g2264317
BLAST score	361
E value	0.0e+00
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	132400
Contig ID	72638_1.R1010
5'-most EST	jC-atXLIB327421P1f01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	1.0e-16
Match length	50
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132401
Contig ID	72639_1.R1010
5'-most EST	LIB35-044-Q1-E1-H11
Method	BLASTX
NCBI GI	g2765244
BLAST score	145
E value	6.0e-09
Match length	74
% identity	47
NCBI Description	(Y12807) invertase inhibitor homolog [Arabidopsis thaliana]

Seq. No.	132402

Contig ID	72646_1.R1010
5'-most EST	jC-atXLIB327421P4d12b1
Method	BLASTN
NCBI GI	g4263694
BLAST score	99
E value	3.0e-48
Match length	123
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132403
Contig ID	72646_2.R1010
5'-most EST	LIB35-045-Q1-E1-A11
Method	BLASTN
NCBI GI	g4263694
BLAST score	99
E value	3.0e-48
Match length	123
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132404
Contig ID	72662_1.R1010
5'-most EST	jC-atXLIB327421P1e06b1
Method	BLASTX
NCBI GI	g3128187
BLAST score	583
E value	5.0e-60
Match length	147
% identity	71
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	132405
Contig ID	72674_1.R1010
5'-most EST	jC-atXLIB327421P1e12b1
Method	BLASTN
NCBI GI	g3510337
BLAST score	426
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	132406
Contig ID	72692_1.R1010
5'-most EST	jC-atX35042Q1E1A03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132407
Contig ID	72703_1.R1010
5'-most EST	jC-atXP27C132C22T7d2
Method	BLASTX
NCBI GI	g2244999
BLAST score	752
E value	6.0e-80
Match length	147
% identity	100
NCBI Description	(Z97341) similarity to phaseolin G-box binding protein PG2 [Arabidopsis thaliana]

Seq. No.	132408
Contig ID	72729_1.R1010
5'-most EST	jC-alX35046Q1E1D08b1
Method	BLASTN
NCBI GI	g3046856
BLAST score	468
E value	0.0e+00
Match length	615
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	132409
Contig ID	72730_1.R1010
5'-most EST	jC-atXLIB327421P2e09b1
Method	BLASTX
NCBI GI	g1653216
BLAST score	195
E value	9.0e-15
Match length	89
% identity	49
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	132410
Contig ID	72755_1.R1010
5'-most EST	g2763172

Seq. No.	132411
Contig ID	72768_1.R1010
5'-most EST	jC-atXLIB327421P1f04b1
Method	BLASTN
NCBI GI	g4757409
BLAST score	255
E value	1.0e-141
Match length	558
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	132412
Contig ID	72777_1.R1010
5'-most EST	jC-atXLIB327421P1f10b1
Method	BLASTX
NCBI GI	g3142300

BLAST score	340
E value	9.0e-32
Match length	76
% identity	86
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	132413
Contig ID	72788_1.R1010
5'-most EST	LIB35-050-Q1-E1-D10
Method	BLASTN
NCBI GI	g3869072
BLAST score	121
E value	2.0e-61
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	132414
Contig ID	72810_1.R1010
5'-most EST	jC-atXLIB327421P2g04b1
Method	BLASTN
NCBI GI	g4335744
BLAST score	306
E value	1.0e-171
Match length	370
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132415
Contig ID	72820_1.R1010
5'-most EST	jC-atXLIB327421P2g08b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	51
E value	1.0e-19
Match length	164
% identity	42
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	132416
Contig ID	72839_1.R1010
5'-most EST	jC-atXLIB327421P1f07b1
Method	BLASTN
NCBI GI	g2702261
BLAST score	486
E value	0.0e+00
Match length	502
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 132417

Contig ID	72860_1.R1010
5'-most EST	jC-atXLIB327421P4f02b1
Method	BLASTX
NCBI GI	g4138916
BLAST score	480
E value	3.0e-48
Match length	117
% identity	75
NCBI Description	(AF059489) expansin precursor [Lycopersicon esculentum]

Seq. No.	132418
Contig ID	72890_1.R1010
5'-most EST	LIB35-048-Q1-E1-F5
Method	BLASTN
NCBI GI	g2924732
BLAST score	290
E value	1.0e-162
Match length	579
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	132419
Contig ID	72892_1.R1010
5'-most EST	jC-atXLIB327421P2g02b1
Method	BLASTX
NCBI GI	g3983103
BLAST score	408
E value	9.0e-40
Match length	134
% identity	58
NCBI Description	(AF097441) phenylalanine-tRNA synthetase [Homo sapiens]

Seq. No.	132420
Contig ID	72919_1.R1010
5'-most EST	jC-atXLIB327421P2f08b1
Method	BLASTN
NCBI GI	g2337888
BLAST score	311
E value	1.0e-175
Match length	339
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	132421
Contig ID	72933_1.R1010
5'-most EST	jC-atXLIB327421P4f03b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	300
E value	1.0e-168
Match length	350
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	132422
Contig ID	72951_1.R1010
5'-most EST	g2047802
Method	BLASTN
NCBI GI	g3859658
BLAST score	352
E value	0.0e+00
Match length	465
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	132423
Contig ID	72951_3.R1010
5'-most EST	jC-atXLIB327421P1g11b1
Method	BLASTN
NCBI GI	g3859658
BLAST score	192
E value	1.0e-103
Match length	361
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	132424
Contig ID	72972_1.R1010
5'-most EST	jC-atXLIB327421P3f09b1
Method	BLASTX
NCBI GI	g2160181
BLAST score	362
E value	2.0e-34
Match length	76
% identity	99
NCBI Description	(AC000132) EST gb_ATTS2829 comes from this gene. [Arabidopsis thaliana]

Seq. No.	132425
Contig ID	73011_1.R1010
5'-most EST	jC-atXLIB327421P1h11b1
Method	BLASTX
NCBI GI	g4056425
BLAST score	617
E value	3.0e-64
Match length	118
% identity	100
NCBI Description	(AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come from this gene. [Arabidopsis thaliana]

Seq. No.	132426
Contig ID	73034_1.R1010
5'-most EST	jC-atXLIB327421P3g04b1
Method	BLASTX
NCBI GI	g2244871
BLAST score	431
E value	2.0e-42
Match length	106
% identity	83

NCBI Description	(Z97338) phosphocholine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	132427
Contig ID	73046_1.R1010
5'-most EST	jC-atXLIB327421P3g12b1
Method	BLASTX
NCBI GI	g3080436
BLAST score	506
E value	4.0e-51
Match length	113
% identity	89
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	132428
Contig ID	73053_1.R1010
5'-most EST	jC-atXLIB327421P4g11b1
Method	BLASTX
NCBI GI	g2668505
BLAST score	180
E value	8.0e-13
Match length	92
% identity	41
NCBI Description	(U61837) putative cyclin G1 interacting protein [Homo sapiens]

Seq. No.	132429
Contig ID	73063_1.R1010
5'-most EST	jC-atXLIB327421P2h03b1
Method	BLASTN
NCBI GI	g4757395
BLAST score	281
E value	1.0e-156
Match length	543
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	132430
Contig ID	73073_1.R1010
5'-most EST	jC-atXLIB327421P2h06b1
Method	BLASTN
NCBI GI	g4519183
BLAST score	286
E value	1.0e-159
Match length	578
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	132431
Contig ID	73073_2.R1010
5'-most EST	jC-alX35052Q1E1E06b1
Method	BLASTN
NCBI GI	g4519183
BLAST score	225
E value	1.0e-123

Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	132432
Contig ID	73082_1.R1010
5'-most EST	g2393674
Method	BLASTX
NCBI GI	g4056462
BLAST score	476
E value	9.0e-48
Match length	96
% identity	96
NCBI Description	(AC005990) Strong similarity to gb_Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF_00171. ESTs gb_F15117, gb_R83958 and gb_586262 come from this gene. [Arabidopsis thaliana]

Seq. No.	132433
Contig ID	73083_1.R1010
5'-most EST	jC-atXLIB327421P1h12b1
Method	BLASTN
NCBI GI	g4589415
BLAST score	228
E value	1.0e-125
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	132434
Contig ID	73116_1.R1010
5'-most EST	jC-atXLIB327421P3g06b1
Method	BLASTX
NCBI GI	g3924823
BLAST score	248
E value	1.0e-20
Match length	119
% identity	41
NCBI Description	(Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST yk491a11.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	132435
Contig ID	73116_2.R1010
5'-most EST	g2413984
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	5.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 132436

Contig ID	73124_1.R1010
5'-most EST	jC-atXLIB327421P4g09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	5.0e-26
Match length	70
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132437
Contig ID	73126_1.R1010
5'-most EST	jC-atXP44C170J22T7085a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	48
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132438
Contig ID	73195_1.R1010
5'-most EST	g493414

Seq. No.	132439
Contig ID	73206_1.R1010
5'-most EST	LIB35-054-Q1-E1-D2
Method	BLASTN
NCBI GI	g3985934
BLAST score	325
E value	0.0e+00
Match length	325
% identity	67
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	132440
Contig ID	73225_1.R1010
5'-most EST	jC-atXLIB327421P1h10b1
Method	BLASTX
NCBI GI	g3763918
BLAST score	363
E value	2.0e-34
Match length	137
% identity	58
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	132441
Contig ID	73226_1.R1010
5'-most EST	jC-atXLIB327431P4f05a1
Method	BLASTN
NCBI GI	g3046847
BLAST score	471
E value	0.0e+00

Match length	471
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	132442
Contig ID	73226_2.R1010
5'-most EST	g2446034
Method	BLASTN
NCBI GI	g3046847
BLAST score	306
E value	1.0e-171
Match length	314
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	132443
Contig ID	73241_1.R1010
5'-most EST	jC-atXLIB327421P3h02b1
Method	BLASTX
NCBI GI	g4559382
BLAST score	222
E value	5.0e-18
Match length	76
% identity	51
NCBI Description	(AC006526) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	132444
Contig ID	73251_1.R1010
5'-most EST	LIB35-055-Q1-E1-A6

Seq. No.	132445
Contig ID	73258_1.R1010
5'-most EST	LIB35-055-Q1-E2-B6

Seq. No.	132446
Contig ID	73259_1.R1010
5'-most EST	LIB35-055-Q1-E2-B7

Seq. No.	132447
Contig ID	73264_1.R1010
5'-most EST	LIB35-055-Q1-E2-C6

Seq. No.	132448
Contig ID	73265_1.R1010
5'-most EST	LIB35-055-Q1-E1-C7
Method	BLASTN
NCBI GI	g4589415
BLAST score	101
E value	1.0e-49
Match length	312
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No. 132449
Contig ID 73271_1.R1010
5'-most EST LIB35-055-Q1-E2-D6

Seq. No. 132450
Contig ID 73272_1.R1010
5'-most EST LIB35-055-Q1-E2-D7

Seq. No. 132451
Contig ID 73276_1.R1010
5'-most EST LIB35-055-Q1-E2-E6

Seq. No. 132452
Contig ID 73277_1.R1010
5'-most EST LIB35-055-Q1-E1-E7
Method BLASTX
NCBI GI g131398
BLAST score 175
E value 8.0e-13
Match length 50
% identity 74
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 132453
Contig ID 73278_1.R1010
5'-most EST jC-atXLIB327422P1a05b1
Method BLASTX
NCBI GI g1001263
BLAST score 690
E value 2.0e-72
Match length 213
% identity 62
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 132454
Contig ID 73282_1.R1010
5'-most EST jC-atXLIB327422P1a10b1
Method BLASTX
NCBI GI g3063466
BLAST score 212
E value 2.0e-16
Match length 171
% identity 30
NCBI Description (AC003981) F22O13.28 [Arabidopsis thaliana]

Seq. No. 132455
Contig ID 73282_2.R1010
5'-most EST g2413414
Method BLASTX

NCBI GI	g3063466
BLAST score	167
E value	2.0e-11
Match length	100
% identity	37
NCBI Description	(AC003981) F22O13.28 [Arabidopsis thaliana]

Seq. No.	132456
Contig ID	73283_1.R1010
5'-most EST	LIB35-055-Q1-E1-F6
Method	BLASTN
NCBI GI	g940369
BLAST score	86
E value	1.0e-40
Match length	146
% identity	90
NCBI Description	Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase (ACS4) gene, complete cds

Seq. No.	132457
Contig ID	73293_1.R1010
5'-most EST	LIB35-055-Q1-E1-H1
Method	BLASTN
NCBI GI	g1769904
BLAST score	176
E value	2.0e-94
Match length	252
% identity	93
NCBI Description	A.thaliana psbP gene

Seq. No.	132458
Contig ID	73296_1.R1010
5'-most EST	LIB35-055-Q1-E2-H6

Seq. No.	132459
Contig ID	73297_1.R1010
5'-most EST	LIB35-055-Q1-E2-H7
Method	BLASTX
NCBI GI	g133028
BLAST score	121
E value	4.0e-20
Match length	109
% identity	61
NCBI Description	50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9) >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor, chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_ (Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi_16501_emb_CAA77594_ (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No.	132460
Contig ID	73383_1.R1010
5'-most EST	jC-atXLIB327421P3h11b1
Method	BLASTN
NCBI GI	g3046854
BLAST score	81
E value	4.0e-37

Match length	89
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	132461
Contig ID	73386_1.R1010
5'-most EST	LIB35-056-Q1-E2-C4
Method	BLASTN
NCBI GI	g4490734
BLAST score	202
E value	1.0e-110
Match length	294
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	132462
Contig ID	73388_1.R1010
5'-most EST	jC-atXLIB327422P2a04b2
Method	BLASTN
NCBI GI	g4469002
BLAST score	577
E value	0.0e+00
Match length	609
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	132463
Contig ID	73390_1.R1010
5'-most EST	jC-atXP111C124K3T7s1
Method	BLASTX
NCBI GI	g2864613
BLAST score	388
E value	1.0e-37
Match length	76
% identity	100
NCBI Description	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	132464
Contig ID	73410_1.R1010
5'-most EST	LIB35-056-Q1-E2-H2

Seq. No.	132465
Contig ID	73417_1.R1010
5'-most EST	jC-atXLIB327421P3h07b1
Method	BLASTN
NCBI GI	g2564047
BLAST score	410
E value	0.0e+00
Match length	539
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	132466
Contig ID	73426_1.R1010
5'-most EST	jC-atXP9C94F11T7s1
Method	BLASTN
NCBI GI	g4263774
BLAST score	423
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132467
Contig ID	73456_1.R1010
5'-most EST	jC-atXLIB327422P2a06b2

Seq. No.	132468
Contig ID	73457_1.R1010
5'-most EST	jC-atXLIB327422P1a07b1
Method	BLASTX
NCBI GI	g2911049
BLAST score	633
E value	4.0e-66
Match length	124
% identity	97
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	132469
Contig ID	73490_1.R1010
5'-most EST	ARABL1-01-Q1-B1-C5
Method	BLASTX
NCBI GI	g1255951
BLAST score	397
E value	6.0e-39
Match length	94
% identity	76
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	132470
Contig ID	73491_1.R1010
5'-most EST	ARABL1-01-Q1-B1-B5

Seq. No.	132471
Contig ID	73496_1.R1010
5'-most EST	jC-atXLIB327431P3a01a1
Method	BLASTX
NCBI GI	g3024708
BLAST score	213
E value	1.0e-16
Match length	101
% identity	45
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID 20/15 KD SUBUNITS (TAFII-20/TAFII-15) (TAFII20/TAFII15) >gi_2135937_pir__JC4676 PolII transcription factor TFTIID chain TAFII20 - human >gi_791055_emb_CAA58826_ (X84002)

PolII transcription factor TFTIID [Homo sapiens] >gi_1345404_dbj_BAA09112_ (D50544) TFIID subunit p22 [Homo sapiens] >gi_1373377 (U57693) TAF20 [Homo sapiens]

Seq. No.	132472
Contig ID	73508_1.R1010
5'-most EST	jC-atXLIB327431P2b01a1
Method	BLASTX
NCBI GI	g4835241
BLAST score	522
E value	6.0e-53
Match length	114
% identity	87
NCBI Description	(AL049862) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132473
Contig ID	73514_1.R1010
5'-most EST	g2757067
Method	BLASTN
NCBI GI	g4713943
BLAST score	139
E value	4.0e-72
Match length	366
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	132474
Contig ID	73529_1.R1010
5'-most EST	ARABL1-01-Q1-B2-F1
Method	BLASTX
NCBI GI	g4263711
BLAST score	315
E value	2.0e-40
Match length	164
% identity	54
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	132475
Contig ID	73536_1.R1010
5'-most EST	jC-atXLIB327431P1c06a1
Method	BLASTN
NCBI GI	g3868723
BLAST score	208
E value	1.0e-113
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	132476
Contig ID	73541_1.R1010
5'-most EST	jC-atXLIB327431P1c09a1
Method	BLASTN
NCBI GI	g3128143
BLAST score	173

E value	2.0e-92
Match length	378
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	132477
Contig ID	73550_1.R1010
5'-most EST	ARABL1-01-Q1-E1-A1
Method	BLASTN
NCBI GI	g4757403
BLAST score	40
E value	4.0e-13
Match length	114
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	132478
Contig ID	73552_1.R1010
5'-most EST	ARABL1-044-Q1-E1-A2
Method	BLASTN
NCBI GI	g4733968
BLAST score	343
E value	0.0e+00
Match length	357
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12P23 genomic sequence, complete sequence

Seq. No.	132479
Contig ID	73557_1.R1010
5'-most EST	jC-atXLIB327426P1g04a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132480
Contig ID	73558_1.R1010
5'-most EST	jC-atXP15C107G13T7050a1
Method	BLASTN
NCBI GI	g3702739
BLAST score	53
E value	2.0e-20
Match length	208
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	132481
Contig ID	73563_1.R1010
5'-most EST	jC-atXLIB327423P3f12a1

Method	BLASTX
NCBI GI	g3915842
BLAST score	213
E value	1.0e-24
Match length	73
% identity	85
NCBI Description	RAS-RELATED PROTEIN RAB11A >gi_2598229_emb_CAA70112_ (Y08904) Rab11 protein [Arabidopsis thaliana]

Seq. No.	132482
Contig ID	73590_1.R1010
5'-most EST	jC-atXLIB327402P2h11a1
Method	BLASTX
NCBI GI	g4510385
BLAST score	381
E value	1.0e-36
Match length	102
% identity	72
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	132483
Contig ID	73601_1.R1010
5'-most EST	jC-atXLIB327431P1c02b1

Seq. No.	132484
Contig ID	73605_1.R1010
5'-most EST	ARABL1-037-Q1-E1-F6
Method	BLASTN
NCBI GI	g2351065
BLAST score	380
E value	0.0e+00
Match length	436
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	132485
Contig ID	73607_1.R1010
5'-most EST	jC-atXLIB327431P2c05b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132486
Contig ID	73611_1.R1010
5'-most EST	jC-atXLIB327431P1c09b1
Method	BLASTN
NCBI GI	g3128143
BLAST score	283
E value	1.0e-158
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	132487
Contig ID	73632_1.R1010
5'-most EST	ARABL1-019-Q1-B1-C2
Method	BLASTX
NCBI GI	g4006829
BLAST score	555
E value	3.0e-57
Match length	120
% identity	93
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	132488
Contig ID	73637_1.R1010
5'-most EST	jC-atXL1019Q1B1B09a1

Seq. No.	132489
Contig ID	73647_1.R1010
5'-most EST	jC-atXLIB327431P3f04a1
Method	BLASTX
NCBI GI	g2924509
BLAST score	847
E value	3.0e-91
Match length	173
% identity	95
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	132490
Contig ID	73651_1.R1010
5'-most EST	g1520746
Method	BLASTX
NCBI GI	g2104536
BLAST score	750
E value	8.0e-80
Match length	173
% identity	80
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	132491
Contig ID	73666_1.R1010
5'-most EST	g2593460
Method	BLASTN
NCBI GI	g3702722
BLAST score	261
E value	1.0e-145
Match length	471
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No.	132492
Contig ID	73674_1.R1010
5'-most EST	jC-atXLIB327438P3c06a2

Seq. No.	132493
Contig ID	73684_1.R1010
5'-most EST	jC-atXP112C132E3T7d2
Method	BLASTX
NCBI GI	g3236237
BLAST score	919
E value	2.0e-99
Match length	204
% identity	91
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	132494
Contig ID	73693_1.R1010
5'-most EST	g935668
Method	BLASTX
NCBI GI	g4544399
BLAST score	453
E value	4.0e-45
Match length	140
% identity	65
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	132495
Contig ID	73699_1.R1010
5'-most EST	jC-atXLIB327438P1d08a1

Seq. No.	132496
Contig ID	73723_1.R1010
5'-most EST	jC-atXLIB327431P3a09a1
Method	BLASTN
NCBI GI	g836895
BLAST score	45
E value	5.0e-16
Match length	52
% identity	98
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	132497
Contig ID	73732_1.R1010
5'-most EST	jC-atXLIB327426P1h12a1
Method	BLASTX
NCBI GI	g2088650
BLAST score	388
E value	1.0e-48
Match length	150
% identity	72
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	132498
Contig ID	73732_2.R1010
5'-most EST	jC-atXLIB327431P1c03a1
Method	BLASTX
NCBI GI	g2088650
BLAST score	850

E value	3.0e-91
Match length	185
% identity	65
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	132499
Contig ID	73739_1.R1010
5'-most EST	jC-atXLIB327431P2b10a1
Method	BLASTN
NCBI GI	g4733953
BLAST score	617
E value	0.0e+00
Match length	625
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	132500
Contig ID	73742_1.R1010
5'-most EST	jC-atXLIB327438P3d11b1
Method	BLASTN
NCBI GI	g56539
BLAST score	103
E value	1.0e-50
Match length	309
% identity	100
NCBI Description	R.norvegicus gene encoding prolactin, exon 5 >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene : exon v and flanks

Seq. No.	132501
Contig ID	73752_1.R1010
5'-most EST	jC-atXP80C240E17T7s1
Method	BLASTX
NCBI GI	g4531444
BLAST score	687
E value	2.0e-72
Match length	134
% identity	100
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	132502
Contig ID	73753_1.R1010
5'-most EST	ARABL1-02-Q1-E1-D8
Method	BLASTN
NCBI GI	g4757392
BLAST score	124
E value	9.0e-64
Match length	136
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	132503
Contig ID	73778_1.R1010
5'-most EST	jC-atXLIB327431P3c06a1

Method	BLASTX
NCBI GI	g2664210
BLAST score	315
E value	8.0e-29
Match length	99
% identity	60
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	132504
Contig ID	73783_1.R1010
5'-most EST	jC-atXLIB327431P4c03a1
Method	BLASTX
NCBI GI	g3540181
BLAST score	407
E value	1.0e-39
Match length	143
% identity	62
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	132505
Contig ID	73804_1.R1010
5'-most EST	g976037

Seq. No.	132506
Contig ID	73809_1.R1010
5'-most EST	jC-alXLIB327436P3e06a1
Method	BLASTX
NCBI GI	g3201633
BLAST score	400
E value	8.0e-39
Match length	83
% identity	99
NCBI Description	(AC004669) putative cell division protein [Arabidopsis thaliana]

Seq. No.	132507
Contig ID	73812_1.R1010
5'-most EST	jC-atXLIB327431P2b09b1
Method	BLASTN
NCBI GI	g4417264
BLAST score	205
E value	1.0e-111
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132508
Contig ID	73813_1.R1010
5'-most EST	jC-atXLIB327431P1b11b1
Method	BLASTN
NCBI GI	g4733953
BLAST score	492
E value	0.0e+00
Match length	508
% identity	99

NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	132509
Contig ID	73833_1.R1010
5'-most EST	jC-atXLIB327431P2c01b1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	2.0e-20
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132510
Contig ID	73845_1.R1010
5'-most EST	jC-atXLIB327415P3f08a1
Method	BLASTX
NCBI GI	g4371298
BLAST score	130
E value	4.0e-07
Match length	78
% identity	42
NCBI Description	(AC006260) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	132511
Contig ID	73855_1.R1010
5'-most EST	jC-atXLIB327438P2b10a1

Seq. No.	132512
Contig ID	73870_1.R1010
5'-most EST	jC-atXLIB327438P3b06a2
Method	BLASTX
NCBI GI	g2832625
BLAST score	54
E value	7.0e-50
Match length	162
% identity	58
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	132513
Contig ID	73900_1.R1010
5'-most EST	g906309
Method	BLASTN
NCBI GI	g2351061
BLAST score	334
E value	0.0e+00
Match length	348
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	132514
Contig ID	73931_1.R1010
5'-most EST	ARABL1-021-Q1-B1-A11
Method	BLASTX

NCBI GI	g2894612
BLAST score	638
E value	2.0e-66
Match length	118
% identity	100
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	132515
Contig ID	73937_1.R1010
5'-most EST	jC-atXLIB327438P1b12a1
Method	BLASTN
NCBI GI	g2656032
BLAST score	111
E value	3.0e-55
Match length	251
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	132516
Contig ID	73948_1.R1010
5'-most EST	g1565767
Method	BLASTX
NCBI GI	g2213600
BLAST score	279
E value	1.0e-26
Match length	113
% identity	56
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	132517
Contig ID	73951_1.R1010
5'-most EST	jC-atXLIB327438P4b10a2
Method	BLASTN
NCBI GI	g3985950
BLAST score	411
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]

Seq. No.	132518
Contig ID	73961_1.R1010
5'-most EST	jC-atXLIB327431P3g09a1
Method	BLASTN
NCBI GI	g2244901
BLAST score	424
E value	0.0e+00
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132519
Contig ID	73963_1.R1010
5'-most EST	jC-atXLIB327438P2c04a1

Method	BLASTN
NCBI GI	g4757401
BLAST score	118
E value	1.0e-59
Match length	316
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	132520
Contig ID	73970_1.R1010
5'-most EST	g2048349
Method	BLASTN
NCBI GI	g3869062
BLAST score	38
E value	7.0e-12
Match length	55
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	132521
Contig ID	73995_1.R1010
5'-most EST	jC-atXLIB327438P3c10a2
Method	BLASTX
NCBI GI	g2392895
BLAST score	750
E value	7.0e-80
Match length	152
% identity	95
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	132522
Contig ID	73999_1.R1010
5'-most EST	ARABL1-023-Q1-B1-C7
Method	BLASTX
NCBI GI	g3021269
BLAST score	515
E value	2.0e-52
Match length	109
% identity	89
NCBI Description	(AL022347) putative protein [Arabidopsis thaliana]

Seq. No.	132523
Contig ID	74007_1.R1010
5'-most EST	jC-atXLIB327409P3h06a1

Seq. No.	132524
Contig ID	74029_1.R1010
5'-most EST	ARABL1-022-Q1-B1-C2
Method	BLASTX
NCBI GI	g1652807
BLAST score	415
E value	4.0e-40
Match length	275
% identity	37

NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]
Seq. No.	132525
Contig ID	74032_1.R1010
5'-most EST	jC-atXLIB327438P3b09a2
Method	BLASTN
NCBI GI	g4584387
BLAST score	257
E value	1.0e-142
Match length	484
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)
Seq. No.	132526
Contig ID	74032_2.R1010
5'-most EST	g315453
Method	BLASTN
NCBI GI	g4584387
BLAST score	248
E value	1.0e-137
Match length	707
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)
Seq. No.	132527
Contig ID	74037_1.R1010
5'-most EST	jC-atXLIB327438P2c06a1
Method	BLASTN
NCBI GI	g531832
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cloning vector pSport2, complete sequence
Seq. No.	132528
Contig ID	74053_1.R1010
5'-most EST	ARABLI-022-Q1-B1-E8
Seq. No.	132529
Contig ID	74055_1.R1010
5'-most EST	ARABLI-022-Q1-B1-F1
Method	BLASTX
NCBI GI	g4539315
BLAST score	278
E value	2.0e-30
Match length	112
% identity	61
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	132530
Contig ID	74068_1.R1010
5'-most EST	jC-atXP73CF3D9T7d2
Method	BLASTX

NCBI GI	g731834
BLAST score	422
E value	6.0e-41
Match length	346
% identity	33
NCBI Description	HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION >gi_1077790_pir__S49797 hypothetical protein YIL083c - yeast (Saccharomyces cerevisiae) >gi_577131_emb_CAA86711.1_ (Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17 [Saccharomyces cerevisiae]

Seq. No.	132531
Contig ID	74068_3.R1010
5'-most EST	ARABL1-022-Q1-B1-G12
Method	BLASTX
NCBI GI	g731834
BLAST score	256
E value	5.0e-22
Match length	123
% identity	50
NCBI Description	HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION >gi_1077790_pir__S49797 hypothetical protein YIL083c - yeast (Saccharomyces cerevisiae) >gi_577131_emb_CAA86711.1_ (Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17 [Saccharomyces cerevisiae]

Seq. No.	132532
Contig ID	74115_1.R1010
5'-most EST	jC-atXLIB327438P2e11a1
Method	BLASTX
NCBI GI	g2462827
BLAST score	550
E value	1.0e-57
Match length	138
% identity	93
NCBI Description	(AF000657) probable thiamin biosynthetic enzyme [Arabidopsis thaliana]

Seq. No.	132533
Contig ID	74136_1.R1010
5'-most EST	ARABL1-023-Q1-B1-F1

Seq. No.	132534
Contig ID	74152_1.R1010
5'-most EST	jC-atXLIB327438P1f08a1
Method	BLASTN
NCBI GI	g4490324
BLAST score	47
E value	3.0e-17
Match length	115
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	132535
Contig ID	74166_1.R1010
5'-most EST	jC-atXLIB327438P4d06a2

Method	BLASTX
NCBI GI	g576509
BLAST score	191
E value	6.0e-20
Match length	110
% identity	50
NCBI Description	(L36857) GTP-binding protein [Pisum sativum]

Seq. No.	132536
Contig ID	74169_1.R1010
5'-most EST	g2764232
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	1.0e-18
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132537
Contig ID	74179_1.R1010
5'-most EST	jC-atXLIB327438P1e03a1
Method	BLASTN
NCBI GI	g4757401
BLAST score	121
E value	2.0e-61
Match length	350
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	132538
Contig ID	74184_1.R1010
5'-most EST	jC-atXLIB327438P2e01a1

Seq. No.	132539
Contig ID	74194_1.R1010
5'-most EST	jC-atXLIB327438P2e09a1
Method	BLASTX
NCBI GI	g2443329
BLAST score	538
E value	5.0e-55
Match length	140
% identity	71
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	132540
Contig ID	74196_1.R1010
5'-most EST	jC-atXLIB327438P2e10a1
Method	BLASTX
NCBI GI	g2642154
BLAST score	333
E value	5.0e-31
Match length	132
% identity	53
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

Seq. No.	132541
Contig ID	74198_1.R1010
5'-most EST	jC-atXLIB327438P1e11a1
Method	BLASTN
NCBI GI	g4220632
BLAST score	39
E value	2.0e-12
Match length	387
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	132542
Contig ID	74205_1.R1010
5'-most EST	jC-atXLIB327438P4e05a2
Method	BLASTN
NCBI GI	g4753645
BLAST score	86
E value	2.0e-40
Match length	402
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)

Seq. No.	132543
Contig ID	74210_1.R1010
5'-most EST	jC-atXP117C141F24T7a1
Method	BLASTN
NCBI GI	g2244901
BLAST score	234
E value	1.0e-128
Match length	606
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132544
Contig ID	74210_2.R1010
5'-most EST	jC-atXL1023Q1B1F04a1
Method	BLASTN
NCBI GI	g2244901
BLAST score	331
E value	0.0e+00
Match length	355
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132545
Contig ID	74222_1.R1010
5'-most EST	ARABL1-046-Q1-B1-B3

Seq. No.	132546
Contig ID	74255_1.R1010
5'-most EST	ARABL1-025-Q1-B1-C2

Method	BLASTX
NCBI GI	g3738333
BLAST score	281
E value	6.0e-25
Match length	82
% identity	73
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	132547
Contig ID	74264_1.R1010
5'-most EST	jC-atXL1025Q1B1D03a1
Method	BLASTX
NCBI GI	g4678308
BLAST score	156
E value	2.0e-10
Match length	118
% identity	18
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	132548
Contig ID	74273_1.R1010
5'-most EST	ARABLI-025-Q1-B1-E11
Method	BLASTX
NCBI GI	g4063750
BLAST score	348
E value	7.0e-33
Match length	121
% identity	59
NCBI Description	(AC005851) putative indole-3-acetate beta-glucosyltransferase synthetase [Arabidopsis thaliana]

Seq. No.	132549
Contig ID	74285_1.R1010
5'-most EST	jC-atXLIB327438P4e08a2
Method	BLASTX
NCBI GI	g4539351
BLAST score	778
E value	3.0e-83
Match length	149
% identity	98
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	132550
Contig ID	74290_1.R1010
5'-most EST	jC-atXLIB327438P1f02a1
Method	BLASTX
NCBI GI	g4587513
BLAST score	218
E value	4.0e-38
Match length	122
% identity	68
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	132551
Contig ID	74298_1.R1010
5'-most EST	jC-atXLIB327438P1f04a1

Method	BLASTX
NCBI GI	g3341697
BLAST score	266
E value	5.0e-23
Match length	54
% identity	96
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132552
Contig ID	74349_1.R1010
5'-most EST	jC-atXP62C202H22T7d2
Method	BLASTX
NCBI GI	g4503375
BLAST score	332
E value	7.0e-65
Match length	290
% identity	48
NCBI Description	dihydropyrimidinase >gi_3122049_sp_Q14117_DPYS_HUMAN DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) >gi_1330236_dbj_BAA11189_ (D78011) dihydropyrimidinase [Homo sapiens] >gi_3608122_dbj_BAA33067_ (AB004678) dihydropyrimidinase [Homo sapiens]

Seq. No.	132553
Contig ID	74354_1.R1010
5'-most EST	ARABLI-026-Q1-B1-E12
Method	BLASTX
NCBI GI	g3461821
BLAST score	267
E value	2.0e-23
Match length	135
% identity	48
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	132554
Contig ID	74355_1.R1010
5'-most EST	jC-atXLIB327438P4e01a2
Method	BLASTX
NCBI GI	g3451075
BLAST score	174
E value	4.0e-60
Match length	122
% identity	94
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	132555
Contig ID	74359_1.R1010
5'-most EST	g1268396
Method	BLASTX
NCBI GI	g2253442
BLAST score	224
E value	5.0e-18
Match length	63
% identity	59
NCBI Description	(AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No.	132556
Contig ID	74362_1.R1010
5'-most EST	g2393298
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	8.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132557
Contig ID	74362_2.R1010
5'-most EST	jC-atXP18C111D4T7d2

Seq. No.	132558
Contig ID	74370_1.R1010
5'-most EST	jC-atXLIB327438P3e08a2
Method	BLASTX
NCBI GI	g2244792
BLAST score	516
E value	3.0e-52
Match length	113
% identity	88
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	132559
Contig ID	74377_1.R1010
5'-most EST	ARABL1-026-Q1-B1-G4
Method	BLASTX
NCBI GI	g125576
BLAST score	264
E value	7.0e-23
Match length	55
% identity	93
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	132560
Contig ID	74399_1.R1010
5'-most EST	jC-atXP20C116B2T7d2
Method	BLASTX
NCBI GI	g208092
BLAST score	67
E value	1.0e-17
Match length	139
% identity	27
NCBI Description	(M11334) synthetic calmodulin [Artificial gene] >gi_208412 (M26151) camodulin [Artificial sequence]

Seq. No.	132561
Contig ID	74414_1.R1010
5'-most EST	g1269284
Method	BLASTX

NCBI GI	g3204125
BLAST score	334
E value	4.0e-31
Match length	95
% identity	71
NCBI Description	(AJ006766) putative Pi starvation-induced protein [Cicer arietinum]

Seq. No.	132562
Contig ID	74415_1.R1010
5'-most EST	jC-atXLIB327438P1g10a1

Seq. No.	132563
Contig ID	74419_1.R1010
5'-most EST	jC-atXLIB327438P2g07a1
Method	BLASTN
NCBI GI	g2967455
BLAST score	381
E value	0.0e+00
Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana gene for sulfate transporter, complete cds, clone:AST12

Seq. No.	132564
Contig ID	74436_1.R1010
5'-most EST	jC-atXLIB327438P4g05b2

Seq. No.	132565
Contig ID	74440_1.R1010
5'-most EST	jC-atXLIB327438P3g06a2
Method	BLASTX
NCBI GI	g3880399
BLAST score	149
E value	2.0e-09
Match length	76
% identity	36
NCBI Description	(Z71267) predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	132566
Contig ID	74478_1.R1010
5'-most EST	jC-atXLIB327438P3f07a2
Method	BLASTX
NCBI GI	g2914693
BLAST score	89
E value	7.0e-59
Match length	138
% identity	54
NCBI Description	(AC003974) putative protein kinase [Arabidopsis thaliana]

Seq. No.	132567
Contig ID	74533_1.R1010
5'-most EST	ARABLI-028-Q1-B1-H1
Method	BLASTN

NCBI GI	g4519191
BLAST score	282
E value	1.0e-157
Match length	286
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	132568
Contig ID	74549_1.R1010
5'-most EST	jC-atXLIB327438P3f05a2
Method	BLASTN
NCBI GI	g4263813
BLAST score	285
E value	1.0e-159
Match length	469
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132569
Contig ID	74555_1.R1010
5'-most EST	jC-atXLIB327438P4f12a2
Method	BLASTX
NCBI GI	g1173638
BLAST score	387
E value	2.0e-37
Match length	135
% identity	56
NCBI Description	(U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]

Seq. No.	132570
Contig ID	74585_1.R1010
5'-most EST	jC-atXLIB327411P2f06a1
Method	BLASTX
NCBI GI	g4512630
BLAST score	204
E value	7.0e-16
Match length	71
% identity	54
NCBI Description	(AC004793) Contains reverse transcriptase domain (rvt) PF_00078. [Arabidopsis thaliana]

Seq. No.	132571
Contig ID	74591_1.R1010
5'-most EST	jC-atXLIB327438P1c09a1
Method	BLASTX
NCBI GI	g3096947
BLAST score	216
E value	3.0e-17
Match length	147
% identity	32
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No. 132572

Contig ID	74593_1.R1010
5'-most EST	jC-atXP123C118J14T7053d1
Method	BLASTN
NCBI GI	g4757411
BLAST score	41
E value	2.0e-13
Match length	148
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	132573
Contig ID	74597_1.R1010
5'-most EST	ARABL1-03-Q1-B1-A1
Method	BLASTX
NCBI GI	g2500430
BLAST score	508
E value	1.0e-51
Match length	111
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S16

Seq. No.	132574
Contig ID	74599_1.R1010
5'-most EST	jC-atXLIB327431P4c12a1
Method	BLASTX
NCBI GI	g4587557
BLAST score	660
E value	3.0e-69
Match length	128
% identity	100
NCBI Description	(AC006577) Similar to gb_U21858 transcription initiation factor TFIID 31KD subunit (TAFII32) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	132575
Contig ID	74610_1.R1010
5'-most EST	jC-atXLIB327431P4g09a1
Method	BLASTX
NCBI GI	g1175016
BLAST score	289
E value	1.0e-25
Match length	231
% identity	31
NCBI Description	WHITE PROTEIN HOMOLOG >gi_1160186_emb_CAA62631_ (X91249) white [Homo sapiens]

Seq. No.	132576
Contig ID	74620_1.R1010
5'-most EST	jC-atXLIB327408P4h06a1

Seq. No.	132577
Contig ID	74638_1.R1010
5'-most EST	jC-atXLIB327431P3d01a1
Method	BLASTN
NCBI GI	g2947056
BLAST score	86

E value	2.0e-40
Match length	421
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132578
Contig ID	74652_1.R1010
5'-most EST	jC-atXP57C191I3T7065a1
Method	BLASTX
NCBI GI	g2911039
BLAST score	445
E value	5.0e-44
Match length	89
% identity	100
NCBI Description	(AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	132579
Contig ID	74652_2.R1010
5'-most EST	ARABLI-03-Q1-B1-F2
Method	BLASTX
NCBI GI	g2911039
BLAST score	159
E value	5.0e-11
Match length	31
% identity	100
NCBI Description	(AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	132580
Contig ID	74657_1.R1010
5'-most EST	ARABLI-03-Q1-B1-F8

Seq. No.	132581
Contig ID	74666_1.R1010
5'-most EST	ARABLI-10-Q1-B1-A2
Method	BLASTX
NCBI GI	g1055162
BLAST score	154
E value	3.0e-10
Match length	97
% identity	39
NCBI Description	(U40029) coded for by C. elegans cDNA yk16b1.3; coded for by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA yk7e12.5; co

Seq. No.	132582
Contig ID	74672_1.R1010
5'-most EST	jC-atXLIB327431P1e06a1
Method	BLASTN
NCBI GI	g2244747
BLAST score	205
E value	1.0e-111
Match length	527

% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132583
Contig ID	74676_1.R1010
5'-most EST	jC-atXLIB327431P2d07a1
Method	BLASTX
NCBI GI	g2980641
BLAST score	112
E value	8.0e-05
Match length	141
% identity	15
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	132584
Contig ID	74681_1.R1010
5'-most EST	jC-atXLIB327438P4f04a2
Method	BLASTN
NCBI GI	g3687221
BLAST score	149
E value	5.0e-78
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132585
Contig ID	74693_1.R1010
5'-most EST	jC-atXL1029Q1B1C07a1
Method	BLASTX
NCBI GI	g2618702
BLAST score	571
E value	4.0e-59
Match length	117
% identity	100
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	132586
Contig ID	74701_1.R1010
5'-most EST	ARABLI-030-Q1-B1-D5

Seq. No.	132587
Contig ID	74702_1.R1010
5'-most EST	jC-atXLIB327438P1g12a1

Seq. No.	132588
Contig ID	74725_1.R1010
5'-most EST	jC-atXLIB327438P1h09a1
Method	BLASTN
NCBI GI	g3869072
BLAST score	126
E value	3.0e-64
Match length	327
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	132589
Contig ID	74765_1.R1010
5'-most EST	ARABL1-031-Q1-B1-F11
Method	BLASTX
NCBI GI	g3451074
BLAST score	398
E value	4.0e-43
Match length	187
% identity	49
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	132590
Contig ID	74774_1.R1010
5'-most EST	jC-atXP125CH6048a1
Method	BLASTX
NCBI GI	g3786324
BLAST score	314
E value	1.0e-28
Match length	113
% identity	52
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	132591
Contig ID	74777_1.R1010
5'-most EST	g2763822
Method	BLASTN
NCBI GI	g2244747
BLAST score	391
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132592
Contig ID	74781_1.R1010
5'-most EST	g2748582

Seq. No.	132593
Contig ID	74803_1.R1010
5'-most EST	jC-atXP15C107J19T7059a1
Method	BLASTX
NCBI GI	g2894598
BLAST score	632
E value	7.0e-66
Match length	166
% identity	75
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	132594
Contig ID	74822_1.R1010
5'-most EST	jC-atXLIB327424P1h09a1
Method	BLASTX
NCBI GI	g3169171
BLAST score	169

E value	8.0e-12
Match length	33
% identity	94
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	132595
Contig ID	74824_1.R1010
5'-most EST	jC-atXLIB327440P1e03a1
Method	BLASTX
NCBI GI	g1531758
BLAST score	277
E value	2.0e-24
Match length	111
% identity	51
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	132596
Contig ID	74835_1.R1010
5'-most EST	jC-atXP75C226G18T7s1
Method	BLASTN
NCBI GI	g4325281
BLAST score	169
E value	4.0e-90
Match length	332
% identity	99
NCBI Description	Arabidopsis thaliana NAC domain protein NAM gene, complete cds

Seq. No.	132597
Contig ID	74854_1.R1010
5'-most EST	jC-atXLIB327440P1g06a1
Method	BLASTX
NCBI GI	g3236261
BLAST score	653
E value	4.0e-68
Match length	227
% identity	59
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	132598
Contig ID	74869_1.R1010
5'-most EST	ARABL1-032-Q1-B1-D7
Method	BLASTN
NCBI GI	g2564050
BLAST score	200
E value	1.0e-108
Match length	382
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	132599
Contig ID	74905_1.R1010

5'-most EST	g2047781
Method	BLASTX
NCBI GI	g1711513
BLAST score	451
E value	8.0e-45
Match length	94
% identity	96
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54) >gi_515681 (U12127) signal recognition particle 54 kDa subunit [Arabidopsis thaliana]

Seq. No.	132600
Contig ID	74913_1.R1010
5'-most EST	jC-atXmonuni25Aa12a1
Method	BLASTX
NCBI GI	g4519539
BLAST score	405
E value	3.0e-39
Match length	99
% identity	80
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	132601
Contig ID	74922_1.R1010
5'-most EST	g2747459
Method	BLASTX
NCBI GI	g3063709
BLAST score	478
E value	5.0e-48
Match length	96
% identity	93
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	132602
Contig ID	74927_1.R1010
5'-most EST	jC-atXP5C89L23T7058a1
Method	BLASTX
NCBI GI	g2583132
BLAST score	362
E value	3.0e-34
Match length	124
% identity	59
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	132603
Contig ID	74934_1.R1010
5'-most EST	g2048549

Seq. No.	132604
Contig ID	74940_1.R1010
5'-most EST	jC-atXP12C103B6T7047a1
Method	BLASTN
NCBI GI	g4757413
BLAST score	601
E value	0.0e+00
Match length	601

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	132605
Contig ID	74950_1.R1010
5'-most EST	jC-atXP73C223G10T7b1
Method	BLASTX
NCBI GI	g4725945
BLAST score	895
E value	1.0e-96
Match length	202
% identity	81
NCBI Description	(AL049730) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	132606
Contig ID	74950_2.R1010
5'-most EST	jC-atXP115C248N15T7076d1
Method	BLASTX
NCBI GI	g4725945
BLAST score	63
E value	8.0e-91
Match length	203
% identity	79
NCBI Description	(AL049730) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	132607
Contig ID	74963_1.R1010
5'-most EST	jC-atXLIB327440P1g11a1
Method	BLASTX
NCBI GI	g4455242
BLAST score	298
E value	7.0e-27
Match length	80
% identity	62
NCBI Description	(AL035523) geranylgeranylated protein ATGP4 [Arabidopsis thaliana]

Seq. No.	132608
Contig ID	74978_1.R1010
5'-most EST	ARABLI-033-Q1-B1-F4
Method	BLASTX
NCBI GI	g2281643
BLAST score	356
E value	1.0e-33
Match length	94
% identity	77
NCBI Description	(AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]

Seq. No.	132609
Contig ID	74985_1.R1010
5'-most EST	ARABLI-033-Q1-B1-G11
Method	BLASTN
NCBI GI	g3128137
BLAST score	228
E value	1.0e-125

Match length 498
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 132610
Contig ID 74997_1.R1010
5'-most EST g2759055

Seq. No. 132611
Contig ID 75003_1.R1010
5'-most EST jC-atXLIB327403P3g06a2

Seq. No. 132612
Contig ID 75015_1.R1010
5'-most EST ARABLI-033-Q1-E1-B5

Seq. No. 132613
Contig ID 75030_1.R1010
5'-most EST ARABLI-033-Q1-E1-D9
Method BLASTN
NCBI GI g4757405
BLAST score 301
E value 1.0e-169
Match length 405
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No. 132614
Contig ID 75051_1.R1010
5'-most EST jC-atXP125C200B8T7019a1
Method BLASTX
NCBI GI g4585879
BLAST score 98
E value 1.0e-53
Match length 188
% identity 73
NCBI Description (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

Seq. No. 132615
Contig ID 75051_2.R1010
5'-most EST jC-atXLIB327408P1e07a1
Method BLASTX
NCBI GI g3402694
BLAST score 285
E value 2.0e-25
Match length 114
% identity 55
NCBI Description (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]

Seq. No. 132616
Contig ID 75052_1.R1010
5'-most EST jC-atXL1033Q1E1G04b1

Seq. No. 132617

Contig ID	75058_1.R1010
5'-most EST	ARABLI-046-Q1-E1-A9
Method	BLASTX
NCBI GI	g3152581
BLAST score	218
E value	9.0e-18
Match length	52
% identity	83
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	132618
Contig ID	75090_1.R1010
5'-most EST	ARABLI-034-Q1-B1-E11
Method	BLASTX
NCBI GI	g2827548
BLAST score	382
E value	9.0e-37
Match length	103
% identity	66
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	132619
Contig ID	75107_1.R1010
5'-most EST	jC-atXLIB327440P4g09a1
Method	BLASTN
NCBI GI	g2894591
BLAST score	300
E value	1.0e-168
Match length	408
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	132620
Contig ID	75128_1.R1010
5'-most EST	jC-atXP37C157G24T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	9.0e-16
Match length	61
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132621
Contig ID	75128_2.R1010
5'-most EST	ARABLI-034-Q1-E1-B6

Seq. No.	132622
Contig ID	75132_1.R1010
5'-most EST	ARABLI-034-Q1-E1-C11
Method	BLASTN
NCBI GI	g4559375
BLAST score	39

E value	3.0e-12
Match length	91
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	132623
Contig ID	75136_2.R1010
5'-most EST	g453795
Method	BLASTN
NCBI GI	g3420042
BLAST score	302
E value	1.0e-169
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132624
Contig ID	75144_1.R1010
5'-most EST	g2048654
Method	BLASTX
NCBI GI	g3298536
BLAST score	338
E value	1.0e-31
Match length	74
% identity	96
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	132625
Contig ID	75150_1.R1010
5'-most EST	jC-atXLIB327411P1e12a1
Method	BLASTX
NCBI GI	g3193314
BLAST score	260
E value	2.0e-22
Match length	97
% identity	55
NCBI Description	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

Seq. No.	132626
Contig ID	75154_1.R1010
5'-most EST	jC-atXP43C170A9T7s1
Method	BLASTN
NCBI GI	g2459406
BLAST score	319
E value	1.0e-179
Match length	343
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132627
Contig ID	75160_1.R1010
5'-most EST	ARABL1-035-Q1-B1-A12
Method	BLASTX

NCBI GI	g3063691
BLAST score	600
E value	1.0e-62
Match length	115
% identity	97
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	132628
Contig ID	75171_1.R1010
5'-most EST	ARABLI-035-Q1-B1-B4
Method	BLASTN
NCBI GI	g2262097
BLAST score	263
E value	1.0e-146
Match length	519
% identity	98
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	132629
Contig ID	75193_1.R1010
5'-most EST	ARABLI-035-Q1-B1-D4
Method	BLASTX
NCBI GI	g746510
BLAST score	225
E value	2.0e-18
Match length	74
% identity	54
NCBI Description	(U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans]

Seq. No.	132630
Contig ID	75219_1.R1010
5'-most EST	jC-atX25063Q1E1E11a1
Method	BLASTX
NCBI GI	g4220533
BLAST score	252
E value	1.0e-21
Match length	103
% identity	51
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	132631
Contig ID	75221_1.R1010
5'-most EST	jC-atXP114C231I18T7s1
Method	BLASTX
NCBI GI	g1172873
BLAST score	456
E value	3.0e-45
Match length	88
% identity	81
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	132632
Contig ID	75236_1.R1010
5'-most EST	jC-atXLIB327404P3c04a1
Method	BLASTN
NCBI GI	g4191771
BLAST score	276
E value	1.0e-153
Match length	547
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132633
Contig ID	75257_1.R1010
5'-most EST	jC-atXLIB327440P1h05b1
Method	BLASTX
NCBI GI	g4263711
BLAST score	499
E value	3.0e-50
Match length	147
% identity	68
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	132634
Contig ID	75260_1.R1010
5'-most EST	jC-atX24005Q1E1A03a1
Method	BLASTN
NCBI GI	g3108025
BLAST score	270
E value	1.0e-150
Match length	491
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	132635
Contig ID	75270_1.R1010
5'-most EST	jC-atXLIB327437P2f03a2
Method	BLASTN
NCBI GI	g3132469
BLAST score	345
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132636
Contig ID	75282_1.R1010
5'-most EST	g2722400

Seq. No.	132637
Contig ID	75309_1.R1010
5'-most EST	g95827
Method	BLASTN
NCBI GI	g4531433

BLAST score	206
E value	1.0e-112
Match length	422
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	132638
Contig ID	75309_3.R1010
5'-most EST	ARABL1-036-Q1-B1-C4
Method	BLASTX
NCBI GI	g4531440
BLAST score	489
E value	4.0e-49
Match length	147
% identity	60
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	132639
Contig ID	75312_1.R1010
5'-most EST	g2581717
Method	BLASTN
NCBI GI	g4757402
BLAST score	43
E value	1.0e-14
Match length	115
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	132640
Contig ID	75319_2.R1010
5'-most EST	g1159583
Method	BLASTX
NCBI GI	g2194125
BLAST score	1865
E value	0.0e+00
Match length	345
% identity	98
NCBI Description	(AC002062) ESTs gb_R30459,gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No.	132641
Contig ID	75321_1.R1010
5'-most EST	jC-atXLIB327417P2c06b1
Method	BLASTX
NCBI GI	g2252830
BLAST score	1077
E value	1.0e-118
Match length	229
% identity	94
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	132642
Contig ID	75351_1.R1010
5'-most EST	g3450318

Method	BLASTN
NCBI GI	g2358139
BLAST score	276
E value	1.0e-153
Match length	546
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	132643
Contig ID	75371_1.R1010
5'-most EST	jC-atXLIB327421P4e06a1
Method	BLASTX
NCBI GI	g549977
BLAST score	217
E value	2.0e-17
Match length	57
% identity	75
NCBI Description	(U12859) cDNA-5-encoded protein [Arabidopsis thaliana]

Seq. No.	132644
Contig ID	75371_2.R1010
5'-most EST	jC-alXLIB327436P1g07a1
Method	BLASTX
NCBI GI	g549977
BLAST score	156
E value	3.0e-10
Match length	31
% identity	100
NCBI Description	(U12859) cDNA-5-encoded protein [Arabidopsis thaliana]

Seq. No.	132645
Contig ID	75380_1.R1010
5'-most EST	ARABLI-036-Q1-E1-D9
Method	BLASTN
NCBI GI	g4582428
BLAST score	253
E value	1.0e-140
Match length	314
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	132646
Contig ID	75383_1.R1010
5'-most EST	jC-atXLIB327411P1d01a1
Method	BLASTX
NCBI GI	g2244860
BLAST score	238
E value	1.0e-19
Match length	99
% identity	56
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	132647
Contig ID	75383_2.R1010
5'-most EST	jC-atXLIB327411P1e01a1

Method	BLASTN
NCBI GI	g3985934
BLAST score	175
E value	2.0e-93
Match length	323
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	132648
Contig ID	75383_3.R1010
5'-most EST	jC-atXP118C142N1T7034a1
Method	BLASTN
NCBI GI	g3985934
BLAST score	179
E value	9.0e-96
Match length	458
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	132649
Contig ID	75394_1.R1010
5'-most EST	g2446035
Method	BLASTX
NCBI GI	g4006887
BLAST score	107
E value	1.0e-04
Match length	115
% identity	70
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	132650
Contig ID	75400_1.R1010
5'-most EST	jC-atX22073Q1E1H11a1
Method	BLASTN
NCBI GI	g2564051
BLAST score	391
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	132651
Contig ID	75402_1.R1010
5'-most EST	jC-atXLIB327409P3c03a1
Method	BLASTX
NCBI GI	g4249409
BLAST score	274
E value	7.0e-24
Match length	137
% identity	53
NCBI Description	(AC006072) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	132652

Contig ID	75442_1.R1010
5'-most EST	jC-atXP71C221G13T7s2
Method	BLASTN
NCBI GI	g4063730
BLAST score	475
E value	0.0e+00
Match length	571
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	132653
Contig ID	75474_1.R1010
5'-most EST	jC-atXLIB327438P4e04b2
Method	BLASTN
NCBI GI	g3859658
BLAST score	265
E value	1.0e-147
Match length	357
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	132654
Contig ID	75486_1.R1010
5'-most EST	jC-atXLIB327426P4a07a1
Method	BLASTN
NCBI GI	g4539290
BLAST score	209
E value	1.0e-114
Match length	298
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	132655
Contig ID	75486_2.R1010
5'-most EST	jC-atXLIB327426P3a07a1
Method	BLASTX
NCBI GI	g4539308
BLAST score	164
E value	2.0e-24
Match length	59
% identity	88
NCBI Description	(AL049480) possible apospory-associated like protein [Arabidopsis thaliana]

Seq. No.	132656
Contig ID	75488_1.R1010
5'-most EST	ARABL1-037-Q1-E1-D3
Method	BLASTX
NCBI GI	g2132842
BLAST score	162
E value	6.0e-11
Match length	73
% identity	45

NCBI Description	probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae) >gi_1419909_emb_CAA99087_ (Z74819) ORF YOL077c [Saccharomyces cerevisiae]

Seq. No.	132657
Contig ID	75494_1.R1010
5'-most EST	jC-atXLIB327408P2a04a1
Method	BLASTX
NCBI GI	g3123712
BLAST score	263
E value	9.0e-23
Match length	73
% identity	66
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	132658
Contig ID	75499_1.R1010
5'-most EST	jC-atXLIB327440P1h07b1

Seq. No.	132659
Contig ID	75507_1.R1010
5'-most EST	jC-atXLIB327402P4e03a1
Method	BLASTN
NCBI GI	g4757403
BLAST score	372
E value	0.0e+00
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	132660
Contig ID	75511_1.R1010
5'-most EST	ARABL1-037-Q1-E1-G6
Method	BLASTN
NCBI GI	g3241924
BLAST score	271
E value	1.0e-151
Match length	511
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	132661
Contig ID	75514_1.R1010
5'-most EST	jC-atX25100Q1E1C11a1
Method	BLASTN
NCBI GI	g4432829
BLAST score	187
E value	1.0e-101
Match length	271
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132662
Contig ID	75516_1.R1010

5'-most EST	jC-atXP57C192B17T7077a1
Method	BLASTN
NCBI GI	g1871173
BLAST score	373
E value	0.0e+00
Match length	435
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	132663
Contig ID	75517_1.R1010
5'-most EST	ARABLI-037-Q1-E1-H12
Method	BLASTN
NCBI GI	g4220468
BLAST score	186
E value	1.0e-100
Match length	606
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132664
Contig ID	75550_1.R1010
5'-most EST	ARABLI-038-Q1-E1-D11
Method	BLASTN
NCBI GI	g2618603
BLAST score	113
E value	1.0e-56
Match length	220
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	132665
Contig ID	75551_1.R1010
5'-most EST	jC-atX25065Q1E1F11a1
Method	BLASTN
NCBI GI	g4589424
BLAST score	131
E value	2.0e-67
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No.	132666
Contig ID	75559_1.R1010
5'-most EST	ARABLI-038-Q1-B1-E1

Seq. No.	132667
Contig ID	75573_1.R1010
5'-most EST	jC-atXL1038Q1E1F02a1

Seq. No.	132668
Contig ID	75610_1.R1010
5'-most EST	jC-atXmonuni10Bg01a1

Method	BLASTN
NCBI GI	g3355463
BLAST score	410
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132669
Contig ID	75619_1.R1010
5'-most EST	jC-atXP1C63C7T7s2
Method	BLASTX
NCBI GI	g1703220
BLAST score	219
E value	1.0e-17
Match length	55
% identity	65
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	132670
Contig ID	75628_1.R1010
5'-most EST	jC-atXP10C95G17T7s2
Method	BLASTN
NCBI GI	g4589424
BLAST score	428
E value	0.0e+00
Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No.	132671
Contig ID	75635_1.R1010
5'-most EST	jC-atXLIB327432P4h03a1
Method	BLASTX
NCBI GI	g2213597
BLAST score	138
E value	4.0e-65
Match length	141
% identity	93
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	132672
Contig ID	75638_1.R1010
5'-most EST	g498678

Seq. No.	132673
Contig ID	75649_1.R1010
5'-most EST	ARABL1-038-Q1-E1-F3
Method	BLASTN
NCBI GI	g2245031
BLAST score	223
E value	1.0e-122
Match length	413
% identity	96

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	132674
Contig ID	75651_1.R1010
5'-most EST	jC-atXP76C227H10T7s1
Method	BLASTX
NCBI GI	g3033397
BLAST score	579
E value	8.0e-60
Match length	109
% identity	100
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.	132675
Contig ID	75694_1.R1010
5'-most EST	jC-atXLIB327409P2h12a1
Method	BLASTX
NCBI GI	g4512697
BLAST score	309
E value	7.0e-28
Match length	124
% identity	50
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]
Seq. No.	132676
Contig ID	75703_1.R1010
5'-most EST	g2446008
Method	BLASTN
NCBI GI	g4803835
BLAST score	453
E value	0.0e+00
Match length	600
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds
Seq. No.	132677
Contig ID	75747_1.R1010
5'-most EST	jC-atXLIB327420P1d05a1
Method	BLASTX
NCBI GI	g2651297
BLAST score	557
E value	4.0e-57
Match length	126
% identity	87
NCBI Description	(AC002336) putative expansin [Arabidopsis thaliana]
Seq. No.	132678
Contig ID	75751_1.R1010
5'-most EST	jC-atXP11C97P6T7s1
Seq. No.	132679
Contig ID	75762_1.R1010
5'-most EST	jC-atXLIB327414P3e03b1
Seq. No.	132680

Contig ID	75789_1.R1010
5'-most EST	jC-atXLIB327437P3f11b2
Method	BLASTX
NCBI GI	g1020315
BLAST score	206
E value	8.0e-16
Match length	120
% identity	41
NCBI Description	(U36310) glycerol-3-phosphate dehydrogenase [Homo sapiens] >gi_1389721 (U40367) glycerol-3-phosphate dehydrogenase [Homo sapiens]

Seq. No.	132681
Contig ID	75807_1.R1010
5'-most EST	jC-atXLIB327431P3c09a1
Method	BLASTX
NCBI GI	g4099921
BLAST score	248
E value	5.0e-21
Match length	91
% identity	54
NCBI Description	(U91982) EREBP-3 homolog [Stylosanthes hamata]

Seq. No.	132682
Contig ID	75813_1.R1010
5'-most EST	jC-atXLIB327431P3d12a1
Method	BLASTN
NCBI GI	g836895
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	132683
Contig ID	75845_1.R1010
5'-most EST	jC-atXLIB327431P3d07a1
Method	BLASTX
NCBI GI	g3319457
BLAST score	179
E value	7.0e-13
Match length	99
% identity	39
NCBI Description	(AF077542) contains similarity to O-linked GlcNAc transferases [Caenorhabditis elegans]

Seq. No.	132684
Contig ID	75845_2.R1010
5'-most EST	g930759

Seq. No.	132685
Contig ID	75876_1.R1010
5'-most EST	jC-atXLIB327414P3a12a1
Method	BLASTN
NCBI GI	g531832
BLAST score	41
E value	1.0e-13

Match length	53
% identity	96
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	132686
Contig ID	75883_1.R1010
5'-most EST	jC-atXLIB327414P4b03a2
Method	BLASTX
NCBI GI	g3043612
BLAST score	74
E value	6.0e-15
Match length	110
% identity	45
NCBI Description	(AB011116) KIAA0544 protein [Homo sapiens]

Seq. No.	132687
Contig ID	75917_1.R1010
5'-most EST	jC-atXLIB327414P2e12a1
Method	BLASTN
NCBI GI	g3241927
BLAST score	316
E value	1.0e-177
Match length	516
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	132688
Contig ID	75922_1.R1010
5'-most EST	jC-atXLIB327414P3c09a1
Method	BLASTN
NCBI GI	g836895
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	132689
Contig ID	75945_1.R1010
5'-most EST	jC-atXLIB327414P3a12b1
Method	BLASTN
NCBI GI	g3702737
BLAST score	59
E value	2.0e-24
Match length	128
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	132690
Contig ID	75948_1.R1010
5'-most EST	jC-atXLIB327414P2b05a1

Seq. No.	132691
Contig ID	75970_1.R1010
5'-most EST	jC-alXLIB327435P1g01b1

Method	BLASTX
NCBI GI	g4249402
BLAST score	115
E value	9.0e-45
Match length	150
% identity	74
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	132692
Contig ID	76008_1.R1010
5'-most EST	jC-atXLIB327414P3a02a1
Method	BLASTX
NCBI GI	g4539313
BLAST score	685
E value	4.0e-72
Match length	124
% identity	99
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	132693
Contig ID	76015_1.R1010
5'-most EST	g2047989

Seq. No.	132694
Contig ID	76015_2.R1010
5'-most EST	jC-atXLIB327414P2g09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	37
E value	3.0e-11
Match length	45
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132695
Contig ID	76016_1.R1010
5'-most EST	ARABLI-041-Q1-B1-B2
Method	BLASTX
NCBI GI	g549077
BLAST score	170
E value	3.0e-15
Match length	112
% identity	50
NCBI Description	3-KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE) (PEROXISOMAL 3-OXOACYL-COA THIOLASE) >gi_480423_pir__S36838 acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) >gi_5532_emb_CAA49605_ (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]

Seq. No.	132696
Contig ID	76039_1.R1010
5'-most EST	jC-atXLIB327414P3b07a1
Method	BLASTX
NCBI GI	g4827060
BLAST score	344

E value	7.0e-32
Match length	178
% identity	46
NCBI Description	xylulokinase (H. influenzae) homolog >gi_3298502_dbj_BAA31527_ (AB015046) xylulokinase [Homo sapiens]

Seq. No.	132697
Contig ID	76050_2.R1010
5'-most EST	jC-atX24036Q1E1G06b1
Method	BLASTN
NCBI GI	g4262221
BLAST score	229
E value	1.0e-126
Match length	229
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132698
Contig ID	76069_1.R1010
5'-most EST	jC-atXLIB327414P1d10a1
Method	BLASTX
NCBI GI	g3283893
BLAST score	402
E value	8.0e-39
Match length	184
% identity	45
NCBI Description	(AF070626) unknown [Homo sapiens]

Seq. No.	132699
Contig ID	76088_1.R1010
5'-most EST	jC-atXLIB327416P1f05a1
Method	BLASTN
NCBI GI	g4757410
BLAST score	369
E value	0.0e+00
Match length	425
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	132700
Contig ID	76093_1.R1010
5'-most EST	jC-atXLIB327414P1b05b1
Method	BLASTX
NCBI GI	g549077
BLAST score	294
E value	2.0e-26
Match length	97
% identity	58
NCBI Description	3-KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE) (PEROXISOMAL 3-OXOACYL-COA THIOLASE) >gi_480423_pir__S36838 acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) >gi_5532_emb_CAA49605_ (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]

Seq. No.	132701
Contig ID	76094_1.R1010
5'-most EST	jC-atXLIB327414P2g08b1
Method	BLASTN
NCBI GI	g2342673
BLAST score	365
E value	0.0e+00
Match length	369
% identity	100
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	132702
Contig ID	76095_1.R1010
5'-most EST	jC-atXLIB327414P1b06b1
Method	BLASTN
NCBI GI	g2505873
BLAST score	345
E value	0.0e+00
Match length	384
% identity	97
NCBI Description	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No.	132703
Contig ID	76110_1.R1010
5'-most EST	jC-atXLIB327414P3b10b1
Method	BLASTX
NCBI GI	g4539371
BLAST score	307
E value	6.0e-28
Match length	85
% identity	73
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	132704
Contig ID	76112_1.R1010
5'-most EST	jC-atXLIB327414P4b06b2
Method	BLASTX
NCBI GI	g3335345
BLAST score	260
E value	9.0e-33
Match length	75
% identity	83
NCBI Description	(AC004512) Contains similarity to ABC transporter gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis thaliana]

Seq. No.	132705
Contig ID	76119_1.R1010
5'-most EST	jC-atXLIB327414P2f07b1
Method	BLASTX
NCBI GI	g3859599
BLAST score	666
E value	7.0e-70
Match length	122
% identity	100

NCBI Description	(AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
Seq. No.	132706
Contig ID	76129_1.R1010
5'-most EST	jC-atXP49C177K8T7074a1
Method	BLASTX
NCBI GI	g4510373
BLAST score	373
E value	2.0e-35
Match length	104
% identity	65
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]
Seq. No.	132707
Contig ID	76131_1.R1010
5'-most EST	jC-atXLIB327402P2a05a1
Seq. No.	132708
Contig ID	76139_1.R1010
5'-most EST	jC-atXP63C203P11T7s2
Method	BLASTX
NCBI GI	g4585905
BLAST score	295
E value	1.0e-26
Match length	59
% identity	100
NCBI Description	(AC007133) unknown protein, 5' partial [Arabidopsis thaliana]
Seq. No.	132709
Contig ID	76155_1.R1010
5'-most EST	jC-atXLIB327414P2h06a1
Method	BLASTN
NCBI GI	g2656029
BLAST score	363
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2
Seq. No.	132710
Contig ID	76184_2.R1010
5'-most EST	g1215925
Method	BLASTX
NCBI GI	g3844596
BLAST score	188
E value	4.0e-14
Match length	67
% identity	51
NCBI Description	(U28941) contains similarity to human copine I (GB:U83246) [Caenorhabditis elegans]
Seq. No.	132711
Contig ID	76190_1.R1010

5'-most EST	jC-atXL1042Q1E1E03b1
Method	BLASTN
NCBI GI	g2673901
BLAST score	145
E value	3.0e-76
Match length	145
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132712
Contig ID	76221_1.R1010
5'-most EST	jC-atXLIB327430P2h11a1
Method	BLASTX
NCBI GI	g3319354
BLAST score	66
E value	9.0e-32
Match length	76
% identity	91
NCBI Description	(AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No.	132713
Contig ID	76240_1.R1010
5'-most EST	jC-atXLIB327414P2g07b1

Seq. No.	132714
Contig ID	76240_2.R1010
5'-most EST	jC-atXP7C92C24T7s1

Seq. No.	132715
Contig ID	76250_1.R1010
5'-most EST	jC-atXP20C114E3T7045a1
Method	BLASTN
NCBI GI	g4713943
BLAST score	273
E value	1.0e-152
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	132716
Contig ID	76284_1.R1010
5'-most EST	ARABL1-042-Q1-E1-H6
Method	BLASTX
NCBI GI	g1305531
BLAST score	410
E value	5.0e-40
Match length	87
% identity	80
NCBI Description	(U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum lycopersicum]

Seq. No.	132717

Contig ID	76335_1.R1010
5'-most EST	jC-atXLIB327414P1c08a1
Method	BLASTN
NCBI GI	g598848
BLAST score	39
E value	2.0e-12
Match length	57
% identity	93
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	132718
Contig ID	76349_1.R1010
5'-most EST	ARABL1-043-Q1-B1-G3

Seq. No.	132719
Contig ID	76359_1.R1010
5'-most EST	jC-atXLIB327431P4e06a1
Method	BLASTX
NCBI GI	g2281088
BLAST score	277
E value	2.0e-24
Match length	146
% identity	39
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	132720
Contig ID	76374_1.R1010
5'-most EST	jC-atXLIB327422P3c03a2
Method	BLASTX
NCBI GI	g1923256
BLAST score	181
E value	2.0e-13
Match length	50
% identity	70
NCBI Description	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]

Seq. No.	132721
Contig ID	76382_1.R1010
5'-most EST	g2445953
Method	BLASTN
NCBI GI	g4589439
BLAST score	382
E value	0.0e+00
Match length	414
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	132722
Contig ID	76410_1.R1010
5'-most EST	jC-atXLIB327431P4e06b1
Method	BLASTX
NCBI GI	g2281086
BLAST score	147
E value	7.0e-25

Match length	108
% identity	56
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	132723
Contig ID	76416_1.R1010
5'-most EST	jC-atXLIB327414P3d05a1
Method	BLASTX
NCBI GI	g3582341
BLAST score	373
E value	1.0e-35
Match length	154
% identity	50
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	132724
Contig ID	76419_1.R1010
5'-most EST	jC-atXLIB327414P4d07a2
Method	BLASTN
NCBI GI	g2182285
BLAST score	410
E value	0.0e+00
Match length	580
% identity	80
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	132725
Contig ID	76429_1.R1010
5'-most EST	jC-atXLIB327414P4d11a2

Seq. No.	132726
Contig ID	76435_1.R1010
5'-most EST	g3450103
Method	BLASTN
NCBI GI	g3927822
BLAST score	462
E value	0.0e+00
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132727
Contig ID	76478_1.R1010
5'-most EST	jC-atX24039Q1E1F04a1
Method	BLASTX
NCBI GI	g4539306
BLAST score	798
E value	1.0e-85
Match length	156
% identity	34
NCBI Description	(AL049480) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	132728

Contig ID	76479_1.R1010
5'-most EST	ARABL1-044-Q1-B1-G12
Method	BLASTN
NCBI GI	g3413696
BLAST score	415
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132729
Contig ID	76505_1.R1010
5'-most EST	jC-alX25029Q1E1C11a1

Seq. No.	132730
Contig ID	76514_1.R1010
5'-most EST	jC-atX22008Q1E1E08a1

Seq. No.	132731
Contig ID	76520_1.R1010
5'-most EST	jC-atXLIB327414P2d05b1
Method	BLASTN
NCBI GI	g4239818
BLAST score	85
E value	8.0e-40
Match length	85
% identity	100
NCBI Description	Arabidopsis thaliana gene for PHR1, complete cds

Seq. No.	132732
Contig ID	76534_1.R1010
5'-most EST	jC-atXL1044Q1E1D07b1
Method	BLASTX
NCBI GI	g2749982
BLAST score	184
E value	8.0e-14
Match length	48
% identity	65
NCBI Description	(AF036705) Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans cDNA yk257d4.5;

Seq. No.	132733
Contig ID	76536_1.R1010
5'-most EST	jC-atXLIB327414P4e03b2
Method	BLASTN
NCBI GI	g4510338
BLAST score	296
E value	1.0e-166
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No. 132734
Contig ID 76539_1.R1010
5'-most EST jC-atX23012Q1E1E08a1

Seq. No. 132735
Contig ID 76545_1.R1010
5'-most EST jC-atXmonuni10Be08a1

Seq. No. 132736
Contig ID 76547_1.R1010
5'-most EST ARABLI-044-Q1-E1-F10
Method BLASTN
NCBI GI g4115930
BLAST score 178
E value 1.0e-95
Match length 321
% identity 98
NCBI Description Arabidopsis thaliana BAC T4B21

Seq. No. 132737
Contig ID 76554_1.R1010
5'-most EST jC-atXP91C247J21T7b1
Method BLASTX
NCBI GI g3236255
BLAST score 302
E value 4.0e-27
Match length 144
% identity 42
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No. 132738
Contig ID 76560_1.R1010
5'-most EST jC-atXLIB327414P1f03b1
Method BLASTX
NCBI GI g4325369
BLAST score 491
E value 2.0e-49
Match length 110
% identity 81
NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No. 132739
Contig ID 76565_1.R1010
5'-most EST g501950
Method BLASTX
NCBI GI g1362093
BLAST score 203
E value 8.0e-16
Match length 75
% identity 56
NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)
>gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 132740
Contig ID 76615_1.R1010
5'-most EST g757610

Seq. No.	132741
Contig ID	76649_1.R1010
5'-most EST	jC-atXLIB327414P4d06b2
Method	BLASTX
NCBI GI	g3395436
BLAST score	436
E value	6.0e-43
Match length	121
% identity	76
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	132742
Contig ID	76671_1.R1010
5'-most EST	jC-atX24007Q1E1G08a1
Method	BLASTN
NCBI GI	g3402695
BLAST score	412
E value	0.0e+00
Match length	440
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132743
Contig ID	76672_1.R1010
5'-most EST	ARABLI-045-Q1-E1-E7
Method	BLASTX
NCBI GI	g4490323
BLAST score	348
E value	9.0e-33
Match length	105
% identity	70
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	132744
Contig ID	76703_1.R1010
5'-most EST	ARABLI-046-Q1-B1-C2
Method	BLASTX
NCBI GI	g4454026
BLAST score	506
E value	3.0e-51
Match length	98
% identity	99
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	132745
Contig ID	76720_1.R1010
5'-most EST	jC-atXLIB327422P4h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	2.0e-17
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132746

Contig ID	76720_2.R1010
5'-most EST	jC-atXP1C63E7T7d1
Method	BLASTX
NCBI GI	g4249384
BLAST score	134
E value	7.0e-12
Match length	120
% identity	35
NCBI Description	(AC005966) Similar to gi_4056506 F3G5.25 nodulin-like protein from Arabidopsis thaliana BAC gb_AC005896. [Arabidopsis thaliana]

Seq. No.	132747
Contig ID	76752_1.R1010
5'-most EST	jC-atXLIB327414P2c08a1
Method	BLASTN
NCBI GI	g2244950
BLAST score	181
E value	4.0e-97
Match length	440
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132748
Contig ID	76777_1.R1010
5'-most EST	jC-atXLIB327428P4f04a2
Method	BLASTX
NCBI GI	g2494116
BLAST score	1396
E value	1.0e-155
Match length	288
% identity	94
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	132749
Contig ID	76777_2.R1010
5'-most EST	jC-atXLIB327414P1e02b1
Method	BLASTX
NCBI GI	g2494116
BLAST score	488
E value	4.0e-49
Match length	95
% identity	98
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	132750
Contig ID	76808_1.R1010
5'-most EST	jC-atX24042Q1E1G03b1
Method	BLASTN
NCBI GI	g3600045
BLAST score	212
E value	1.0e-116
Match length	376
% identity	99

NCBI Description	Arabidopsis thaliana BAC F2P3
Seq. No.	132751
Contig ID	76810_1.R1010
5'-most EST	jC-atXLIB327414P2c09b1
Method	BLASTN
NCBI GI	g4056476
BLAST score	380
E value	0.0e+00
Match length	380
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	132752
Contig ID	76811_1.R1010
5'-most EST	jC-atXLIB327414P2c08b1
Method	BLASTN
NCBI GI	g2244950
BLAST score	403
E value	0.0e+00
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	132753
Contig ID	76813_1.R1010
5'-most EST	jC-atXLIB327422P3f06a2
Method	BLASTX
NCBI GI	g2980781
BLAST score	247
E value	1.0e-20
Match length	94
% identity	55
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]
Seq. No.	132754
Contig ID	76824_1.R1010
5'-most EST	jC-atXLIB327414P3d09a1
Method	BLASTN
NCBI GI	g3075383
BLAST score	310
E value	1.0e-174
Match length	525
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	132755
Contig ID	76833_1.R1010
5'-most EST	ARABLI-047-Q1-B1-C12
Method	BLASTN
NCBI GI	g2924655
BLAST score	202
E value	1.0e-110
Match length	263

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence [Arabidopsis thaliana]

Seq. No.	132756
Contig ID	76839_1.R1010
5'-most EST	jC-atXL1047Q1E1C07b1
Method	BLASTN
NCBI GI	g2760166
BLAST score	161
E value	2.0e-85
Match length	204
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK20, complete sequence [Arabidopsis thaliana]

Seq. No.	132757
Contig ID	76851_1.R1010
5'-most EST	jC-atXP123C117E1T7036a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132758
Contig ID	76857_1.R1010
5'-most EST	jC-atXLIB327414P4e06a2
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	4.0e-17
Match length	50
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132759
Contig ID	76859_1.R1010
5'-most EST	jC-atXLIB327414P3e07a1
Method	BLASTX
NCBI GI	g2244899
BLAST score	720
E value	2.0e-76
Match length	143
% identity	100
NCBI Description	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]

Seq. No.	132760
Contig ID	76868_1.R1010
5'-most EST	jC-atXLIB327414P2c12a1
Method	BLASTX
NCBI GI	g3337367
BLAST score	432
E value	1.0e-42
Match length	146

% identity	62
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.	132761
Contig ID	76894_1.R1010
5'-most EST	jC-atXLIB327404P3h08a1
Method	BLASTN
NCBI GI	g2459406
BLAST score	169
E value	3.0e-90
Match length	281
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	132762
Contig ID	76895_1.R1010
5'-most EST	jC-atXLIB327419P2c07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	53
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	132763
Contig ID	76898_1.R1010
5'-most EST	jC-atXLIB327414P2d08b1
Seq. No.	132764
Contig ID	76905_1.R1010
5'-most EST	jC-atXLIB327414P2d04b1
Method	BLASTN
NCBI GI	g4584387
BLAST score	228
E value	1.0e-125
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)
Seq. No.	132765
Contig ID	76917_1.R1010
5'-most EST	jC-atXLIB327414P4e06b2
Seq. No.	132766
Contig ID	76919_1.R1010
5'-most EST	jC-atXP112C128G19T7d2
Method	BLASTN
NCBI GI	g2244870
BLAST score	252
E value	1.0e-139
Match length	537
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132767
Contig ID	76919_2.R1010
5'-most EST	jC-atXP112C128G19T7a1
Method	BLASTN
NCBI GI	g2244870
BLAST score	271
E value	1.0e-150
Match length	525
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	132768
Contig ID	76924_1.R1010
5'-most EST	jC-atXLIB327414P2c12b1
Method	BLASTX
NCBI GI	g3337367
BLAST score	332
E value	7.0e-31
Match length	72
% identity	83
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132769
Contig ID	76951_1.R1010
5'-most EST	jC-atXLIB327431P2d01a1
Method	BLASTX
NCBI GI	g2190542
BLAST score	669
E value	2.0e-70
Match length	134
% identity	100
NCBI Description	(AC001229) F5I14.5 gene product [Arabidopsis thaliana]

Seq. No.	132770
Contig ID	76960_1.R1010
5'-most EST	jC-atXP1C72D7T7d1
Method	BLASTN
NCBI GI	g1871173
BLAST score	475
E value	0.0e+00
Match length	641
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	132771
Contig ID	76966_1.R1010
5'-most EST	jC-atXLIB327431P1d04a1
Method	BLASTX
NCBI GI	g1345504
BLAST score	172
E value	7.0e-12
Match length	137
% identity	34
NCBI Description	(X74756) ATAF2 [Arabidopsis thaliana]

Seq. No.	132772
Contig ID	76966_2.R1010
5'-most EST	jC-atXP41C166C6T7d1
Method	BLASTX
NCBI GI	g3367576
BLAST score	180
E value	1.0e-14
Match length	146
% identity	35
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	132773
Contig ID	76992_1.R1010
5'-most EST	jC-atXLIB327431P4d06a1
Method	BLASTX
NCBI GI	g2635863
BLAST score	211
E value	2.0e-24
Match length	120
% identity	50
NCBI Description	(Z99121) similar to heavy metal-transporting ATPase [Bacillus subtilis]

Seq. No.	132774
Contig ID	76999_1.R1010
5'-most EST	ARABLI-10-Q1-B1-D1
Method	BLASTN
NCBI GI	g2618602
BLAST score	317
E value	1.0e-178
Match length	365
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	132775
Contig ID	77038_1.R1010
5'-most EST	ARABLI-06-Q1-B1-C2

Seq. No.	132776
Contig ID	77044_1.R1010
5'-most EST	jC-atXP85CG4D10T7b1
Method	BLASTX
NCBI GI	g4510402
BLAST score	94
E value	2.0e-34
Match length	94
% identity	89
NCBI Description	(AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No.	132777
Contig ID	77045_1.R1010
5'-most EST	jC-atXLIB327422P3b04b2
Method	BLASTX
NCBI GI	g1498315
BLAST score	413

E value	4.0e-40
Match length	139
% identity	66
NCBI Description	(U56419) IAP100 [Pisum sativum]

Seq. No.	132778
Contig ID	77046_1.R1010
5'-most EST	jC-atXLIB327431P1d09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	42
E value	4.0e-14
Match length	49
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132779
Contig ID	77052_1.R1010
5'-most EST	jC-atXLIB327431P1d12a1
Method	BLASTX
NCBI GI	g2961356
BLAST score	389
E value	3.0e-37
Match length	186
% identity	42
NCBI Description	(AL022140) alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	132780
Contig ID	77052_2.R1010
5'-most EST	jC-atXLIB327414P1g08a1
Method	BLASTX
NCBI GI	g2129562
BLAST score	248
E value	5.0e-21
Match length	113
% identity	38
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]

Seq. No.	132781
Contig ID	77053_1.R1010
5'-most EST	g2749008
Method	BLASTN
NCBI GI	g2668397
BLAST score	43
E value	1.0e-14
Match length	47
% identity	98
NCBI Description	Mus musculus mGLT-1 mRNA, complete cds

Seq. No.	132782
Contig ID	77084_1.R1010
5'-most EST	jC-atXLIB327429P1h03a2

Method	BLASTX
NCBI GI	g4680489
BLAST score	197
E value	5.0e-15
Match length	81
% identity	53
NCBI Description	(AF119222) hypothetical protein [Oryza sativa]

Seq. No.	132783
Contig ID	77086_1.R1010
5'-most EST	ARABL1-07-Q1-B1-A6
Method	BLASTN
NCBI GI	g4589410
BLAST score	185
E value	1.0e-99
Match length	361
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	132784
Contig ID	77102_1.R1010
5'-most EST	g4714040
Method	BLASTN
NCBI GI	g2191157
BLAST score	688
E value	0.0e+00
Match length	815
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	132785
Contig ID	77109_1.R1010
5'-most EST	g3450489
Method	BLASTX
NCBI GI	g3600055
BLAST score	97
E value	9.0e-18
Match length	79
% identity	65
NCBI Description	(AF080120) contains similarity to Pisum sativum disease resistance response protein 206-d (GB:U11716) [Arabidopsis thaliana]

Seq. No.	132786
Contig ID	77113_1.R1010
5'-most EST	jC-atXLIB327429P3h06a2

Seq. No.	132787
Contig ID	77141_1.R1010
5'-most EST	jC-atXLIB327431P4e07a1
Method	BLASTX
NCBI GI	g2842478
BLAST score	435
E value	6.0e-43
Match length	151
% identity	58

NCBI Description	(AL021749) receptor protein kinase like protein [Arabidopsis thaliana]
Seq. No.	132788
Contig ID	77151_1.R1010
5'-most EST	jC-atXLIB327431P1f01a1
Method	BLASTN
NCBI GI	g4581084
BLAST score	441
E value	0.0e+00
Match length	707
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence
Seq. No.	132789
Contig ID	77176_1.R1010
5'-most EST	ARABLI-08-Q1-B1-C12
Method	BLASTN
NCBI GI	g4159700
BLAST score	309
E value	1.0e-173
Match length	601
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence
Seq. No.	132790
Contig ID	77185_2.R1010
5'-most EST	ARABLI-08-Q1-B1-D10
Method	BLASTN
NCBI GI	g2252823
BLAST score	56
E value	1.0e-22
Match length	125
% identity	93
NCBI Description	Arabidopsis thaliana BAC IG005I10
Seq. No.	132791
Contig ID	77190_1.R1010
5'-most EST	jC-atXLIB327429P4h06a2
Method	BLASTN
NCBI GI	g4159709
BLAST score	588
E value	0.0e+00
Match length	613
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence
Seq. No.	132792
Contig ID	77212_1.R1010
5'-most EST	jC-atXLIB327431P4e01a1
Method	BLASTX
NCBI GI	g4049344
BLAST score	267
E value	3.0e-23

Match length	104
% identity	63
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	132793
Contig ID	77213_1.R1010
5'-most EST	jC-atXLIB327431P3e01b1

Seq. No.	132794
Contig ID	77218_1.R1010
5'-most EST	jC-atXLIB327431P4e08a1
Method	BLASTX
NCBI GI	g4507141
BLAST score	173
E value	3.0e-12
Match length	105
% identity	42
NCBI Description	sorting nexin 2 >gi_3152938 (AF065482) sorting nexin 2 [Homo sapiens]

Seq. No.	132795
Contig ID	77239_1.R1010
5'-most EST	g1054363

Seq. No.	132796
Contig ID	77255_1.R1010
5'-most EST	g930865
Method	BLASTN
NCBI GI	g2351061
BLAST score	374
E value	0.0e+00
Match length	720
% identity	63
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	132797
Contig ID	77255_2.R1010
5'-most EST	jC-atXLIB327438P3a10a2
Method	BLASTN
NCBI GI	g2351061
BLAST score	338
E value	0.0e+00
Match length	375
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	132798
Contig ID	77261_1.R1010
5'-most EST	jC-atXLIB327431P4g12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95

NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	132799
Contig ID	77267_1.R1010
5'-most EST	jC-atXLIB327431P3h11a1
Method	BLASTX
NCBI GI	g4104058
BLAST score	258
E value	7.0e-22
Match length	137
% identity	39
NCBI Description	(AF031195) blue copper-binding protein homolog [Triticum aestivum]
Seq. No.	132800
Contig ID	77295_1.R1010
5'-most EST	jC-atXLIB327431P2h12a1
Method	BLASTX
NCBI GI	g1172558
BLAST score	167
E value	2.0e-11
Match length	59
% identity	53
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_480122_pir__S36454 porin por1 - garden pea >gi_396819_emb_CAA80988_ (Z25540) Porin [Pisum sativum]
Seq. No.	132801
Contig ID	77309_1.R1010
5'-most EST	jC-atXLIB327431P4h11a1
Method	BLASTX
NCBI GI	g4432818
BLAST score	188
E value	6.0e-14
Match length	66
% identity	62
NCBI Description	(AC006593) putative ethylene responsive element binding protein [Arabidopsis thaliana]
Seq. No.	132802
Contig ID	77313_1.R1010
5'-most EST	jC-atXP2C77D11T7055a1
Method	BLASTX
NCBI GI	g3641868
BLAST score	308
E value	7.0e-28
Match length	108
% identity	56
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]
Seq. No.	132803
Contig ID	77314_1.R1010
5'-most EST	jC-atXLIB327431P3h09a1
Method	BLASTN
NCBI GI	g836895
BLAST score	44

E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	132804
Contig ID	77320_1.R1010
5'-most EST	ARABL1-18-Q1-B1-E11

Seq. No.	132805
Contig ID	77344_1.R1010
5'-most EST	jC-atXL118Q1B1G09a1

Seq. No.	132806
Contig ID	77369_1.R1010
5'-most EST	jC-atXP82CG1G3T7b1
Method	BLASTX
NCBI GI	g2829918
BLAST score	473
E value	4.0e-47
Match length	178
% identity	58
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	132807
Contig ID	77399_1.R1010
5'-most EST	jC-atXLIB327431P4d11a1
Method	BLASTX
NCBI GI	g4567204
BLAST score	157
E value	2.0e-10
Match length	33
% identity	82
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	132808
Contig ID	77414_1.R1010
5'-most EST	jC-atX23022Q2E1C09a1
Method	BLASTX
NCBI GI	g2827551
BLAST score	167
E value	9.0e-12
Match length	41
% identity	76
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	132809
Contig ID	77417_1.R1010
5'-most EST	jC-atXLI09Q1B1B10a1
Method	BLASTX
NCBI GI	g2245066
BLAST score	437
E value	2.0e-43
Match length	131
% identity	61
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	132810
Contig ID	77419_1.R1010
5'-most EST	jC-atXLI09Q1B1B12a1
Method	BLASTX
NCBI GI	g2213595
BLAST score	495
E value	2.0e-53
Match length	211
% identity	51
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	132811
Contig ID	77420_1.R1010
5'-most EST	jC-atXLI09Q1B1B02a1

Seq. No.	132812
Contig ID	77421_1.R1010
5'-most EST	jC-atXLIB327429P1h06a2
Method	BLASTX
NCBI GI	g4191774
BLAST score	324
E value	6.0e-30
Match length	145
% identity	41
NCBI Description	(AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	132813
Contig ID	77430_1.R1010
5'-most EST	jC-atXLIB327431P1f08a1
Method	BLASTX
NCBI GI	g3021268
BLAST score	308
E value	3.0e-37
Match length	155
% identity	59
NCBI Description	(AL022347) putative protein [Arabidopsis thaliana]

Seq. No.	132814
Contig ID	77463_1.R1010
5'-most EST	jC-atX23021Q2E1F09a1
Method	BLASTX
NCBI GI	g4455251
BLAST score	676
E value	5.0e-71
Match length	132
% identity	100
NCBI Description	(AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	132815
Contig ID	77481_1.R1010
5'-most EST	jC-atXLIB327431P4e09a1
Method	BLASTX
NCBI GI	g629597
BLAST score	217

E value	3.0e-17
Match length	64
% identity	66
NCBI Description	proline-rich protein - rape >gi_545029_bbs_142669 (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]

Seq. No.	132816
Contig ID	77481_2.R1010
5'-most EST	g16893
Method	BLASTX
NCBI GI	g629597
BLAST score	321
E value	8.0e-30
Match length	117
% identity	61
NCBI Description	proline-rich protein - rape >gi_545029_bbs_142669 (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]

Seq. No.	132817
Contig ID	77484_1.R1010
5'-most EST	jC-atXLIB327431P2e09a1
Method	BLASTX
NCBI GI	g4220461
BLAST score	991
E value	1.0e-108
Match length	208
% identity	90
NCBI Description	(AC006216) ESTs gb_T75642 and gb_AA650997 come from this gene. [Arabidopsis thaliana]

Seq. No.	132818
Contig ID	77510_1.R1010
5'-most EST	jC-atXLIB327429P1h07a2
Method	BLASTN
NCBI GI	g4678231
BLAST score	271
E value	1.0e-150
Match length	373
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F23I14 genomic sequence, complete sequence

Seq. No.	132819
Contig ID	77519_1.R1010
5'-most EST	jC-atXLIB327431P3h05a1
Method	BLASTX
NCBI GI	g4559395
BLAST score	489
E value	3.0e-49
Match length	92
% identity	100
NCBI Description	(AC006526) putative cyclic nucleotide-regulated ion channel protein [Arabidopsis thaliana]

Seq. No. 132820

Contig ID	77527_1.R1010
5'-most EST	g907048
Method	BLASTX
NCBI GI	g1076451
BLAST score	183
E value	4.0e-13
Match length	99
% identity	43
NCBI Description	hypothetical protein 2 - rape >gi_2970639 (AF052241) unknown [Brassica napus]

Seq. No.	132821
Contig ID	77561_1.R1010
5'-most EST	jC-atXLIB327431P3e09a1
Method	BLASTX
NCBI GI	g4263792
BLAST score	599
E value	4.0e-62
Match length	154
% identity	80
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	132822
Contig ID	77563_1.R1010
5'-most EST	jC-atXLIB327431P1f06a1
Method	BLASTX
NCBI GI	g3746073
BLAST score	115
E value	4.0e-25
Match length	171
% identity	37
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132823
Contig ID	77564_1.R1010
5'-most EST	g558164

Seq. No.	132824
Contig ID	77572_1.R1010
5'-most EST	ARABLI-11-Q1-B1-B10
Method	BLASTN
NCBI GI	g4191760
BLAST score	112
E value	4.0e-56
Match length	361
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	132825
Contig ID	77577_1.R1010
5'-most EST	jC-atXLIB327431P3f01a1
Method	BLASTX
NCBI GI	g4580393
BLAST score	258
E value	4.0e-22
Match length	119

% identity	45
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]
Seq. No.	132826
Contig ID	77580_1.R1010
5'-most EST	g2047987
Method	BLASTN
NCBI GI	g4538990
BLAST score	133
E value	2.0e-68
Match length	475
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)
Seq. No.	132827
Contig ID	77600_1.R1010
5'-most EST	jC-atXLIB327431P1g07a1
Method	BLASTX
NCBI GI	g10874
BLAST score	132
E value	4.0e-10
Match length	179
% identity	24
NCBI Description	(X02974) pot. w(+) polypeptide [Drosophila melanogaster]
Seq. No.	132828
Contig ID	77600_2.R1010
5'-most EST	g907225
Seq. No.	132829
Contig ID	77601_1.R1010
5'-most EST	jC-atXLIB327431P2g07a1
Method	BLASTX
NCBI GI	g2191136
BLAST score	1131
E value	1.0e-124
Match length	221
% identity	98
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]
Seq. No.	132830
Contig ID	77646_1.R1010
5'-most EST	jC-atXLIB327431P4f02a1
Method	BLASTX
NCBI GI	g2213583
BLAST score	288
E value	1.0e-25
Match length	125
% identity	49
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.	132831
Contig ID	77655_1.R1010

5'-most EST	jC-atXLIB327431P4f08a1
Method	BLASTN
NCBI GI	g3746057
BLAST score	236
E value	1.0e-130
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132832
Contig ID	77667_1.R1010
5'-most EST	ARABLI-12-Q1-B1-D7
Method	BLASTX
NCBI GI	g4406780
BLAST score	273
E value	6.0e-24
Match length	51
% identity	100
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	132833
Contig ID	77676_1.R1010
5'-most EST	jC-atXLI11Q1B1E04a1
Method	BLASTX
NCBI GI	g4105794
BLAST score	250
E value	5.0e-21
Match length	121
% identity	42
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	132834
Contig ID	77693_1.R1010
5'-most EST	jC-atXLIB327410P1g06a1
Method	BLASTX
NCBI GI	g1653702
BLAST score	340
E value	1.0e-31
Match length	119
% identity	60
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	132835
Contig ID	77730_1.R1010
5'-most EST	jC-atXLI13Q1B1C08a1
Method	BLASTN
NCBI GI	g3395421
BLAST score	333
E value	0.0e+00
Match length	461
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132836
Contig ID	77734_1.R1010
5'-most EST	jC-atXLIB327431P3f05a1
Method	BLASTN
NCBI GI	g4587986
BLAST score	331
E value	0.0e+00
Match length	541
% identity	93
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	132837
Contig ID	77739_1.R1010
5'-most EST	jC-atXLIB327431P2g01a1
Method	BLASTN
NCBI GI	g3176694
BLAST score	437
E value	0.0e+00
Match length	462
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132838
Contig ID	77767_1.R1010
5'-most EST	jC-atXLIB327431P2g11a1
Method	BLASTX
NCBI GI	g2129652
BLAST score	659
E value	9.0e-71
Match length	156
% identity	92
NCBI Description	myosin heavy chain homolog - Arabidopsis thaliana (fragment) >gi_699495 (U19616) myosin heavy chain homolog [Arabidopsis thaliana]

Seq. No.	132839
Contig ID	77821_1.R1010
5'-most EST	jC-atXLIB327431P3f10a1
Method	BLASTX
NCBI GI	g3236258
BLAST score	651
E value	5.0e-68
Match length	125
% identity	100
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	132840
Contig ID	77842_1.R1010
5'-most EST	jC-atXLI14Q1B1F11a1
Method	BLASTX
NCBI GI	g4689366
BLAST score	714
E value	9.0e-76
Match length	132

% identity	100
NCBI Description	(AF134155) RING finger protein [Arabidopsis thaliana]

Seq. No.	132841
Contig ID	77853_1.R1010
5'-most EST	jC-atXLIB327431P3g03a1
Method	BLASTN
NCBI GI	g4713943
BLAST score	477
E value	0.0e+00
Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	132842
Contig ID	77862_1.R1010
5'-most EST	ARABLI-14-Q1-B1-H3
Method	BLASTX
NCBI GI	g7758
BLAST score	193
E value	7.0e-15
Match length	81
% identity	47
NCBI Description	(X58374) crn [Drosophila melanogaster]

Seq. No.	132843
Contig ID	77865_1.R1010
5'-most EST	g2596366
Method	BLASTN
NCBI GI	g3046850
BLAST score	119
E value	3.0e-60
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	132844
Contig ID	77870_1.R1010
5'-most EST	jC-atXLIB327431P2h07a1
Method	BLASTX
NCBI GI	g1730806
BLAST score	293
E value	3.0e-26
Match length	115
% identity	47
NCBI Description	HYPOTHETICAL 45.7 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION >gi_2131908_pir__S63130 hypothetical protein YNL175c - yeast (Saccharomyces cerevisiae) >gi_1302151_emb_CAA96066_ (Z71451) ORF YNL175c [Saccharomyces cerevisiae]

Seq. No.	132845
Contig ID	77905_1.R1010
5'-most EST	jC-atXLIB327438P2a07a1
Method	BLASTN
NCBI GI	g4558586

BLAST score	173
E value	2.0e-92
Match length	281
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	132846
Contig ID	77937_1.R1010
5'-most EST	ARABLI-15-Q1-B1-H6
Method	BLASTX
NCBI GI	g2983476
BLAST score	293
E value	2.0e-26
Match length	102
% identity	52
NCBI Description	(AE000715) hypothetical protein [Aquifex aeolicus]

Seq. No.	132847
Contig ID	77988_1.R1010
5'-most EST	jC-atXLIB327438P1a08a1
Method	BLASTN
NCBI GI	g4572664
BLAST score	206
E value	1.0e-112
Match length	520
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	132848
Contig ID	78008_1.R1010
5'-most EST	jC-atXLIB327431P2h10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132849
Contig ID	78019_1.R1010
5'-most EST	jC-atXP123C118D19T7010d1
Method	BLASTN
NCBI GI	g2828183
BLAST score	306
E value	1.0e-171
Match length	475
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	132850
Contig ID	78019_3.R1010
5'-most EST	jC-atXP124C121D5T7d1

Method	BLASTX
NCBI GI	g4337175
BLAST score	333
E value	5.0e-31
Match length	126
% identity	49
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	132851
Contig ID	78039_1.R1010
5'-most EST	jC-atXP94CH5F8T7089d1
Method	BLASTX
NCBI GI	g3269287
BLAST score	499
E value	3.0e-90
Match length	180
% identity	97
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	132852
Contig ID	78057_1.R1010
5'-most EST	jC-alXLIB327434P1a02a1
Method	BLASTX
NCBI GI	g3559816
BLAST score	288
E value	1.0e-25
Match length	80
% identity	66
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	132853
Contig ID	78063_1.R1010
5'-most EST	jC-alXLIB327434P1a05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132854
Contig ID	78072_1.R1010
5'-most EST	jC-alXLIB327434P1a10a1
Method	BLASTX
NCBI GI	g4218991
BLAST score	162
E value	6.0e-11
Match length	117
% identity	35
NCBI Description	(AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	132855
Contig ID	78078_1.R1010

5'-most EST	jC-alXLIB327434P1b01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132856
Contig ID	78095_1.R1010
5'-most EST	jC-atXLIB327417P1h02a1
Method	BLASTX
NCBI GI	g3041672
BLAST score	220
E value	2.0e-17
Match length	127
% identity	43
NCBI Description	DNA POLYMERASE I (POL I)

Seq. No.	132857
Contig ID	78097_1.R1010
5'-most EST	jC-atXP3C83B10T7058a1

Seq. No.	132858
Contig ID	78109_1.R1010
5'-most EST	jC-atXP73CF3C7T7b1
Method	BLASTN
NCBI GI	g4335711
BLAST score	650
E value	0.0e+00
Match length	650
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132859
Contig ID	78125_1.R1010
5'-most EST	jC-alXLIB327434P1d03a1
Method	BLASTX
NCBI GI	g3152565
BLAST score	265
E value	6.0e-23
Match length	100
% identity	63
NCBI Description	(AC002986) EST gb_N65759 comes from this gene. [Arabidopsis thaliana]

Seq. No.	132860
Contig ID	78129_1.R1010
5'-most EST	jC-alXLIB327434P1d06b1
Method	BLASTN
NCBI GI	g2264303
BLAST score	202
E value	1.0e-109
Match length	202
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]
Seq. No.	132861
Contig ID	78131_1.R1010
5'-most EST	jC-alXLIB327434P1d08a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	132862
Contig ID	78135_1.R1010
5'-most EST	jC-atXP37C156G15T7d2
Method	BLASTX
NCBI GI	g3386622
BLAST score	535
E value	4.0e-93
Match length	201
% identity	90
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.	132863
Contig ID	78135_2.R1010
5'-most EST	jC-alXLIB327434P1d10a1
Method	BLASTX
NCBI GI	g2979563
BLAST score	456
E value	2.0e-45
Match length	88
% identity	98
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.	132864
Contig ID	78140_1.R1010
5'-most EST	jC-alXLIB327434P1e01a1
Method	BLASTX
NCBI GI	g3746067
BLAST score	558
E value	2.0e-57
Match length	125
% identity	90
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]
Seq. No.	132865
Contig ID	78146_1.R1010
5'-most EST	jC-alXLIB327434P1e04a1
Method	BLASTN
NCBI GI	g3985934
BLAST score	133
E value	2.0e-68
Match length	512
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	132866
Contig ID	78148_1.R1010
5'-most EST	jC-atXLIB327433P2a06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	1.0e-08
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	132867
Contig ID	78148_2.R1010
5'-most EST	jC-alXLIB327434P1e05a1

Seq. No.	132868
Contig ID	78152_1.R1010
5'-most EST	jC-alXLIB327434P1e07a1
Method	BLASTX
NCBI GI	g4587585
BLAST score	310
E value	3.0e-28
Match length	60
% identity	98
NCBI Description	(AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132869
Contig ID	78156_1.R1010
5'-most EST	jC-alXLIB327434P1e10a1
Method	BLASTN
NCBI GI	g4691223
BLAST score	248
E value	1.0e-137
Match length	759
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	132870
Contig ID	78159_1.R1010
5'-most EST	jC-alXLIB327434P1e11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132871
Contig ID	78185_1.R1010
5'-most EST	jC-alXLIB327434P1g02a1

Seq. No.	132872

Contig ID 78201_1.R1010
5'-most EST jC-alXLIB327436P4b02a1
Method BLASTN
NCBI GI g4539290
BLAST score 425
E value 0.0e+00
Match length 462
% identity 97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No. 132873
Contig ID 78215_1.R1010
5'-most EST jC-alXLIB327434P1h06a1
Method BLASTN
NCBI GI g2245073
BLAST score 486
E value 0.0e+00
Match length 486
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 132874
Contig ID 78223_1.R1010
5'-most EST jC-atXP118C144B12T7091d2
Method BLASTX
NCBI GI g3024859
BLAST score 186
E value 2.0e-13
Match length 87
% identity 41
NCBI Description HYPOTHETICAL PROTEIN AF0130 >gi_2650515 (AE001097) acetylpolyamine aminohydrolase (aphA) [Archaeoglobus fulgidus]

Seq. No. 132875
Contig ID 78225_1.R1010
5'-most EST jC-alXLIB327434P1h12a1
Method BLASTX
NCBI GI g3183285
BLAST score 206
E value 8.0e-16
Match length 157
% identity 34
NCBI Description HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION >gi_1742787_dbj_BAA15475_ (D90813) ORF_ID:o322#7; similar to [SwissProt Accession Number Q06373] [Escherichia coli] >gi_1787999 (AE000266) orf, hypothetical protein [Escherichia coli]

Seq. No. 132876
Contig ID 78301_1.R1010
5'-most EST jC-alXLIB327434P2f04a1
Method BLASTN
NCBI GI g3928074
BLAST score 141

E value	4.0e-73
Match length	380
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132877
Contig ID	78337_1.R1010
5'-most EST	jC-alXLIB327434P3a06a1
Method	BLASTN
NCBI GI	g2828188
BLAST score	284
E value	1.0e-158
Match length	547
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	132878
Contig ID	78339_1.R1010
5'-most EST	jC-atXP90C242P19T7s2
Method	BLASTX
NCBI GI	g2228771
BLAST score	184
E value	4.0e-13
Match length	81
% identity	56
NCBI Description	(AF001453) Dc3 promoter-binding factor-1 [Helianthus annuus]

Seq. No.	132879
Contig ID	78361_1.R1010
5'-most EST	jC-alXLIB327434P4b10a1
Method	BLASTN
NCBI GI	g4220644
BLAST score	341
E value	0.0e+00
Match length	509
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	132880
Contig ID	78392_1.R1010
5'-most EST	jC-alXLIB327434P3d07a1
Method	BLASTX
NCBI GI	g1363488
BLAST score	615
E value	6.0e-64
Match length	117
% identity	100
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	132881

Contig ID	78411_1.R1010
5'-most EST	jC-alXLIB327434P3e07a1
Method	BLASTX
NCBI GI	g2252841
BLAST score	372
E value	2.0e-35
Match length	165
% identity	53
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	132882
Contig ID	78474_1.R1010
5'-most EST	jC-alXLIB327434P4a02a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	294
E value	1.0e-164
Match length	540
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	132883
Contig ID	78476_1.R1010
5'-most EST	jC-alXLIB327434P4a03a1
Method	BLASTX
NCBI GI	g3540199
BLAST score	173
E value	7.0e-65
Match length	162
% identity	76
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	132884
Contig ID	78482_1.R1010
5'-most EST	g2413911
Method	BLASTX
NCBI GI	g4582441
BLAST score	572
E value	7.0e-59
Match length	104
% identity	98
NCBI Description	(AC007142) unknown protein [Arabidopsis thaliana]

Seq. No.	132885
Contig ID	78482_2.R1010
5'-most EST	g2047792
Method	BLASTX
NCBI GI	g4582441
BLAST score	214
E value	5.0e-17
Match length	54
% identity	80
NCBI Description	(AC007142) unknown protein [Arabidopsis thaliana]

Seq. No. 132886

Contig ID	78484_1.R1010
5'-most EST	jC-alXLIB327434P4a07a1
Method	BLASTX
NCBI GI	g4510357
BLAST score	215
E value	1.0e-46
Match length	100
% identity	89
NCBI Description	(AC006921) putative invertase [Arabidopsis thaliana] >gi_4678229_gb_AAD26974.1_AC007135_10 (AC007135) putative invertase [Arabidopsis thaliana]

Seq. No.	132887
Contig ID	78503_1.R1010
5'-most EST	jC-alXLIB327434P4b05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	70
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	132888
Contig ID	78524_1.R1010
5'-most EST	jC-alXLIB327434P4c05a1
Method	BLASTX
NCBI GI	g112801
BLAST score	335
E value	4.0e-31
Match length	128
% identity	55
NCBI Description	4-COUMARATE--COA LIGASE 2 (4CL) >gi_282937_pir__S15695 4-coumarate--CoA ligase (EC 6.2.1.12) (clone Pc4CL-2) - parsley >gi_20436_emb_CAA31697_ (X13325) 4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544) [Petroselinum crispum]

Seq. No.	132889
Contig ID	78540_1.R1010
5'-most EST	jC-alXLIB327434P4d01a1
Method	BLASTX
NCBI GI	g4508070
BLAST score	429
E value	4.0e-42
Match length	83
% identity	96
NCBI Description	(AC005882) 24349 [Arabidopsis thaliana]

Seq. No.	132890
Contig ID	78556_1.R1010
5'-most EST	jC-alXLIB327434P4d10a1
Method	BLASTX
NCBI GI	g2190550
BLAST score	622
E value	1.0e-64
Match length	144

% identity	89
NCBI Description	(AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]

Seq. No.	132891
Contig ID	78558_1.R1010
5'-most EST	jC-alXLIB327434P4d11a1
Method	BLASTN
NCBI GI	g2264315
BLAST score	415
E value	0.0e+00
Match length	564
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	132892
Contig ID	78626_1.R1010
5'-most EST	jC-alXLIB327434P4h01a1
Method	BLASTX
NCBI GI	g404688
BLAST score	421
E value	3.0e-41
Match length	130
% identity	57
NCBI Description	(L19074) cytochrome P450 [Catharanthus roseus]

Seq. No.	132893
Contig ID	78636_1.R1010
5'-most EST	jC-alXLIB327434P4h06a1
Method	BLASTX
NCBI GI	g2232354
BLAST score	315
E value	9.0e-29
Match length	124
% identity	50
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	132894
Contig ID	78652_1.R1010
5'-most EST	jC-alXLIB327435P1a04a1

Seq. No.	132895
Contig ID	78656_1.R1010
5'-most EST	jC-alXLIB327435P1a06b1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132896
Contig ID	78659_1.R1010
5'-most EST	jC-alXLIB327435P1a08b1
Method	BLASTX

NCBI GI	g2244833
BLAST score	179
E value	6.0e-13
Match length	139
% identity	16
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	132897
Contig ID	78660_1.R1010
5'-most EST	jC-alXLIB327435P1a09b1
Method	BLASTX
NCBI GI	g3367593
BLAST score	235
E value	2.0e-19
Match length	69
% identity	58
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	132898
Contig ID	78663_1.R1010
5'-most EST	jC-alXLIB327435P1a12b1

Seq. No.	132899
Contig ID	78664_1.R1010
5'-most EST	jC-alXLIB327435P1b01a1
Method	BLASTN
NCBI GI	g4713943
BLAST score	419
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	132900
Contig ID	78668_1.R1010
5'-most EST	jC-alXLIB327435P1b03b1
Method	BLASTX
NCBI GI	g2804278
BLAST score	303
E value	2.0e-27
Match length	73
% identity	78
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	132901
Contig ID	78677_1.R1010
5'-most EST	jC-alXLIB327435P1b10b1
Method	BLASTN
NCBI GI	g3985934
BLAST score	439
E value	0.0e+00
Match length	556
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	132902
Contig ID	78681_1.R1010
5'-most EST	jC-alXLIB327435P1c01b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	293
E value	1.0e-164
Match length	369
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	132903
Contig ID	78685_1.R1010
5'-most EST	jC-atXP123C119N23T7058d1
Method	BLASTX
NCBI GI	g4186184
BLAST score	166
E value	3.0e-11
Match length	134
% identity	31
NCBI Description	(AF111168) unknown [Homo sapiens]

Seq. No.	132904
Contig ID	78689_1.R1010
5'-most EST	jC-alXLIB327435P1c07a1
Method	BLASTX
NCBI GI	g4406767
BLAST score	418
E value	6.0e-41
Match length	98
% identity	89
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	132905
Contig ID	78696_1.R1010
5'-most EST	jC-alXLIB327435P1c12b1
Method	BLASTN
NCBI GI	g4582411
BLAST score	43
E value	8.0e-15
Match length	59
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, complete sequence

Seq. No.	132906
Contig ID	78702_1.R1010
5'-most EST	jC-alXLIB327435P1d04a1
Method	BLASTX
NCBI GI	g1549379
BLAST score	183
E value	3.0e-13
Match length	73

% identity	43
NCBI Description	(U62737) putative protein [Synechococcus PCC7942]
Seq. No.	132907
Contig ID	78703_1.R1010
5'-most EST	jC-atXP73CF3C1T7d2
Method	BLASTN
NCBI GI	g1070003
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222
Seq. No.	132908
Contig ID	78706_1.R1010
5'-most EST	jC-alXLIB327435P1d08a1
Seq. No.	132909
Contig ID	78712_1.R1010
5'-most EST	jC-alXLIB327435P1d12b1
Method	BLASTN
NCBI GI	g3241922
BLAST score	354
E value	0.0e+00
Match length	695
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.	132910
Contig ID	78720_1.R1010
5'-most EST	jC-alXLIB327435P1e05b1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	61
% identity	98
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	132911
Contig ID	78724_1.R1010
5'-most EST	jC-alXLIB327435P1e07b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	132912
Contig ID	78728_1.R1010
5'-most EST	g2757522

Method	BLASTN
NCBI GI	g3335331
BLAST score	178
E value	2.0e-95
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132913
Contig ID	78734_1.R1010
5'-most EST	jC-alXLIB327435P1f03a1
Method	BLASTN
NCBI GI	g2459406
BLAST score	421
E value	0.0e+00
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132914
Contig ID	78738_1.R1010
5'-most EST	jC-atXP123C121A4T7080d1
Method	BLASTX
NCBI GI	g4544399
BLAST score	889
E value	6.0e-96
Match length	170
% identity	100
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	132915
Contig ID	78745_1.R1010
5'-most EST	jC-alXLIB327435P1f09b1
Method	BLASTX
NCBI GI	g1653767
BLAST score	378
E value	5.0e-36
Match length	172
% identity	45
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	132916
Contig ID	78752_1.R1010
5'-most EST	jC-alXLIB327435P1g02b1
Method	BLASTX
NCBI GI	g3063468
BLAST score	159
E value	1.0e-10
Match length	36
% identity	78
NCBI Description	(AC003981) F22O13.30 [Arabidopsis thaliana]

Seq. No.	132917
Contig ID	78762_1.R1010

5'-most EST	jC-atXP69C219P6T7024d1
Method	BLASTX
NCBI GI	g481812
BLAST score	204
E value	1.0e-15
Match length	40
% identity	90
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	132918
Contig ID	78762_2.R1010
5'-most EST	jC-alXLIB327435P1g08b1
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	6.0e-22
Match length	66
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132919
Contig ID	78769_1.R1010
5'-most EST	jC-alXLIB327435P1h01b1
Method	BLASTX
NCBI GI	g2769696
BLAST score	197
E value	9.0e-15
Match length	108
% identity	37
NCBI Description	(AC003982) unknown function; 60% similar to Z50177 (PID:g927403) (PID:g927402) [Homo sapiens]

Seq. No.	132920
Contig ID	78769_2.R1010
5'-most EST	g397312
Method	BLASTN
NCBI GI	g2997683
BLAST score	51
E value	2.0e-19
Match length	164
% identity	88
NCBI Description	Arabidopsis thaliana putative transcriptional co-activator (KIWI) mRNA, complete cds

Seq. No.	132921
Contig ID	78774_1.R1010
5'-most EST	jC-alXLIB327435P1h05a1
Method	BLASTX
NCBI GI	g462578
BLAST score	114
E value	2.0e-35
Match length	97
% identity	80
NCBI Description	MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR (NADP-MDH) >gi_421790_pir__S33066 malate dehydrogenase

(NADP+) (EC 1.1.1.82) - common ice plant
>gi_19530_emb_CAA45270_ (X63727) malate dehydrogenase (NADP+) [Mesembryanthemum crystallinum]

Seq. No.	132922
Contig ID	78782_1.R1010
5'-most EST	jC-alXLIB327435P1h09b1
Method	BLASTX
NCBI GI	g2982942
BLAST score	329
E value	3.0e-49
Match length	159
% identity	64
NCBI Description	(AE000679) GMP synthase [Aquifex aeolicus]

Seq. No.	132923
Contig ID	78787_1.R1010
5'-most EST	jC-alXLIB327435P1h12b1
Method	BLASTN
NCBI GI	g4757403
BLAST score	37
E value	3.0e-11
Match length	61
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	132924
Contig ID	78794_1.R1010
5'-most EST	jC-alXLIB327435P2a04a1

Seq. No.	132925
Contig ID	78898_1.R1010
5'-most EST	jC-atXP81C240J10T7d1
Method	BLASTX
NCBI GI	g4544399
BLAST score	442
E value	9.0e-91
Match length	172
% identity	100
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	132926
Contig ID	78958_1.R1010
5'-most EST	jC-alXLIB327435P3a02a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	226
E value	1.0e-124
Match length	673
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	132927
Contig ID	78958_2.R1010

5'-most EST	jC-atXP79C240C3T7d2
Method	BLASTN
NCBI GI	g3063690
BLAST score	211
E value	1.0e-115
Match length	581
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	132928
Contig ID	79004_1.R1010
5'-most EST	jC-alXLIB327435P3c06a1
Method	BLASTX
NCBI GI	g3461814
BLAST score	114
E value	3.0e-50
Match length	165
% identity	64
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132929
Contig ID	79015_1.R1010
5'-most EST	jC-alXLIB327435P3d02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132930
Contig ID	79022_1.R1010
5'-most EST	jC-alXLIB327435P3d06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	132931
Contig ID	79040_1.R1010
5'-most EST	jC-alXLIB327435P3e04a1
Method	BLASTX
NCBI GI	g2463509
BLAST score	130
E value	3.0e-35
Match length	107
% identity	70
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	132932
Contig ID	79042_1.R1010

5'-most EST	jC-alXLIB327435P3e05a1
Method	BLASTN
NCBI GI	g3449329
BLAST score	240
E value	1.0e-132
Match length	331
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	132933
Contig ID	79052_1.R1010
5'-most EST	jC-alXLIB327435P3e10a1
Method	BLASTX
NCBI GI	g4406759
BLAST score	148
E value	4.0e-09
Match length	97
% identity	37
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132934
Contig ID	79054_1.R1010
5'-most EST	jC-atXLIB327422P2c08a2
Method	BLASTN
NCBI GI	g2760167
BLAST score	225
E value	1.0e-123
Match length	641
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	132935
Contig ID	79076_1.R1010
5'-most EST	jC-alXLIB327435P3f12a1
Method	BLASTX
NCBI GI	g1707008
BLAST score	74
E value	5.0e-49
Match length	161
% identity	73
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No.	132936
Contig ID	79093_1.R1010
5'-most EST	jC-alXLIB327435P3h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 132937

Contig ID	79128_1.R1010
5'-most EST	jC-alXLIB327435P4a08a1
Method	BLASTX
NCBI GI	g3335359
BLAST score	410
E value	7.0e-40
Match length	138
% identity	58
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	132938
Contig ID	79134_1.R1010
5'-most EST	jC-atXLIB327432P3c08a1
Method	BLASTX
NCBI GI	g2708745
BLAST score	476
E value	2.0e-47
Match length	115
% identity	81
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	132939
Contig ID	79172_1.R1010
5'-most EST	jC-alXLIB327435P4c06a1
Method	BLASTN
NCBI GI	g4512646
BLAST score	324
E value	0.0e+00
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No.	132940
Contig ID	79181_1.R1010
5'-most EST	jC-alXLIB327435P4c12a1
Method	BLASTX
NCBI GI	g1076511
BLAST score	53
E value	4.0e-41
Match length	122
% identity	78
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	132941
Contig ID	79197_1.R1010
5'-most EST	jC-alXLIB327435P4d08a1
Method	BLASTN
NCBI GI	g4063735
BLAST score	341
E value	0.0e+00
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5

cM, complete sequence [Arabidopsis thaliana]

Seq. No.	132942
Contig ID	79207_1.R1010
5'-most EST	jC-alXLIB327435P4e01a1
Method	BLASTN
NCBI GI	g4584387
BLAST score	258
E value	1.0e-143
Match length	396
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	132943
Contig ID	79284_1.R1010
5'-most EST	jC-atXP113C134L4T7074a2
Method	BLASTN
NCBI GI	g2924733
BLAST score	309
E value	1.0e-173
Match length	606
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	132944
Contig ID	79397_1.R1010
5'-most EST	jC-alXLIB327436P1f07a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	221
E value	1.0e-121
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	132945
Contig ID	79408_1.R1010
5'-most EST	jC-alXLIB327436P1g01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	9.0e-21
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132946
Contig ID	79410_1.R1010
5'-most EST	jC-atXP123C117P15T7056a1
Method	BLASTN
NCBI GI	g2342717
BLAST score	324
E value	0.0e+00

Match length	376
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132947
Contig ID	79449_1.R1010
5'-most EST	jC-alXLIB327436P2a04a1

Seq. No.	132948
Contig ID	79461_1.R1010
5'-most EST	jC-alXLIB327436P2a10a1

Seq. No.	132949
Contig ID	79466_1.R1010
5'-most EST	jC-atXLIB327408P3c06a1
Method	BLASTX
NCBI GI	g3582333
BLAST score	494
E value	1.0e-49
Match length	110
% identity	81
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	132950
Contig ID	79484_1.R1010
5'-most EST	jC-atXLIB327428P4a10a2
Method	BLASTX
NCBI GI	g4586260
BLAST score	174
E value	4.0e-12
Match length	66
% identity	53
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	132951
Contig ID	79488_1.R1010
5'-most EST	jC-alXLIB327436P2c02a1
Method	BLASTN
NCBI GI	g3600045
BLAST score	61
E value	2.0e-25
Match length	101
% identity	90
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	132952
Contig ID	79492_1.R1010
5'-most EST	jC-alXLIB327436P2c04a1
Method	BLASTN
NCBI GI	g2072337
BLAST score	218
E value	1.0e-119
Match length	276
% identity	94
NCBI Description	Arabidopsis thaliana ISWI-like protein mRNA, partial cds

Seq. No.	132953
Contig ID	79552_1.R1010
5'-most EST	jC-alXLIB327436P2f07a1
Method	BLASTX
NCBI GI	g4104457
BLAST score	272
E value	9.0e-24
Match length	58
% identity	78
NCBI Description	(AF036172) 2-oxoglutarate/malate translocator [Zea mays]

Seq. No.	132954
Contig ID	79562_1.R1010
5'-most EST	jC-alXLIB327436P2g02a1
Method	BLASTN
NCBI GI	g4539331
BLAST score	426
E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	132955
Contig ID	79564_1.R1010
5'-most EST	jC-alXLIB327436P2g04a1
Method	BLASTN
NCBI GI	g4097546
BLAST score	318
E value	1.0e-179
Match length	390
% identity	92
NCBI Description	Arabidopsis thaliana farnesylated protein ATFP3 mRNA, partial cds

Seq. No.	132956
Contig ID	79604_1.R1010
5'-most EST	jC-alXLIB327436P3a03a1
Method	BLASTN
NCBI GI	g4314374
BLAST score	584
E value	0.0e+00
Match length	621
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132957
Contig ID	79606_1.R1010
5'-most EST	jC-alXLIB327436P3a04a1

Seq. No.	132958
Contig ID	79608_1.R1010
5'-most EST	g2393160
Method	BLASTN
NCBI GI	g2564045
BLAST score	334

E value	0.0e+00
Match length	525
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	132959
Contig ID	79612_1.R1010
5'-most EST	jC-alXLIB327436P4a07a1
Method	BLASTN
NCBI GI	g2252848
BLAST score	328
E value	0.0e+00
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	132960
Contig ID	79615_1.R1010
5'-most EST	jC-alXLIB327436P3a09a1
Method	BLASTN
NCBI GI	g3869074
BLAST score	178
E value	2.0e-95
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	132961
Contig ID	79616_1.R1010
5'-most EST	jC-atXLIB327408P2c10b1
Method	BLASTN
NCBI GI	g3869074
BLAST score	254
E value	1.0e-140
Match length	330
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	132962
Contig ID	79625_1.R1010
5'-most EST	jC-alXLIB327436P3b02a1
Method	BLASTX
NCBI GI	g3913079
BLAST score	281
E value	1.0e-24
Match length	163
% identity	40
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE (ACOAT) >gi_2622444 (AE000897) N-acetylornithine aminotransferase [Methanobacterium thermoautotrophicum]

Seq. No.	132963
Contig ID	79631_1.R1010
5'-most EST	jC-alXLIB327436P3b08a1

Method	BLASTX
NCBI GI	g2191171
BLAST score	173
E value	3.0e-12
Match length	56
% identity	61
NCBI Description	(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) [Arabidopsis thaliana]

Seq. No.	132964
Contig ID	79634_1.R1010
5'-most EST	jC-alXLIB327436P3b10a1
Method	BLASTX
NCBI GI	g2244973
BLAST score	129
E value	4.0e-29
Match length	87
% identity	80
NCBI Description	(Z97340) similarity to extensin class 1 protein [Arabidopsis thaliana]

Seq. No.	132965
Contig ID	79637_1.R1010
5'-most EST	jC-alXLIB327436P3b12a1
Method	BLASTN
NCBI GI	g4585891
BLAST score	322
E value	0.0e+00
Match length	374
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T103 genomic sequence, complete sequence

Seq. No.	132966
Contig ID	79655_1.R1010
5'-most EST	jC-alXLIB327436P3c11a1

Seq. No.	132967
Contig ID	79681_1.R1010
5'-most EST	jC-alXLIB327436P3e03a1

Seq. No.	132968
Contig ID	79688_1.R1010
5'-most EST	jC-alXLIB327436P3e07a1
Method	BLASTN
NCBI GI	g4567237
BLAST score	369
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	132969
Contig ID	79691_1.R1010
5'-most EST	jC-alXLIB327436P3e10a1

Seq. No.	132970
Contig ID	79695_1.R1010
5'-most EST	jC-alXLIB327436P3e12a1

Seq. No.	132971
Contig ID	79697_1.R1010
5'-most EST	jC-alXLIB327436P3f01a1
Method	BLASTN
NCBI GI	g3128166
BLAST score	262
E value	1.0e-145
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132972
Contig ID	79723_2.R1010
5'-most EST	jC-alXLIB327436P3g03a1
Method	BLASTX
NCBI GI	g1778093
BLAST score	276
E value	3.0e-24
Match length	109
% identity	51
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	132973
Contig ID	79731_1.R1010
5'-most EST	jC-alXLIB327436P3g07a1
Method	BLASTX
NCBI GI	g1707015
BLAST score	1041
E value	1.0e-113
Match length	200
% identity	99
NCBI Description	(U78721) protein phosphatase 2C isolog [Arabidopsis thaliana]

Seq. No.	132974
Contig ID	79733_1.R1010
5'-most EST	jC-alXLIB327436P3g08a1
Method	BLASTX
NCBI GI	g4490751
BLAST score	400
E value	4.0e-39
Match length	79
% identity	99
NCBI Description	(AL035708) proliferating-cell nucleolar antigen-like protein [Arabidopsis thaliana]

Seq. No.	132975
Contig ID	79742_1.R1010
5'-most EST	jC-atXP54C187A11T7053a1

Seq. No.	132976
Contig ID	79742_3.R1010
5'-most EST	jC-alXLIB327436P3h01a1
Method	BLASTX
NCBI GI	g4539459
BLAST score	182
E value	3.0e-13
Match length	38
% identity	71
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	132977
Contig ID	79750_1.R1010
5'-most EST	jC-atX25069Q1E1B11a1

Seq. No.	132978
Contig ID	79763_1.R1010
5'-most EST	jC-alXLIB327436P4a01a1
Method	BLASTN
NCBI GI	g4388816
BLAST score	144
E value	6.0e-75
Match length	420
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132979
Contig ID	79764_1.R1010
5'-most EST	jC-alXLIB327436P4a01b1
Method	BLASTN
NCBI GI	g4388816
BLAST score	380
E value	0.0e+00
Match length	425
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132980
Contig ID	79788_1.R1010
5'-most EST	g2048165
Method	BLASTX
NCBI GI	g4006878
BLAST score	285
E value	3.0e-25
Match length	100
% identity	50
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	132981
Contig ID	79794_1.R1010
5'-most EST	jC-atXLIB327424P4c11a1
Method	BLASTX
NCBI GI	g2924512
BLAST score	497
E value	3.0e-50

Match length	97
% identity	98
NCBI Description	(AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No.	132982
Contig ID	79855_1.R1010
5'-most EST	jC-alXLIB327436P4e10a1
Method	BLASTX
NCBI GI	g3643599
BLAST score	433
E value	1.0e-42
Match length	88
% identity	95
NCBI Description	(AC005395) putative trytophanyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	132983
Contig ID	79873_1.R1010
5'-most EST	jC-alXLIB327436P4f07a1
Method	BLASTX
NCBI GI	g2342688
BLAST score	309
E value	3.0e-28
Match length	99
% identity	56
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). [Arabidopsis thaliana]

Seq. No.	132984
Contig ID	79896_1.R1010
5'-most EST	jC-alXLIB327436P4g07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	132985
Contig ID	79922_1.R1010
5'-most EST	jC-alXLIB327436P4h10a1
Method	BLASTN
NCBI GI	g1877523
BLAST score	323
E value	0.0e+00
Match length	399
% identity	95
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	132986
Contig ID	79926_1.R1010
5'-most EST	jC-alXLIB327436P4h12a1
Method	BLASTX

NCBI GI g3818624
BLAST score 487
E value 5.0e-49
Match length 94
% identity 99
NCBI Description (AF095912) actin related protein 2; ARP2 [Arabidopsis thaliana]

Seq. No. 132987
Contig ID 79945_1.R1010
5'-most EST jC-atXLIB327408P3a10a1
Method BLASTN
NCBI GI g3985931
BLAST score 498
E value 0.0e+00
Match length 565
% identity 85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No. 132988
Contig ID 79959_1.R1010
5'-most EST jC-atXLIB327408P3b05a1
Method BLASTN
NCBI GI g2288979
BLAST score 480
E value 0.0e+00
Match length 500
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 132989
Contig ID 79961_1.R1010
5'-most EST jC-atXLIB327419P1a09a2
Method BLASTN
NCBI GI g3367500
BLAST score 632
E value 0.0e+00
Match length 704
% identity 99
NCBI Description REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No. 132990
Contig ID 80000_1.R1010
5'-most EST jC-atXLIB327408P3d02a1
Method BLASTN
NCBI GI g2290120
BLAST score 54
E value 3.0e-21
Match length 66
% identity 95
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 132991

Contig ID	80020_1.R1010
5'-most EST	jC-atXLIB327408P3d12a1
Method	BLASTX
NCBI GI	g3600033
BLAST score	316
E value	1.0e-28
Match length	114
% identity	86
NCBI Description	(AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No.	132992
Contig ID	80026_1.R1010
5'-most EST	jC-atXLIB327408P3f02a1
Method	BLASTN
NCBI GI	g2645198
BLAST score	737
E value	0.0e+00
Match length	1175
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132993
Contig ID	80028_1.R1010
5'-most EST	jC-atXLIB327408P3e04a1
Method	BLASTX
NCBI GI	g4056493
BLAST score	175
E value	2.0e-12
Match length	158
% identity	51
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	132994
Contig ID	80036_1.R1010
5'-most EST	jC-atXLIB327408P3e08a1
Method	BLASTX
NCBI GI	g3287857
BLAST score	368
E value	6.0e-35
Match length	118
% identity	63
NCBI Description	3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA DEHYDROGENASE) (BHBD) >gi_1209052 (U32229) HbdA [Bradyrhizobium japonicum]

Seq. No.	132995
Contig ID	80058_1.R1010
5'-most EST	jC-atXP83CG3G5T7087d1
Method	BLASTX
NCBI GI	g4505765
BLAST score	325
E value	5.0e-30
Match length	124
% identity	53

NCBI Description	phosphoglucomutase 1 >gi_284351_pir__A41801 phosphoglucomutase (EC 5.4.2.2) 1 - human >gi_189926 (M83088) PGM1 [Homo sapiens]

Seq. No.	132996
Contig ID	80096_1.R1010
5'-most EST	jC-atXLIB327408P3h02a1
Method	BLASTN
NCBI GI	g3420042
BLAST score	554
E value	0.0e+00
Match length	729
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	132997
Contig ID	80102_1.R1010
5'-most EST	jC-atXLIB327408P3h05a1
Method	BLASTX
NCBI GI	g4585995
BLAST score	291
E value	7.0e-26
Match length	85
% identity	69
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	132998
Contig ID	80106_1.R1010
5'-most EST	jC-atXLIB327408P3h07a1
Method	BLASTX
NCBI GI	g2832616
BLAST score	261
E value	3.0e-22
Match length	215
% identity	44
NCBI Description	(AL021711) heat shock transcription factor - like protein [Arabidopsis thaliana]

Seq. No.	132999
Contig ID	80120_1.R1010
5'-most EST	jC-atXLIB327408P4a02a1

Seq. No.	133000
Contig ID	80122_1.R1010
5'-most EST	jC-atXP53C185D3T7031a1
Method	BLASTX
NCBI GI	g3831441
BLAST score	165
E value	4.0e-11
Match length	44
% identity	89
NCBI Description	(AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133001
Contig ID	80146_1.R1010
5'-most EST	jC-atXP40C161L4T7050a1

Method	BLASTX
NCBI GI	g3328126
BLAST score	510
E value	1.0e-51
Match length	124
% identity	80
NCBI Description	(AF072691) putative basic helix-loop-helix DNA binding protein TCP2 [Arabidopsis thaliana]

Seq. No.	133002
Contig ID	80152_1.R1010
5'-most EST	jC-atXLIB327408P4b06a1
Method	BLASTN
NCBI GI	g4539331
BLAST score	430
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	133003
Contig ID	80171_1.R1010
5'-most EST	jC-atXLIB327408P4c04a1
Method	BLASTX
NCBI GI	g3063460
BLAST score	643
E value	3.0e-67
Match length	128
% identity	100
NCBI Description	(AC003981) F22O13.22 [Arabidopsis thaliana]

Seq. No.	133004
Contig ID	80175_1.R1010
5'-most EST	jC-atXLIB327408P4c06a1
Method	BLASTX
NCBI GI	g2738248
BLAST score	619
E value	3.0e-64
Match length	128
% identity	94
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	133005
Contig ID	80181_1.R1010
5'-most EST	jC-atXLIB327408P4c09a1

Seq. No.	133006
Contig ID	80181_2.R1010
5'-most EST	jC-alX24090Q1E1F05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	79
% identity	92

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	133007
Contig ID	80215_1.R1010
5'-most EST	jC-atXLIB327440P1b03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	7.0e-22
Match length	55
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133008
Contig ID	80221_1.R1010
5'-most EST	jC-atXLIB327408P4e05a1
Method	BLASTX
NCBI GI	g2494304
BLAST score	325
E value	5.0e-30
Match length	125
% identity	54
NCBI Description	TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) >gi_2144003_pir__I59376 translation initiation factor eIF-2B alpha-subunit - rat >gi_623033 (U05821) translation initiation factor eIF-2B alpha-subunit [Rattus norvegicus] >gi_1050328 (L41679) GTP-exchange protein [Rattus norvegicus] >gi_1096885_prf__2112359A initiation factor eIF-2B [Rattus norvegicus]

Seq. No.	133009
Contig ID	80247_1.R1010
5'-most EST	jC-atXP35C154B14T7d1
Method	BLASTX
NCBI GI	g2262100
BLAST score	531
E value	1.0e-137
Match length	243
% identity	100
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	133010
Contig ID	80250_1.R1010
5'-most EST	jC-atXLIB327407P1h12a2
Method	BLASTX
NCBI GI	g2760326
BLAST score	207
E value	3.0e-16
Match length	54
% identity	69
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	133011
Contig ID	80250_2.R1010
5'-most EST	jC-atXLIB327425P2d08a1

Method	BLASTX
NCBI GI	g2760326
BLAST score	215
E value	3.0e-17
Match length	57
% identity	68
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	133012
Contig ID	80254_1.R1010
5'-most EST	jC-atXLIB327408P4f10a1
Method	BLASTN
NCBI GI	g4519193
BLAST score	165
E value	1.0e-87
Match length	420
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	133013
Contig ID	80278_1.R1010
5'-most EST	jC-atXLIB327425P2g10a1
Method	BLASTN
NCBI GI	g3319339
BLAST score	554
E value	0.0e+00
Match length	554
% identity	100
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	133014
Contig ID	80299_1.R1010
5'-most EST	jC-atXLIB327408P4h10a1
Method	BLASTX
NCBI GI	g3643596
BLAST score	367
E value	7.0e-42
Match length	93
% identity	94
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133015
Contig ID	80328_1.R1010
5'-most EST	jC-atXLIB327409P1b01a1
Method	BLASTN
NCBI GI	g3128141
BLAST score	516
E value	0.0e+00
Match length	805
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	133016
Contig ID	80413_1.R1010
5'-most EST	jC-atXLIB327409P1e11a1

Method	BLASTN
NCBI GI	g4519195
BLAST score	299
E value	1.0e-167
Match length	775
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	133017
Contig ID	80415_1.R1010
5'-most EST	jC-atXLIB327409P1e12a1
Method	BLASTX
NCBI GI	g2829887
BLAST score	312
E value	2.0e-28
Match length	142
% identity	52
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	133018
Contig ID	80427_1.R1010
5'-most EST	jC-atXLIB327409P1f08a1
Method	BLASTX
NCBI GI	g4468984
BLAST score	134
E value	6.0e-19
Match length	108
% identity	50
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	133019
Contig ID	80437_1.R1010
5'-most EST	jC-atXLIB327409P3g02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	6.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133020
Contig ID	80449_1.R1010
5'-most EST	jC-atXLIB327401P1h03a1
Method	BLASTX
NCBI GI	g4567255
BLAST score	189
E value	7.0e-34
Match length	173
% identity	53
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133021
Contig ID	80480_1.R1010
5'-most EST	jC-atXLIB327409P2a01a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133022
Contig ID	80484_1.R1010
5'-most EST	jC-atXLIB327409P2a03a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	482
E value	0.0e+00
Match length	534
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	133023
Contig ID	80511_1.R1010
5'-most EST	jC-atXLIB327430P1e08a1
Method	BLASTN
NCBI GI	g4468976
BLAST score	403
E value	0.0e+00
Match length	546
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	133024
Contig ID	80517_1.R1010
5'-most EST	jC-atXLIB327409P2b08a1
Method	BLASTN
NCBI GI	g4262221
BLAST score	244
E value	1.0e-134
Match length	478
% identity	76
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133025
Contig ID	80525_1.R1010
5'-most EST	jC-atXLIB327409P2b12a1
Method	BLASTX
NCBI GI	g3212865
BLAST score	288
E value	2.0e-25
Match length	134
% identity	49
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	133026
Contig ID	80546_2.R1010

5'-most EST	jC-atXP92C247M14T7058d1
Method	BLASTX
NCBI GI	g2154997
BLAST score	282
E value	1.0e-28
Match length	142
% identity	50
NCBI Description	(Y12503) Man9-mannosidase [Sus scrofa]

Seq. No.	133027
Contig ID	80546_3.R1010
5'-most EST	jC-atXLIB327409P2c11a1
Method	BLASTX
NCBI GI	g1708900
BLAST score	310
E value	4.0e-28
Match length	100
% identity	63
NCBI Description	MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 2 (MAN(9)-ALPHA-MANNOSIDASE) >gi_2133634_pir__S60710 alpha 1,2 mannosidase mas-1 precursor - fruit fly (Drosophila melanogaster) >gi_840752_emb_CAA57963_ (X82641) alpha 1,2 mannosidase [Drosophila melanogaster]

Seq. No.	133028
Contig ID	80548_1.R1010
5'-most EST	jC-atXLIB327409P2g11a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	249
E value	1.0e-137
Match length	396
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	133029
Contig ID	80552_1.R1010
5'-most EST	jC-atXLIB327409P2d02a1
Method	BLASTX
NCBI GI	g4490706
BLAST score	507
E value	5.0e-51
Match length	162
% identity	65
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	133030
Contig ID	80558_1.R1010
5'-most EST	jC-atXLIB327409P2d05a1
Method	BLASTX
NCBI GI	g2262111
BLAST score	706
E value	2.0e-74
Match length	138
% identity	99
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis

thaliana]

Seq. No.	133031
Contig ID	80560_1.R1010
5'-most EST	jC-atXLIB327409P2d06a1
Method	BLASTN
NCBI GI	g4432829
BLAST score	359
E value	0.0e+00
Match length	756
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133032
Contig ID	80562_1.R1010
5'-most EST	jC-atXLIB327409P2d07a1
Method	BLASTX
NCBI GI	g134028
BLAST score	153
E value	9.0e-10
Match length	76
% identity	46
NCBI Description	30S RIBOSOMAL PROTEIN S9 (BS10) >gi_70924_pir__R3BS9 ribosomal protein S9 - Bacillus stearothermophilus

Seq. No.	133033
Contig ID	80564_1.R1010
5'-most EST	jC-atXLIB327403P1e06a1
Method	BLASTX
NCBI GI	g3355467
BLAST score	255
E value	1.0e-21
Match length	149
% identity	38
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133034
Contig ID	80566_1.R1010
5'-most EST	jC-atXLIB327409P2d09a1
Method	BLASTX
NCBI GI	g1168646
BLAST score	50
E value	3.0e-25
Match length	163
% identity	39
NCBI Description	GTP-BINDING PROTEIN ERA HOMOLOG (BEX PROTEIN) >gi_606745 (U18532) Bex [Bacillus subtilis] >gi_1303826_dbj_BAA12482_ (D84432) YqfH [Bacillus subtilis] >gi_2634961_emb_CAB14458_ (Z99116) GTP-binding protein [Bacillus subtilis] >gi_2634975_emb_CAB14471_ (Z99117) GTP-binding protein [Bacillus subtilis]

Seq. No.	133035
Contig ID	80570_1.R1010
5'-most EST	jC-atXLIB327409P2d11a1

Seq. No.	133036
Contig ID	80581_1.R1010
5'-most EST	jC-atXLIB327409P2e05a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	222
E value	1.0e-121
Match length	443
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	133037
Contig ID	80587_1.R1010
5'-most EST	jC-atXLIB327409P2e08a1
Method	BLASTN
NCBI GI	g4220643
BLAST score	366
E value	0.0e+00
Match length	714
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	133038
Contig ID	80595_1.R1010
5'-most EST	jC-atXLIB327409P2e12a1
Method	BLASTX
NCBI GI	g4454468
BLAST score	204
E value	6.0e-52
Match length	132
% identity	76
NCBI Description	(AC006234) putative NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	133039
Contig ID	80600_1.R1010
5'-most EST	jC-atXLIB327432P4c06a1
Method	BLASTX
NCBI GI	g4586244
BLAST score	146
E value	4.0e-19
Match length	142
% identity	46
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	133040
Contig ID	80603_1.R1010
5'-most EST	jC-atXP82CG2F2T7d3
Method	BLASTX
NCBI GI	g3953481
BLAST score	459
E value	1.0e-121
Match length	259
% identity	91
NCBI Description	(AC002328) F22O2.26 [Arabidopsis thaliana]

Seq. No.	133041
Contig ID	80606_1.R1010
5'-most EST	jC-atXLIB327409P2f06a1
Method	BLASTX
NCBI GI	g3367522
BLAST score	145
E value	8.0e-59
Match length	174
% identity	75
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	133042
Contig ID	80610_1.R1010
5'-most EST	jC-atXLIB327401P2h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133043
Contig ID	80618_1.R1010
5'-most EST	jC-atXLIB327409P2f12a1

Seq. No.	133044
Contig ID	80622_1.R1010
5'-most EST	jC-atXLIB327409P2h03a1
Method	BLASTN
NCBI GI	g2564044
BLAST score	265
E value	1.0e-147
Match length	746
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	133045
Contig ID	80638_1.R1010
5'-most EST	jC-atXLIB327409P2g10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	5.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133046
Contig ID	80657_1.R1010
5'-most EST	jC-atXLIB327409P2h08a1
Method	BLASTN
NCBI GI	g3046847
BLAST score	180

E value	2.0e-96
Match length	672
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	133047
Contig ID	80678_1.R1010
5'-most EST	jC-atXLIB327409P3a07a1
Method	BLASTX
NCBI GI	g2811048
BLAST score	75
E value	4.0e-12
Match length	95
% identity	48
NCBI Description	DEVB PROTEIN HOMOLOG >gi_2131051_emb_CAB09261_ (Z95844) devB [Mycobacterium tuberculosis]

Seq. No.	133048
Contig ID	80688_1.R1010
5'-most EST	jC-atXLIB327409P3a12a1

Seq. No.	133049
Contig ID	80707_1.R1010
5'-most EST	jC-atXLIB327409P3b10a1

Seq. No.	133050
Contig ID	80709_1.R1010
5'-most EST	jC-atXLIB327409P3b11a1

Seq. No.	133051
Contig ID	80711_1.R1010
5'-most EST	jC-atXLIB327409P3b12a1
Method	BLASTX
NCBI GI	g4678345
BLAST score	430
E value	5.0e-42
Match length	160
% identity	49
NCBI Description	(AL049659) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	133052
Contig ID	80711_2.R1010
5'-most EST	g2047638
Method	BLASTX
NCBI GI	g4678345
BLAST score	308
E value	6.0e-28
Match length	144
% identity	41
NCBI Description	(AL049659) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	133053
Contig ID	80713_1.R1010
5'-most EST	jC-atXLIB327409P3c01a1

Method	BLASTX
NCBI GI	g3881836
BLAST score	87
E value	3.0e-43
Match length	172
% identity	59
NCBI Description	(Z78019) Similarity to Yeast LPG22P protein (TR:G1151240); cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this ge

Seq. No.	133054
Contig ID	80713_2.R1010
5'-most EST	jC-atXP89C245A2T7004d1
Method	BLASTN
NCBI GI	g3046856
BLAST score	651
E value	0.0e+00
Match length	666
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	133055
Contig ID	80737_1.R1010
5'-most EST	jC-atXLIB327409P3d01a1
Method	BLASTN
NCBI GI	g2351071
BLAST score	410
E value	0.0e+00
Match length	503
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	133056
Contig ID	80742_1.R1010
5'-most EST	jC-atXLIB327409P3d04a1
Method	BLASTX
NCBI GI	g2809246
BLAST score	314
E value	1.0e-28
Match length	140
% identity	46
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	133057
Contig ID	80744_1.R1010
5'-most EST	jC-atXLIB327430P1b07a1

Seq. No.	133058
Contig ID	80744_3.R1010
5'-most EST	jC-atXLIB327401P2g05a1

Seq. No.	133059
Contig ID	80748_1.R1010

5'-most EST	jC-atXLIB327409P3d07a1
Method	BLASTX
NCBI GI	g3135271
BLAST score	108
E value	3.0e-62
Match length	178
% identity	65
NCBI Description	(AC003058) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	133060
Contig ID	80750_1.R1010
5'-most EST	jC-atXLIB327409P3d08a1
Method	BLASTX
NCBI GI	g4455159
BLAST score	543
E value	2.0e-55
Match length	160
% identity	65
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	133061
Contig ID	80764_1.R1010
5'-most EST	jC-atXLIB327409P3e03a1
Method	BLASTX
NCBI GI	g4678332
BLAST score	919
E value	2.0e-99
Match length	237
% identity	83
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	133062
Contig ID	80782_1.R1010
5'-most EST	jC-atXLIB327409P3e12a1
Method	BLASTN
NCBI GI	g4469002
BLAST score	444
E value	0.0e+00
Match length	520
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	133063
Contig ID	80784_1.R1010
5'-most EST	jC-atXLIB327409P3f01a1
Method	BLASTX
NCBI GI	g4432844
BLAST score	556
E value	5.0e-57
Match length	130
% identity	88
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	133064

Contig ID 80863_1.R1010
5'-most EST jC-atXLIB327409P4a08a1

Seq. No. 133065
Contig ID 80917_1.R1010
5'-most EST jC-atXLIB327409P4d02a1

Seq. No. 133066
Contig ID 80931_1.R1010
5'-most EST jC-atXLIB327409P4d10a1
Method BLASTN
NCBI GI g2462264
BLAST score 49
E value 2.0e-18
Match length 53
% identity 98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133067
Contig ID 80935_1.R1010
5'-most EST jC-atXLIB327409P4d12a1
Method BLASTX
NCBI GI g1076473
BLAST score 379
E value 2.0e-36
Match length 83
% identity 87
NCBI Description Gln 1.1 protein - radish >gi_1526562_dbj_BAA04994_ (D25324) glutamine synthetase [Raphanus sativus]

Seq. No. 133068
Contig ID 80942_1.R1010
5'-most EST jC-atXLIB327409P4e04a1
Method BLASTN
NCBI GI g4325336
BLAST score 295
E value 1.0e-165
Match length 431
% identity 97
NCBI Description Arabidopsis thaliana BAC F15P23

Seq. No. 133069
Contig ID 80952_1.R1010
5'-most EST jC-atXP34C150H15T7a1
Method BLASTN
NCBI GI g2264302
BLAST score 97
E value 8.0e-47
Match length 204
% identity 88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 133070
Contig ID 80954_1.R1010
5'-most EST jC-atXP20C115G22T7047a1
Method BLASTX

NCBI GI	g2864602
BLAST score	669
E value	4.0e-70
Match length	186
% identity	71
NCBI Description	(Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No.	133071
Contig ID	80971_1.R1010
5'-most EST	jC-atXLIB327409P4f07a1
Method	BLASTX
NCBI GI	g4468807
BLAST score	500
E value	2.0e-50
Match length	110
% identity	89
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No.	133072
Contig ID	80975_1.R1010
5'-most EST	jC-atXLIB327409P4g12a1
Method	BLASTN
NCBI GI	g3241920
BLAST score	97
E value	5.0e-47
Match length	277
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	133073
Contig ID	80977_1.R1010
5'-most EST	jC-atXLIB327409P4f11a1
Method	BLASTN
NCBI GI	g3176693
BLAST score	263
E value	1.0e-146
Match length	368
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133074
Contig ID	80983_1.R1010
5'-most EST	jC-atXP112C127P7T7a1
Method	BLASTX
NCBI GI	g3201627
BLAST score	359
E value	8.0e-34
Match length	125
% identity	59
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	133075
Contig ID	80983_2.R1010
5'-most EST	jC-atXLIB327409P4g02a1

Method	BLASTX
NCBI GI	g3201627
BLAST score	122
E value	8.0e-74
Match length	190
% identity	74
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	133076
Contig ID	80987_1.R1010
5'-most EST	jC-atXLIB327409P4g04a1
Method	BLASTN
NCBI GI	g3702731
BLAST score	413
E value	0.0e+00
Match length	421
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	133077
Contig ID	80992_1.R1010
5'-most EST	jC-atXP12C99O5T7030a1
Method	BLASTX
NCBI GI	g1350680
BLAST score	460
E value	9.0e-46
Match length	143
% identity	69
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	133078
Contig ID	81016_1.R1010
5'-most EST	jC-atXLIB327409P4h09a1
Method	BLASTN
NCBI GI	g3451055
BLAST score	450
E value	0.0e+00
Match length	524
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	133079
Contig ID	81024_1.R1010
5'-most EST	jC-atXLIB327410P1a01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	1.0e-21
Match length	59
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133080
Contig ID	81024_2.R1010

5'-most EST	jC-atXLIB327410P1b03a1
Seq. No.	133081
Contig ID	81036_1.R1010
5'-most EST	jC-atXLIB327410P1a07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	133082
Contig ID	81056_1.R1010
5'-most EST	jC-atXLIB327410P1b08a1
Method	BLASTN
NCBI GI	g4191760
BLAST score	391
E value	0.0e+00
Match length	527
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]
Seq. No.	133083
Contig ID	81062_1.R1010
5'-most EST	jC-atXLIB327410P1b12a1
Method	BLASTN
NCBI GI	g3702724
BLAST score	324
E value	0.0e+00
Match length	606
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.	133084
Contig ID	81064_1.R1010
5'-most EST	jC-atXLIB327410P1c01a1
Method	BLASTX
NCBI GI	g2642432
BLAST score	449
E value	2.0e-44
Match length	160
% identity	63
NCBI Description	(AC002391) putative elicitor response element binding protein (WRKY3) [Arabidopsis thaliana]
Seq. No.	133085
Contig ID	81077_1.R1010
5'-most EST	jC-atXP44C170I15T7021a1
Seq. No.	133086
Contig ID	81077_2.R1010
5'-most EST	g2576806

Seq. No.	133087
Contig ID	81133_1.R1010
5'-most EST	jC-atXLIB327410P1f06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	6.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133088
Contig ID	81163_1.R1010
5'-most EST	jC-atXLIB327410P1g11a1
Method	BLASTN
NCBI GI	g4455348
BLAST score	274
E value	1.0e-152
Match length	638
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	133089
Contig ID	81169_1.R1010
5'-most EST	jC-atXLIB327410P1h02a1
Method	BLASTX
NCBI GI	g3641868
BLAST score	314
E value	2.0e-28
Match length	108
% identity	56
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	133090
Contig ID	81177_1.R1010
5'-most EST	jC-atXLIB327410P1h07a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	5.0e-23
Match length	61
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133091
Contig ID	81184_1.R1010
5'-most EST	jC-atXLIB327410P2a01a1
Method	BLASTX
NCBI GI	g4103635
BLAST score	191
E value	3.0e-14
Match length	78
% identity	46
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	133092
Contig ID	81191_1.R1010
5'-most EST	jC-atXLIB327410P2a06a1
Method	BLASTN
NCBI GI	g4757678
BLAST score	283
E value	1.0e-158
Match length	404
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	133093
Contig ID	81199_1.R1010
5'-most EST	jC-atXLIB327410P2a11a1
Method	BLASTN
NCBI GI	g2618600
BLAST score	375
E value	0.0e+00
Match length	391
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	133094
Contig ID	81207_1.R1010
5'-most EST	jC-atXLIB327410P2b05a1
Method	BLASTX
NCBI GI	g3522943
BLAST score	344
E value	3.0e-32
Match length	128
% identity	36
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	133095
Contig ID	81216_1.R1010
5'-most EST	jC-atXLIB327410P2b11a1
Method	BLASTX
NCBI GI	g3335353
BLAST score	351
E value	4.0e-33
Match length	79
% identity	84
NCBI Description	(AC004512) Similar to cytochrome P450 gb_X90458 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	133096
Contig ID	81227_1.R1010
5'-most EST	jC-atXLIB327410P2c09a1
Method	BLASTX
NCBI GI	g2688822
BLAST score	277
E value	2.0e-24
Match length	62
% identity	82
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase

[Prunus armeniaca]

Seq. No.	133097
Contig ID	81240_1.R1010
5'-most EST	jC-atXLIB327410P2d11a1
Method	BLASTN
NCBI GI	g2252823
BLAST score	162
E value	8.0e-86
Match length	542
% identity	43
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	133098
Contig ID	81252_1.R1010
5'-most EST	jC-atXLIB327410P2e07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	6.0e-22
Match length	63
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133099
Contig ID	81254_1.R1010
5'-most EST	jC-atXLIB327410P3d10a1
Method	BLASTX
NCBI GI	g4049342
BLAST score	423
E value	1.0e-41
Match length	98
% identity	50
NCBI Description	(AL034567) adenylate translocator (brittle-1)-like protein [Arabidopsis thaliana]

Seq. No.	133100
Contig ID	81262_1.R1010
5'-most EST	jC-atXLIB327410P2f04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133101
Contig ID	81269_1.R1010
5'-most EST	jC-atXLIB327410P2f09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	49
E value	3.0e-18
Match length	61
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No.	133102
Contig ID	81285_1.R1010
5'-most EST	jC-atXLIB327410P2g08a1
Method	BLASTX
NCBI GI	g4585877
BLAST score	160
E value	1.0e-10
Match length	110
% identity	38
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	133103
Contig ID	81307_1.R1010
5'-most EST	jC-atXLIB327410P2h08a1
Method	BLASTX
NCBI GI	g3928543
BLAST score	493
E value	1.0e-49
Match length	117
% identity	75
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	133104
Contig ID	81323_1.R1010
5'-most EST	jC-atXLIB327431P3f04b1
Method	BLASTN
NCBI GI	g2924505
BLAST score	437
E value	0.0e+00
Match length	457
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	133105
Contig ID	81323_2.R1010
5'-most EST	jC-atXLIB327410P3a05a1
Method	BLASTN
NCBI GI	g2924505
BLAST score	391
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	133106
Contig ID	81344_1.R1010
5'-most EST	jC-atXLIB327410P3b05a1
Method	BLASTX
NCBI GI	g3927825
BLAST score	176
E value	1.0e-12
Match length	65

% identity	65
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	133107
Contig ID	81366_1.R1010
5'-most EST	jC-atXLIB327410P3c11a1
Method	BLASTN
NCBI GI	g2564051
BLAST score	382
E value	0.0e+00
Match length	678
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	133108
Contig ID	81374_1.R1010
5'-most EST	jC-atXLIB327410P3d05a1
Method	BLASTX
NCBI GI	g4191796
BLAST score	102
E value	9.0e-39
Match length	89
% identity	92
NCBI Description	(AC005917) putative senescence-associated protein 5 [Arabidopsis thaliana]

Seq. No.	133109
Contig ID	81387_1.R1010
5'-most EST	jC-atXLIB327410P3e04a1
Method	BLASTX
NCBI GI	g2129593
BLAST score	402
E value	5.0e-39
Match length	93
% identity	88
NCBI Description	geranylgeranyl pyrophosphate synthase GGPS3 - Arabidopsis thaliana (fragment) >gi_1229166 (U44877) geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	133110
Contig ID	81397_1.R1010
5'-most EST	jC-atXLIB327410P3e10a1
Method	BLASTX
NCBI GI	g4056482
BLAST score	525
E value	3.0e-53
Match length	167
% identity	59
NCBI Description	(AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	133111
Contig ID	81401_1.R1010
5'-most EST	jC-atXLIB327410P3e12a1
Method	BLASTN
NCBI GI	g2245073

BLAST score	283
E value	1.0e-158
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133112
Contig ID	81406_1.R1010
5'-most EST	jC-atXLIB327410P3f05a1
Method	BLASTN
NCBI GI	g2245073
BLAST score	186
E value	1.0e-100
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133113
Contig ID	81408_1.R1010
5'-most EST	jC-atXLIB327410P3f06a1
Method	BLASTN
NCBI GI	g3449316
BLAST score	410
E value	0.0e+00
Match length	506
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	133114
Contig ID	81424_1.R1010
5'-most EST	jC-atXLIB327410P3g05a1

Seq. No.	133115
Contig ID	81432_1.R1010
5'-most EST	jC-atXLIB327410P3g10a1
Method	BLASTX
NCBI GI	g3482974
BLAST score	196
E value	1.0e-14
Match length	74
% identity	58
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	133116
Contig ID	81443_1.R1010
5'-most EST	jC-atXLIB327410P3h04a1

Seq. No.	133117
Contig ID	81447_1.R1010
5'-most EST	jC-atXLIB327410P3h06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	45

E value	6.0e-16
Match length	64
% identity	92
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133118
Contig ID	81449_1.R1010
5'-most EST	jC-atXLIB327410P3h07a1
Method	BLASTX
NCBI GI	g4521249
BLAST score	210
E value	2.0e-16
Match length	73
% identity	58
NCBI Description	(AB013912) DNA helicase [Mus musculus]

Seq. No.	133119
Contig ID	81453_1.R1010
5'-most EST	jC-atXLIB327410P3h09a1
Method	BLASTN
NCBI GI	g3367500
BLAST score	411
E value	0.0e+00
Match length	415
% identity	41
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	133120
Contig ID	81481_1.R1010
5'-most EST	jC-atXLIB327410P4b01a1
Method	BLASTN
NCBI GI	g3341671
BLAST score	258
E value	1.0e-143
Match length	399
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133121
Contig ID	81502_1.R1010
5'-most EST	jC-atXLIB327439P2d10a2

Seq. No.	133122
Contig ID	81513_1.R1010
5'-most EST	jC-atXLIB327410P4d11a1
Method	BLASTX
NCBI GI	g3860321
BLAST score	839
E value	5.0e-90
Match length	206
% identity	71
NCBI Description	(AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No. 133123

Contig ID 81522_1.R1010
5'-most EST jC-atXLIB327410P4e05a1
Method BLASTN
NCBI GI g3702732
BLAST score 236
E value 1.0e-130
Match length 381
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No. 133124
Contig ID 81535_1.R1010
5'-most EST jC-atXP95CG12C3T7002b1

Seq. No. 133125
Contig ID 81539_1.R1010
5'-most EST jC-atXLIB327410P4f09a1

Seq. No. 133126
Contig ID 81541_1.R1010
5'-most EST jC-atXLIB327410P4f10a1
Method BLASTX
NCBI GI g3033375
BLAST score 398
E value 2.0e-38
Match length 135
% identity 53
NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No. 133127
Contig ID 81541_2.R1010
5'-most EST g2047376
Method BLASTX
NCBI GI g3033375
BLAST score 318
E value 3.0e-29
Match length 129
% identity 50
NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No. 133128
Contig ID 81570_1.R1010
5'-most EST jC-atXLIB327410P4h04a1
Method BLASTX
NCBI GI g3395441
BLAST score 69
E value 5.0e-36
Match length 96
% identity 90
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 133129
Contig ID 81592_1.R1010
5'-most EST jC-atXLIB327411P1a03a1

Seq. No.	133130
Contig ID	81596_1.R1010
5'-most EST	jC-atXLIB327411P1a05a1
Method	BLASTX
NCBI GI	g1652856
BLAST score	146
E value	5.0e-09
Match length	101
% identity	34
NCBI Description	(D90909) hypothetical protein [Synechocystis sp.]

Seq. No.	133131
Contig ID	81600_1.R1010
5'-most EST	jC-atXLIB327411P1a07a1
Method	BLASTN
NCBI GI	g4732169
BLAST score	41
E value	1.0e-13
Match length	89
% identity	87
NCBI Description	Arabidopsis thaliana BAC T3E15

Seq. No.	133132
Contig ID	81606_1.R1010
5'-most EST	jC-atXLIB327411P1a10a1
Method	BLASTX
NCBI GI	g2194130
BLAST score	258
E value	4.0e-22
Match length	137
% identity	41
NCBI Description	(AC002062) Similar to Nicotiana 5-epi-aristolochene synthase (gb_L04680). [Arabidopsis thaliana]

Seq. No.	133133
Contig ID	81610_1.R1010
5'-most EST	jC-atXLIB327411P1a12a1
Method	BLASTX
NCBI GI	g3913425
BLAST score	377
E value	4.0e-36
Match length	68
% identity	99
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	133134
Contig ID	81613_1.R1010
5'-most EST	jC-atXLIB327411P1b02b1
Method	BLASTN
NCBI GI	g4220644
BLAST score	289
E value	1.0e-161
Match length	474
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	133135
Contig ID	81622_1.R1010
5'-most EST	jC-atXLIB327411P1b09a1

Seq. No.	133136
Contig ID	81628_1.R1010
5'-most EST	jC-atXLIB327411P1b12a1
Method	BLASTN
NCBI GI	g540252
BLAST score	51
E value	1.0e-19
Match length	55
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	133137
Contig ID	81632_1.R1010
5'-most EST	jC-atXLIB327411P2c01a1
Method	BLASTX
NCBI GI	g3335359
BLAST score	249
E value	8.0e-35
Match length	148
% identity	63
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	133138
Contig ID	81636_1.R1010
5'-most EST	jC-atXLIB327411P1c04a1
Method	BLASTX
NCBI GI	g2253010
BLAST score	98
E value	2.0e-24
Match length	83
% identity	69
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	133139
Contig ID	81638_1.R1010
5'-most EST	jC-atXLIB327411P1c05a1
Method	BLASTN
NCBI GI	g3702728
BLAST score	313
E value	1.0e-176
Match length	447
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	133140
Contig ID	81641_1.R1010
5'-most EST	jC-atXLIB327411P1c07a1
Method	BLASTN

NCBI GI g3281847
BLAST score 129
E value 4.0e-66
Match length 411
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No. 133141
Contig ID 81668_1.R1010
5'-most EST jC-atXLIB327411P1d10a1
Method BLASTN
NCBI GI g4519193
BLAST score 435
E value 0.0e+00
Match length 447
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No. 133142
Contig ID 81678_1.R1010
5'-most EST jC-atXLIB327432P3b11a1
Method BLASTX
NCBI GI g3297817
BLAST score 204
E value 8.0e-16
Match length 105
% identity 38
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 133143
Contig ID 81680_1.R1010
5'-most EST jC-atXLIB327411P1e04a1
Method BLASTN
NCBI GI g4662647
BLAST score 330
E value 0.0e+00
Match length 424
% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F3K12 genomic sequence, complete sequence

Seq. No. 133144
Contig ID 81684_1.R1010
5'-most EST jC-atXLIB327411P1e06a1
Method BLASTN
NCBI GI g3600029
BLAST score 57
E value 4.0e-23
Match length 114
% identity 95
NCBI Description Arabidopsis thaliana BAC T12H20

Seq. No. 133145
Contig ID 81688_1.R1010
5'-most EST jC-atXLIB327411P1e08a1

Method	BLASTX
NCBI GI	g4580761
BLAST score	67
E value	2.0e-51
Match length	156
% identity	67
NCBI Description	(AF061088) P-glycoprotein [Gossypium robinsonii]

Seq. No.	133146
Contig ID	81692_1.R1010
5'-most EST	jC-atXLIB327411P1e10a1
Method	BLASTX
NCBI GI	g4678335
BLAST score	448
E value	2.0e-44
Match length	90
% identity	94
NCBI Description	(AL049658) L-galactono-1, 4-lactone dehydrogenase-like protein [Arabidopsis thaliana]

Seq. No.	133147
Contig ID	81694_1.R1010
5'-most EST	jC-atXLIB327411P1e11a1
Method	BLASTN
NCBI GI	g3252804
BLAST score	184
E value	7.0e-99
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133148
Contig ID	81705_1.R1010
5'-most EST	g634985
Method	BLASTX
NCBI GI	g3450842
BLAST score	626
E value	4.0e-65
Match length	214
% identity	60
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	133149
Contig ID	81726_1.R1010
5'-most EST	jC-atXLIB327411P1g05a1
Method	BLASTN
NCBI GI	g4559319
BLAST score	347
E value	0.0e+00
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	133150

Contig ID	81731_1.R1010
5'-most EST	jC-atXLIB327411P1g07b1
Method	BLASTN
NCBI GI	g2264317
BLAST score	283
E value	1.0e-158
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	133151
Contig ID	81732_1.R1010
5'-most EST	jC-atXLIB327411P1g08a1
Method	BLASTN
NCBI GI	g2578821
BLAST score	443
E value	0.0e+00
Match length	463
% identity	99
NCBI Description	Arabidopsis thaliana gene for geranyl geranyl pyrophosphate synthase, complete cds

Seq. No.	133152
Contig ID	81750_1.R1010
5'-most EST	jC-atXLIB327411P1h05a1

Seq. No.	133153
Contig ID	81755_1.R1010
5'-most EST	jC-atXLIB327411P1h08a1
Method	BLASTN
NCBI GI	g4432829
BLAST score	249
E value	1.0e-137
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133154
Contig ID	81763_1.R1010
5'-most EST	jC-atXLIB327411P2a01a1
Method	BLASTN
NCBI GI	g3241922
BLAST score	45
E value	5.0e-16
Match length	198
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	133155
Contig ID	81799_1.R1010
5'-most EST	jC-atXLIB327411P2c02a1
Method	BLASTN
NCBI GI	g4490324
BLAST score	416

E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	133156
Contig ID	81815_1.R1010
5'-most EST	jC-atXLIB327411P2d04a1
Method	BLASTX
NCBI GI	g3822223
BLAST score	208
E value	2.0e-83
Match length	177
% identity	91
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	133157
Contig ID	81818_1.R1010
5'-most EST	jC-atXLIB327411P2d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	133158
Contig ID	81835_1.R1010
5'-most EST	jC-atXLIB327411P2e02a1
Method	BLASTX
NCBI GI	g4454484
BLAST score	1287
E value	1.0e-142
Match length	281
% identity	88
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	133159
Contig ID	81836_1.R1010
5'-most EST	jC-atXLIB327418P3a05a2
Method	BLASTX
NCBI GI	g4581139
BLAST score	540
E value	3.0e-55
Match length	100
% identity	51
NCBI Description	(AC006919) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	133160
Contig ID	81837_1.R1010
5'-most EST	jC-atXLIB327411P2e04a1
Method	BLASTX

NCBI GI	g1076534
BLAST score	404
E value	3.0e-39
Match length	94
% identity	77
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden pea >gi_497120 (U06461) monodehydroascorbate reductase [Pisum sativum]

Seq. No.	133161
Contig ID	81847_1.R1010
5'-most EST	jC-atXLIB327411P2f01a1
Method	BLASTX
NCBI GI	g3928093
BLAST score	504
E value	6.0e-51
Match length	100
% identity	100
NCBI Description	(AC005770) IVR-like protein [Arabidopsis thaliana]

Seq. No.	133162
Contig ID	81897_1.R1010
5'-most EST	jC-atXLIB327411P2h08a1
Method	BLASTX
NCBI GI	g2213882
BLAST score	159
E value	2.0e-10
Match length	60
% identity	50
NCBI Description	(AF004165) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	133163
Contig ID	81903_1.R1010
5'-most EST	jC-atXLIB327411P2h11a1
Method	BLASTX
NCBI GI	g2541876
BLAST score	241
E value	4.0e-20
Match length	126
% identity	40
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	133164
Contig ID	81928_1.R1010
5'-most EST	jC-atXP70C222C8T7095a1
Method	BLASTN
NCBI GI	g4757392
BLAST score	421
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No. 133165

Contig ID 81930_1.R1010
5'-most EST jC-atXLIB327407P4b04a1
Method BLASTN
NCBI GI g2288979
BLAST score 66
E value 2.0e-28
Match length 147
% identity 93
NCBI Description Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133166
Contig ID 81931_1.R1010
5'-most EST jC-atXLIB327407P4b04b1
Method BLASTX
NCBI GI g2288988
BLAST score 684
E value 4.0e-72
Match length 136
% identity 93
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 133167
Contig ID 81940_1.R1010
5'-most EST jC-atXP70C221F4T7076a1
Method BLASTX
NCBI GI g4580517
BLAST score 297
E value 5.0e-62
Match length 120
% identity 99
NCBI Description (AF036302) scarecrow-like 5 [Arabidopsis thaliana]

Seq. No. 133168
Contig ID 81947_2.R1010
5'-most EST g510749

Seq. No. 133169
Contig ID 81973_1.R1010
5'-most EST jC-atXLIB327407P4d06a1

Seq. No. 133170
Contig ID 81998_1.R1010
5'-most EST jC-atXLIB327407P4e12a1
Method BLASTN
NCBI GI g2264313
BLAST score 93
E value 2.0e-44
Match length 255
% identity 87
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No. 133171
Contig ID 82037_1.R1010
5'-most EST jC-atXLIB327408P1a03a1
Method BLASTX

NCBI GI	g3913425
BLAST score	204
E value	8.0e-16
Match length	40
% identity	93
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	133172
Contig ID	82043_1.R1010
5'-most EST	jC-atXP86CG8E6T7b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	755
E value	0.0e+00
Match length	804
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	133173
Contig ID	82043_2.R1010
5'-most EST	g2747509
Method	BLASTN
NCBI GI	g4159704
BLAST score	410
E value	0.0e+00
Match length	671
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	133174
Contig ID	82047_1.R1010
5'-most EST	jC-atXLIB327408P1a08a1
Method	BLASTN
NCBI GI	g3702731
BLAST score	465
E value	0.0e+00
Match length	556
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	133175
Contig ID	82053_1.R1010
5'-most EST	jC-atXLIB327408P1a11a1
Method	BLASTX
NCBI GI	g4490308
BLAST score	555
E value	2.0e-76
Match length	150
% identity	100
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 133176

Contig ID 82059_1.R1010
5'-most EST jC-atXLIB327408P1b02a1

Seq. No. 133177
Contig ID 82061_1.R1010
5'-most EST jC-atXLIB327408P1b03a1
Method BLASTN
NCBI GI g4467094
BLAST score 392
E value 0.0e+00
Match length 417
% identity 65
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No. 133178
Contig ID 82061_3.R1010
5'-most EST jC-atXP10C96I1T7s2
Method BLASTX
NCBI GI g4468993
BLAST score 455
E value 4.0e-45
Match length 95
% identity 89
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 133179
Contig ID 82101_1.R1010
5'-most EST jC-atXLIB327408P1d01a1
Method BLASTX
NCBI GI g2651310
BLAST score 528
E value 9.0e-54
Match length 116
% identity 89
NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No. 133180
Contig ID 82103_1.R1010
5'-most EST jC-atXLIB327408P1d02a1

Seq. No. 133181
Contig ID 82105_1.R1010
5'-most EST jC-atXLIB327408P1d03a1

Seq. No. 133182
Contig ID 82111_1.R1010
5'-most EST jC-atXLIB327433P2g07a1
Method BLASTX
NCBI GI g722377
BLAST score 122
E value 5.0e-19
Match length 79
% identity 57
NCBI Description (U23139) highly similar to beta-ureidopropionase (SP:BUP_RAT) [Caenorhabditis elegans]

Seq. No.	133183
Contig ID	82117_1.R1010
5'-most EST	jC-atXLIB327408P1d09a1
Method	BLASTN
NCBI GI	g2245073
BLAST score	342
E value	0.0e+00
Match length	681
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133184
Contig ID	82152_1.R1010
5'-most EST	jC-atXLIB327408P1f04b1
Method	BLASTX
NCBI GI	g2497538
BLAST score	655
E value	1.0e-68
Match length	151
% identity	89
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	133185
Contig ID	82175_1.R1010
5'-most EST	jC-atXLIB327408P1g04a1
Method	BLASTN
NCBI GI	g2529657
BLAST score	326
E value	0.0e+00
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133186
Contig ID	82179_1.R1010
5'-most EST	jC-atXP117C140M20T7a1
Method	BLASTX
NCBI GI	g4262186
BLAST score	410
E value	9.0e-40
Match length	172
% identity	58
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	133187
Contig ID	82187_1.R1010
5'-most EST	jC-atXLIB327408P1g10a1

Seq. No.	133188
Contig ID	82191_1.R1010
5'-most EST	jC-atXLIB327408P1h12a1
Method	BLASTN

NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133189
Contig ID	82201_1.R1010
5'-most EST	jC-atXLIB327408P1h05a1
Method	BLASTX
NCBI GI	g2281334
BLAST score	227
E value	2.0e-18
Match length	89
% identity	51
NCBI Description	(U83619) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	133190
Contig ID	82213_1.R1010
5'-most EST	jC-atXLIB327408P1h11a1
Method	BLASTX
NCBI GI	g4099090
BLAST score	159
E value	2.0e-10
Match length	53
% identity	68
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	133191
Contig ID	82236_1.R1010
5'-most EST	jC-atXLIB327408P2a11a1
Method	BLASTX
NCBI GI	g1170606
BLAST score	354
E value	3.0e-33
Match length	105
% identity	63
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	133192
Contig ID	82246_1.R1010
5'-most EST	jC-atXLIB327408P2b04a1

Seq. No.	133193
Contig ID	82248_1.R1010
5'-most EST	jC-atXLIB327408P2b05a1

Seq. No.	133194

Contig ID 82259_1.R1010
5'-most EST jC-atXLIB327408P2b11a1

Seq. No. 133195
Contig ID 82282_1.R1010
5'-most EST jC-atXLIB327408P2c11a1
Method BLASTX
NCBI GI g3236240
BLAST score 460
E value 9.0e-50
Match length 130
% identity 75
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 133196
Contig ID 82282_2.R1010
5'-most EST g1053415
Method BLASTX
NCBI GI g3236240
BLAST score 145
E value 2.0e-09
Match length 38
% identity 71
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 133197
Contig ID 82284_1.R1010
5'-most EST jC-atXP22C114O15T7082a1
Method BLASTX
NCBI GI g4006899
BLAST score 443
E value 1.0e-43
Match length 139
% identity 58
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 133198
Contig ID 82286_1.R1010
5'-most EST jC-atXLIB327408P2d01a1
Method BLASTN
NCBI GI g3402695
BLAST score 73
E value 1.0e-32
Match length 203
% identity 85
NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133199
Contig ID 82294_1.R1010
5'-most EST jC-atXLIB327408P2d05a1
Method BLASTX
NCBI GI g4585988
BLAST score 627
E value 4.0e-65
Match length 143
% identity 84

NCBI Description	(AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]

Seq. No.	133200
Contig ID	82296_1.R1010
5'-most EST	jC-atXLIB327408P2d06a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	673
E value	0.0e+00
Match length	697
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	133201
Contig ID	82296_2.R1010
5'-most EST	jC-atXLIB327427P1g05a2
Method	BLASTN
NCBI GI	g4757662
BLAST score	530
E value	0.0e+00
Match length	630
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	133202
Contig ID	82298_1.R1010
5'-most EST	g1053527
Method	BLASTX
NCBI GI	g3329316
BLAST score	228
E value	2.0e-23
Match length	94
% identity	58
NCBI Description	(AE001357) cytosine deaminase [Chlamydia trachomatis]

Seq. No.	133203
Contig ID	82298_2.R1010
5'-most EST	jC-atXLIB327408P2d07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133204
Contig ID	82315_1.R1010
5'-most EST	jC-atXLIB327408P2e04a1

Seq. No.	133205
Contig ID	82323_1.R1010
5'-most EST	jC-atXLIB327408P2e08a1

Seq. No.	133206
Contig ID	82338_1.R1010
5'-most EST	jC-atXLIB327408P2f04b1
Method	BLASTN
NCBI GI	g3985931
BLAST score	304
E value	1.0e-170
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	133207
Contig ID	82345_1.R1010
5'-most EST	jC-atXLIB327408P2f08a1
Method	BLASTX
NCBI GI	g3688170
BLAST score	534
E value	2.0e-54
Match length	100
% identity	99
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	133208
Contig ID	82363_1.R1010
5'-most EST	jC-atXLIB327405P2f12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	6.0e-22
Match length	62
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133209
Contig ID	82365_1.R1010
5'-most EST	jC-atXLIB327408P2h07a1
Method	BLASTX
NCBI GI	g2213629
BLAST score	356
E value	1.0e-33
Match length	89
% identity	81
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	133210
Contig ID	82390_1.R1010
5'-most EST	jC-atXLIB327408P2h08a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	721
E value	0.0e+00
Match length	828
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No. 133211
Contig ID 82392_1.R1010
5'-most EST jC-atXLIB327408P2h09a1

Seq. No. 133212
Contig ID 82396_1.R1010
5'-most EST jC-atXLIB327408P2h11a1
Method BLASTN
NCBI GI g4455262
BLAST score 338
E value 0.0e+00
Match length 437
% identity 97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No. 133213
Contig ID 82398_1.R1010
5'-most EST jC-atXLIB327413P2e08a1
Method BLASTX
NCBI GI g4262174
BLAST score 97
E value 3.0e-34
Match length 97
% identity 84
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 133214
Contig ID 82400_1.R1010
5'-most EST jC-atXP22C114P19T7075a1
Method BLASTX
NCBI GI g4455159
BLAST score 794
E value 1.0e-84
Match length 162
% identity 96
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 133215
Contig ID 82402_1.R1010
5'-most EST jC-atXLIB327414P2a02a1
Method BLASTN
NCBI GI g2924728
BLAST score 319
E value 1.0e-179
Match length 364
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No. 133216
Contig ID 82410_1.R1010
5'-most EST jC-atXLIB327414P2a06a1
Method BLASTX
NCBI GI g4539383
BLAST score 421

E value	3.0e-41
Match length	82
% identity	100
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	133217
Contig ID	82437_1.R1010
5'-most EST	jC-atXLIB327414P2b08a1
Method	BLASTX
NCBI GI	g4827050
BLAST score	455
E value	7.0e-45
Match length	306
% identity	37
NCBI Description	ubiquitin specific protease 14 (tRNA-guanine transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No.	133218
Contig ID	82607_1.R1010
5'-most EST	jC-atXLIB327406P3g11b2
Method	BLASTN
NCBI GI	g3046856
BLAST score	95
E value	2.0e-45
Match length	481
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	133219
Contig ID	82666_1.R1010
5'-most EST	jC-atXLIB327414P3f06a1
Method	BLASTX
NCBI GI	g4586050
BLAST score	427
E value	7.0e-42
Match length	87
% identity	97
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana] >gi_4588009_gb_AAD25950.1_AF085279_23 (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133220
Contig ID	82674_1.R1010
5'-most EST	jC-atXLIB327414P3f10a1
Method	BLASTX
NCBI GI	g2244818
BLAST score	187
E value	7.0e-14
Match length	100
% identity	50
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133221
Contig ID	82680_1.R1010
5'-most EST	jC-atXLIB327414P3g01a1
Method	BLASTN
NCBI GI	g3413696
BLAST score	275
E value	1.0e-153
Match length	396
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133222
Contig ID	82686_1.R1010
5'-most EST	jC-atXLIB327440P4d12a1
Method	BLASTN
NCBI GI	g2264317
BLAST score	455
E value	0.0e+00
Match length	526
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	133223
Contig ID	82690_1.R1010
5'-most EST	jC-atXLIB327416P2f03a1
Method	BLASTX
NCBI GI	g4559342
BLAST score	409
E value	8.0e-40
Match length	102
% identity	80
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	133224
Contig ID	82698_1.R1010
5'-most EST	jC-atXLIB327414P3g11a1
Method	BLASTX
NCBI GI	g4510383
BLAST score	52
E value	3.0e-25
Match length	78
% identity	82
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	133225
Contig ID	82710_1.R1010
5'-most EST	jC-atXLIB327414P3h05a1
Method	BLASTX
NCBI GI	g974294
BLAST score	332
E value	1.0e-30
Match length	109
% identity	58
NCBI Description	(U31309) LP6 [Pinus taeda]

Seq. No.	133226
Contig ID	82714_1.R1010
5'-most EST	jC-atXLIB327414P3h07a1
Method	BLASTX
NCBI GI	g1890317
BLAST score	364
E value	1.0e-34
Match length	84
% identity	81
NCBI Description	(Y11791) peroxidase ATP26a [Arabidopsis thaliana]

Seq. No.	133227
Contig ID	82720_1.R1010
5'-most EST	jC-atXLIB327414P3h11a1
Method	BLASTN
NCBI GI	g468770
BLAST score	366
E value	0.0e+00
Match length	412
% identity	97
NCBI Description	A.thaliana genes for chloroplast ribosomal protein L12 and tRNA-Pro

Seq. No.	133228
Contig ID	82747_1.R1010
5'-most EST	jC-atXLIB327420P1e01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133229
Contig ID	82751_1.R1010
5'-most EST	jC-atXLIB327415P4b03a1
Method	BLASTN
NCBI GI	g2351073
BLAST score	37
E value	4.0e-11
Match length	92
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	133230
Contig ID	82754_1.R1010
5'-most EST	jC-atXLIB327425P2g01a1
Method	BLASTX
NCBI GI	g3779021
BLAST score	533
E value	3.0e-57
Match length	119
% identity	93

NCBI Description	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	133231
Contig ID	82754_2.R1010
5'-most EST	jC-atXLIB327415P4b05a1
Method	BLASTX
NCBI GI	g3779021
BLAST score	700
E value	5.0e-74
Match length	135
% identity	97
NCBI Description	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	133232
Contig ID	82758_1.R1010
5'-most EST	jC-atXLIB327415P4b07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	48
E value	1.0e-17
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133233
Contig ID	82800_1.R1010
5'-most EST	jC-atXLIB327415P4d07a1
Method	BLASTX
NCBI GI	g2104536
BLAST score	301
E value	4.0e-27
Match length	51
% identity	100
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	133234
Contig ID	82810_1.R1010
5'-most EST	jC-atXLIB327415P4e01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	3.0e-21
Match length	66
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133235
Contig ID	82814_1.R1010
5'-most EST	jC-atXLIB327415P4e03a1
Method	BLASTN
NCBI GI	g2760169
BLAST score	315
E value	1.0e-177

Match length	389
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	133236
Contig ID	82820_1.R1010
5'-most EST	jC-atXLIB327415P4e06a1
Method	BLASTN
NCBI GI	g4415928
BLAST score	304
E value	1.0e-170
Match length	425
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133237
Contig ID	82826_1.R1010
5'-most EST	jC-atXLIB327415P4e09a1
Method	BLASTN
NCBI GI	g2696018
BLAST score	432
E value	0.0e+00
Match length	503
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	133238
Contig ID	82830_1.R1010
5'-most EST	jC-atXLIB327415P4e11a1

Seq. No.	133239
Contig ID	82840_1.R1010
5'-most EST	jC-atXLIB327415P4f04a1
Method	BLASTN
NCBI GI	g3831437
BLAST score	479
E value	0.0e+00
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133240
Contig ID	82852_1.R1010
5'-most EST	jC-atXP46C174D21T7087a1

Seq. No.	133241
Contig ID	82868_1.R1010
5'-most EST	jC-atXLIB327415P4g11a1
Method	BLASTX
NCBI GI	g3831440
BLAST score	445
E value	4.0e-44
Match length	100

% identity	86
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	133242
Contig ID	82920_1.R1010
5'-most EST	jC-atXLIB327412P1b10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	4.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	133243
Contig ID	82968_1.R1010
5'-most EST	jC-atXLIB327412P3e04a1
Method	BLASTX
NCBI GI	g4521247
BLAST score	455
E value	3.0e-45
Match length	104
% identity	82
NCBI Description	(AB007770) translation elongation factor 1 alpha [Aspergillus oryzae]
Seq. No.	133244
Contig ID	82974_1.R1010
5'-most EST	jC-atXLIB327412P1f07a1
Method	BLASTX
NCBI GI	g4490293
BLAST score	380
E value	2.0e-36
Match length	90
% identity	83
NCBI Description	(AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]
Seq. No.	133245
Contig ID	82975_1.R1010
5'-most EST	jC-atXP3C80E6T7008a1
Method	BLASTX
NCBI GI	g1134882
BLAST score	418
E value	8.0e-41
Match length	87
% identity	83
NCBI Description	(Z68291) cysteine protease [Pisum sativum]
Seq. No.	133246
Contig ID	82975_4.R1010
5'-most EST	g438290
Seq. No.	133247
Contig ID	82993_1.R1010

5'-most EST	jC-atXLIB327412P3g06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	2.0e-18
Match length	65
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133248
Contig ID	83015_1.R1010
5'-most EST	jC-atXLIB327412P2b05a1
Method	BLASTX
NCBI GI	g3193296
BLAST score	451
E value	9.0e-45
Match length	132
% identity	60
NCBI Description	(AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No.	133249
Contig ID	83021_1.R1010
5'-most EST	jC-atXLIB327412P2b09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	5.0e-20
Match length	64
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133250
Contig ID	83040_1.R1010
5'-most EST	jC-atXLIB327412P2d02a1
Method	BLASTN
NCBI GI	g2832667
BLAST score	298
E value	1.0e-167
Match length	427
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	133251
Contig ID	83054_1.R1010
5'-most EST	jC-atXLIB327439P3c01a2
Method	BLASTN
NCBI GI	g4589418
BLAST score	431
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	133252

Contig ID 83063_1.R1010
5'-most EST g2047796

Seq. No. 133253
Contig ID 83063_2.R1010
5'-most EST jC-atXLIB327412P2f02a1
Method BLASTX
NCBI GI g3738334
BLAST score 283
E value 6.0e-25
Match length 104
% identity 60
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 133254
Contig ID 83089_1.R1010
5'-most EST jC-atXLIB327412P3a02a1

Seq. No. 133255
Contig ID 83104_1.R1010
5'-most EST jC-atXLIB327413P2g05a1
Method BLASTX
NCBI GI g3080420
BLAST score 574
E value 3.0e-59
Match length 108
% identity 100
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 133256
Contig ID 83113_1.R1010
5'-most EST jC-atX35002Q1E1E08a1
Method BLASTN
NCBI GI g4512656
BLAST score 337
E value 0.0e+00
Match length 337
% identity 82
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No. 133257
Contig ID 83118_1.R1010
5'-most EST jC-atXLIB327412P3b10a1
Method BLASTX
NCBI GI g4587530
BLAST score 724
E value 2.0e-76
Match length 221
% identity 58
NCBI Description (AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No. 133258
Contig ID 83122_1.R1010

5'-most EST	jC-atXLIB327412P3b12a1
Method	BLASTN
NCBI GI	g4539402
BLAST score	66
E value	2.0e-28
Match length	118
% identity	61
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)

Seq. No.	133259
Contig ID	83144_1.R1010
5'-most EST	jC-atXP5C89J22T7046a1
Method	BLASTX
NCBI GI	g3367596
BLAST score	251
E value	4.0e-21
Match length	82
% identity	60
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	133260
Contig ID	83152_1.R1010
5'-most EST	jC-atXLIB327412P3d05a1

Seq. No.	133261
Contig ID	83250_1.R1010
5'-most EST	jC-atXLIB327412P4c01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133262
Contig ID	83289_1.R1010
5'-most EST	jC-atXLIB327412P4d12a1
Method	BLASTX
NCBI GI	g4587550
BLAST score	268
E value	3.0e-23
Match length	67
% identity	78
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	133263
Contig ID	83296_1.R1010
5'-most EST	jC-atXLIB327412P4e06a1
Method	BLASTX
NCBI GI	g2660664
BLAST score	253
E value	2.0e-21
Match length	46
% identity	100

NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]
Seq. No.	133264
Contig ID	83298_1.R1010
5'-most EST	jC-atXLIB327412P4e09a1
Method	BLASTX
NCBI GI	g3548806
BLAST score	348
E value	1.0e-32
Match length	110
% identity	56
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.	133265
Contig ID	83316_1.R1010
5'-most EST	jC-atXLIB327426P3h08a1
Method	BLASTN
NCBI GI	g2529657
BLAST score	422
E value	0.0e+00
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	133266
Contig ID	83428_1.R1010
5'-most EST	jC-atXLIB327413P2b06a1
Method	BLASTX
NCBI GI	g3757519
BLAST score	273
E value	6.0e-24
Match length	75
% identity	79
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.	133267
Contig ID	83433_1.R1010
5'-most EST	jC-atXLIB327413P2b11a1
Method	BLASTN
NCBI GI	g4469002
BLAST score	402
E value	0.0e+00
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)
Seq. No.	133268
Contig ID	83438_1.R1010
5'-most EST	jC-atXLIB327413P2c05a1
Method	BLASTN
NCBI GI	g2264320
BLAST score	62
E value	4.0e-26
Match length	150
% identity	26

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]
Seq. No.	133269
Contig ID	83443_1.R1010
5'-most EST	jC-atXLIB327413P2c10a1
Method	BLASTN
NCBI GI	g4589413
BLAST score	384
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K10D11, complete sequence
Seq. No.	133270
Contig ID	83445_1.R1010
5'-most EST	jC-atXLIB327413P2c12a1
Seq. No.	133271
Contig ID	83449_1.R1010
5'-most EST	jC-atXLIB327411P3h05a1
Method	BLASTN
NCBI GI	g4587986
BLAST score	351
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence
Seq. No.	133272
Contig ID	83455_1.R1010
5'-most EST	g2393278
Method	BLASTN
NCBI GI	g4159707
BLAST score	124
E value	4.0e-63
Match length	283
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence
Seq. No.	133273
Contig ID	83461_1.R1010
5'-most EST	jC-atXLIB327413P2e07a1
Method	BLASTX
NCBI GI	g3738289
BLAST score	667
E value	7.0e-70
Match length	167
% identity	78
NCBI Description	(AC005309) Not56-like protein [Arabidopsis thaliana]
Seq. No.	133274
Contig ID	83479_1.R1010
5'-most EST	jC-atXLIB327413P2g04a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133275
Contig ID	83481_1.R1010
5'-most EST	jC-atXLIB327413P2g07a1
Method	BLASTN
NCBI GI	g4680765
BLAST score	367
E value	0.0e+00
Match length	493
% identity	99
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	133276
Contig ID	83488_1.R1010
5'-most EST	jC-atXLIB327413P2h03a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	45
E value	6.0e-16
Match length	106
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	133277
Contig ID	83494_1.R1010
5'-most EST	jC-atXLIB327413P2h10a1
Method	BLASTX
NCBI GI	g2146728
BLAST score	385
E value	5.0e-37
Match length	95
% identity	73
NCBI Description	cyclin cyc1b - Arabidopsis thaliana >gi_1360646 (L27223) cyclin [Arabidopsis thaliana]

Seq. No.	133278
Contig ID	83495_1.R1010
5'-most EST	jC-atXLIB327413P2h11a1
Method	BLASTX
NCBI GI	g4585994
BLAST score	478
E value	7.0e-48
Match length	103
% identity	94
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	133279
Contig ID	83507_1.R1010

5'-most EST	jC-atXLIB327413P3d04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133280
Contig ID	83522_1.R1010
5'-most EST	jC-alX24004Q1E1C01a1

Seq. No.	133281
Contig ID	83542_1.R1010
5'-most EST	jC-atXLIB327413P4a03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	8.0e-18
Match length	67
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133282
Contig ID	83553_1.R1010
5'-most EST	jC-atXLIB327413P4a09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	45
E value	1.0e-15
Match length	65
% identity	92
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133283
Contig ID	83564_1.R1010
5'-most EST	jC-atXLIB327413P4b03a1
Method	BLASTN
NCBI GI	g3789706
BLAST score	272
E value	1.0e-151
Match length	348
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133284
Contig ID	83566_1.R1010
5'-most EST	jC-atXLIB327413P4b04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97

NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	133285
Contig ID	83577_1.R1010
5'-most EST	jC-atXLIB327413P4b10a1
Seq. No.	133286
Contig ID	83578_1.R1010
5'-most EST	jC-atXP5C90D8T7087a1
Method	BLASTX
NCBI GI	g1345655
BLAST score	71
E value	8.0e-77
Match length	165
% identity	90
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD) >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	133287
Contig ID	83616_1.R1010
5'-most EST	jC-atXLIB327413P4d10a1
Method	BLASTX
NCBI GI	g3242717
BLAST score	201
E value	3.0e-15
Match length	89
% identity	43
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]
Seq. No.	133288
Contig ID	83628_1.R1010
5'-most EST	jC-atXLIB327413P4e06b1
Method	BLASTN
NCBI GI	g4510408
BLAST score	414
E value	0.0e+00
Match length	508
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T1E2 genomic sequence, complete sequence
Seq. No.	133289
Contig ID	83635_1.R1010
5'-most EST	jC-atXLIB327413P4e10a1
Method	BLASTN
NCBI GI	g2924653
BLAST score	286
E value	1.0e-159
Match length	536
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.	133290
Contig ID	83662_1.R1010
5'-most EST	jC-atXLIB327413P4f12a1

Method	BLASTN
NCBI GI	g4490734
BLAST score	256
E value	1.0e-142
Match length	364
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	133291
Contig ID	83668_1.R1010
5'-most EST	jC-atXLIB327413P4g03a1

Seq. No.	133292
Contig ID	83684_1.R1010
5'-most EST	jC-atXLIB327413P4h02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	7.0e-22
Match length	67
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133293
Contig ID	83698_2.R1010
5'-most EST	g576971
Method	BLASTX
NCBI GI	g1657523
BLAST score	81
E value	5.0e-14
Match length	93
% identity	52
NCBI Description	(U73857) similar to cinnamyl-alcohol dehydrogenase of P. crispum [Escherichia coli]

Seq. No.	133294
Contig ID	83788_1.R1010
5'-most EST	jC-atXP15C106F5T7015a1
Method	BLASTX
NCBI GI	g4262147
BLAST score	699
E value	1.0e-73
Match length	170
% identity	84
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	133295
Contig ID	83788_2.R1010
5'-most EST	jC-atXLIB327414P1f12a1
Method	BLASTX
NCBI GI	g4262147
BLAST score	263
E value	9.0e-23
Match length	71

% identity	77
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	133296
Contig ID	83823_1.R1010
5'-most EST	jC-atXLIB327414P1h11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	59
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133297
Contig ID	83896_1.R1010
5'-most EST	jC-atXLIB327416P1a01a1
Method	BLASTX
NCBI GI	g115510
BLAST score	167
E value	3.0e-11
Match length	179
% identity	36
NCBI Description	CALMODULIN >gi_71681_pir__MCEG calmodulin - Euglena gracilis

Seq. No.	133298
Contig ID	83907_1.R1010
5'-most EST	jC-atXLIB327416P1c03a1
Method	BLASTX
NCBI GI	g3193320
BLAST score	639
E value	7.0e-67
Match length	132
% identity	97
NCBI Description	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No.	133299
Contig ID	83913_1.R1010
5'-most EST	jC-atXLIB327416P1c07a1
Method	BLASTX
NCBI GI	g3641252
BLAST score	347
E value	1.0e-32
Match length	92
% identity	68
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	133300
Contig ID	83926_1.R1010
5'-most EST	jC-atXLIB327416P1d05a1

Method	BLASTX
NCBI GI	g2244784
BLAST score	219
E value	1.0e-17
Match length	74
% identity	59
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133301
Contig ID	83930_1.R1010
5'-most EST	g2581724
Method	BLASTX
NCBI GI	g2062167
BLAST score	106
E value	1.0e-11
Match length	171
% identity	34
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	133302
Contig ID	83930_2.R1010
5'-most EST	jC-atXLIB327416P1d08a1
Method	BLASTX
NCBI GI	g4586042
BLAST score	199
E value	3.0e-15
Match length	96
% identity	41
NCBI Description	(AC007020) putative APG protein isolog [Arabidopsis thaliana]

Seq. No.	133303
Contig ID	83936_1.R1010
5'-most EST	jC-atXLIB327416P1d11a1

Seq. No.	133304
Contig ID	83954_1.R1010
5'-most EST	jC-atXLIB327416P1e12a1
Method	BLASTN
NCBI GI	g2244788
BLAST score	469
E value	0.0e+00
Match length	477
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133305
Contig ID	83963_1.R1010
5'-most EST	jC-atXLIB327416P1f06a1
Method	BLASTN
NCBI GI	g4455168
BLAST score	201
E value	1.0e-109
Match length	445
% identity	98

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)
Seq. No.	133306
Contig ID	83964_1.R1010
5'-most EST	jC-atXLIB327416P1f06b1
Method	BLASTX
NCBI GI	g4455181
BLAST score	431
E value	2.0e-42
Match length	85
% identity	98
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]
Seq. No.	133307
Contig ID	83973_1.R1010
5'-most EST	jC-atXLIB327416P1f12b1
Seq. No.	133308
Contig ID	83983_1.R1010
5'-most EST	jC-atXLIB327416P1g06a1
Method	BLASTX
NCBI GI	g2935342
BLAST score	138
E value	2.0e-43
Match length	91
% identity	97
NCBI Description	(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]
Seq. No.	133309
Contig ID	83987_1.R1010
5'-most EST	jC-atXLIB327416P1g09a1
Method	BLASTN
NCBI GI	g2264303
BLAST score	161
E value	3.0e-85
Match length	402
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]
Seq. No.	133310
Contig ID	84011_1.R1010
5'-most EST	jC-atXLIB327416P1h11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	7.0e-19
Match length	58
% identity	97
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	133311
Contig ID	84043_1.R1010
5'-most EST	g2576689
Method	BLASTX

NCBI GI	g4309732
BLAST score	151
E value	1.0e-09
Match length	40
% identity	65
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133312
Contig ID	84052_1.R1010
5'-most EST	jC-atXLIB327416P2c12a1
Method	BLASTN
NCBI GI	g4678196
BLAST score	401
E value	0.0e+00
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence, complete sequence

Seq. No.	133313
Contig ID	84064_1.R1010
5'-most EST	jC-atXLIB327416P2d07a1
Method	BLASTN
NCBI GI	g2264304
BLAST score	289
E value	1.0e-161
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	133314
Contig ID	84068_1.R1010
5'-most EST	jC-atXLIB327416P2d09a1
Method	BLASTN
NCBI GI	g2924653
BLAST score	381
E value	0.0e+00
Match length	413
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	133315
Contig ID	84077_1.R1010
5'-most EST	jC-atXP67C213P4T7056a1
Method	BLASTX
NCBI GI	g4559372
BLAST score	370
E value	3.0e-35
Match length	74
% identity	99
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	133316

Contig ID 84077_3.R1010
5'-most EST jC-atXP71C221L24T7s2
Method BLASTX
NCBI GI g4559372
BLAST score 279
E value 9.0e-25
Match length 55
% identity 98
NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No. 133317
Contig ID 84080_1.R1010
5'-most EST jC-atXLIB327416P2e04a1
Method BLASTX
NCBI GI g2832623
BLAST score 147
E value 5.0e-09
Match length 66
% identity 41
NCBI Description (AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 133318
Contig ID 84080_2.R1010
5'-most EST jC-atXP59C194M9T7d1
Method BLASTX
NCBI GI g2832623
BLAST score 349
E value 5.0e-33
Match length 137
% identity 56
NCBI Description (AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 133319
Contig ID 84105_1.R1010
5'-most EST jC-atXLIB327416P2f07a1

Seq. No. 133320
Contig ID 84122_1.R1010
5'-most EST jC-atXLIB327416P2h04a1
Method BLASTN
NCBI GI g2760171
BLAST score 264
E value 1.0e-146
Match length 391
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]

Seq. No. 133321
Contig ID 84130_1.R1010
5'-most EST jC-atXLIB327416P2g08a1
Method BLASTN
NCBI GI g4584387

BLAST score 48
E value 1.0e-17
Match length 56
% identity 96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No. 133322
Contig ID 84135_1.R1010
5'-most EST jC-atXLIB327416P2h10a1

Seq. No. 133323
Contig ID 84162_1.R1010
5'-most EST jC-atXLIB327416P3a04a1
Method BLASTN
NCBI GI g2582640
BLAST score 60
E value 1.0e-24
Match length 75
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 133324
Contig ID 84174_1.R1010
5'-most EST jC-atXLIB327416P3b05b1
Method BLASTX
NCBI GI g2645697
BLAST score 322
E value 1.0e-29
Match length 100
% identity 61
NCBI Description (AF031940) alcohol dehydrogenase [Sinorhizobium meliloti]

Seq. No. 133325
Contig ID 84204_1.R1010
5'-most EST jC-atXP112C127I22T7d2
Method BLASTX
NCBI GI g4468805
BLAST score 907
E value 1.0e-107
Match length 201
% identity 100
NCBI Description (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No. 133326
Contig ID 84204_2.R1010
5'-most EST jC-atXP112C127I22T7a1
Method BLASTX
NCBI GI g4468805
BLAST score 500
E value 2.0e-50
Match length 124
% identity 84
NCBI Description (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	133327
Contig ID	84206_1.R1010
5'-most EST	jC-atXLIB327416P4e06a1

Seq. No.	133328
Contig ID	84220_1.R1010
5'-most EST	jC-atXLIB327416P3d10a1

Seq. No.	133329
Contig ID	84238_1.R1010
5'-most EST	jC-atXLIB327416P3e07a1
Method	BLASTX
NCBI GI	g3790102
BLAST score	349
E value	7.0e-33
Match length	79
% identity	82
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	133330
Contig ID	84247_1.R1010
5'-most EST	jC-atXLIB327416P3e12a1

Seq. No.	133331
Contig ID	84274_1.R1010
5'-most EST	jC-atXLIB327416P3g04a1
Method	BLASTN
NCBI GI	g3869075
BLAST score	374
E value	0.0e+00
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	133332
Contig ID	84276_1.R1010
5'-most EST	jC-atXLIB327416P3g05a1
Method	BLASTX
NCBI GI	g2281093
BLAST score	478
E value	5.0e-48
Match length	88
% identity	53
NCBI Description	(AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No.	133333
Contig ID	84281_1.R1010
5'-most EST	jC-atXLIB327416P3g08a1
Method	BLASTN
NCBI GI	g2160155
BLAST score	219
E value	1.0e-120
Match length	406
% identity	96

NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	133334
Contig ID	84285_1.R1010
5'-most EST	jC-atXLIB327416P3g10a1
Seq. No.	133335
Contig ID	84291_1.R1010
5'-most EST	jC-atXLIB327416P3h01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	9.0e-19
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	133336
Contig ID	84299_1.R1010
5'-most EST	jC-atXP22C116N2T7014a1
Method	BLASTN
NCBI GI	g4589445
BLAST score	57
E value	5.0e-23
Match length	101
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence
Seq. No.	133337
Contig ID	84301_1.R1010
5'-most EST	jC-atXLIB327416P3h06a1
Method	BLASTN
NCBI GI	g4691223
BLAST score	308
E value	1.0e-173
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)
Seq. No.	133338
Contig ID	84303_1.R1010
5'-most EST	g2763393
Method	BLASTX
NCBI GI	g1168529
BLAST score	321
E value	2.0e-29
Match length	121
% identity	60
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir__S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	133339
Contig ID	84306_1.R1010
5'-most EST	jC-atXLIB327416P3h09a1
Method	BLASTN
NCBI GI	g3449327
BLAST score	166
E value	4.0e-88
Match length	378
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	133340
Contig ID	84338_1.R1010
5'-most EST	jC-atXLIB327416P4c02a1

Seq. No.	133341
Contig ID	84342_1.R1010
5'-most EST	jC-atXLIB327416P4c04a1
Method	BLASTX
NCBI GI	g3170230
BLAST score	334
E value	4.0e-31
Match length	71
% identity	94
NCBI Description	(AF041848) fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No.	133342
Contig ID	84344_1.R1010
5'-most EST	jC-atXLIB327416P4c05a1
Method	BLASTN
NCBI GI	g1871173
BLAST score	305
E value	1.0e-171
Match length	507
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	133343
Contig ID	84348_1.R1010
5'-most EST	g2749422

Seq. No.	133344
Contig ID	84350_1.R1010
5'-most EST	jC-atXLIB327416P4c08a1

Seq. No.	133345
Contig ID	84360_1.R1010
5'-most EST	jC-atXLIB327404P1e05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133346
Contig ID 84387_1.R1010
5'-most EST jC-atXLIB327416P4e03a1
Method BLASTX
NCBI GI g4522012
BLAST score 531
E value 3.0e-54
Match length 123
% identity 81
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 133347
Contig ID 84391_1.R1010
5'-most EST jC-atXLIB327416P4e05a1
Method BLASTN
NCBI GI g2695704
BLAST score 317
E value 1.0e-178
Match length 420
% identity 97
NCBI Description A.thaliana constans gene

Seq. No. 133348
Contig ID 84400_1.R1010
5'-most EST jC-atXLIB327416P4e11a1
Method BLASTX
NCBI GI g2583123
BLAST score 489
E value 3.0e-49
Match length 95
% identity 100
NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No. 133349
Contig ID 84402_1.R1010
5'-most EST jC-atXLIB327416P4e12a1

Seq. No. 133350
Contig ID 84410_1.R1010
5'-most EST jC-atXLIB327416P4f04b1

Seq. No. 133351
Contig ID 84417_1.R1010
5'-most EST jC-atXLIB327416P4f08a1

Seq. No. 133352
Contig ID 84420_1.R1010
5'-most EST g576948
Method BLASTX
NCBI GI g4097545
BLAST score 59
E value 3.0e-23
Match length 84
% identity 80

NCBI Description (U64905) ATFP2 [Arabidopsis thaliana]

Seq. No. 133353
Contig ID 84422_1.R1010
5'-most EST jC-atXP24C123M18T7071a1

Seq. No. 133354
Contig ID 84423_1.R1010
5'-most EST jC-atXLIB327416P4f11b1
Method BLASTN
NCBI GI g3821780
BLAST score 25
E value 5.0e-04
Match length 36
% identity 60
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 133355
Contig ID 84428_1.R1010
5'-most EST jC-atXLIB327416P4g02a1
Method BLASTX
NCBI GI g2980641
BLAST score 239
E value 6.0e-20
Match length 70
% identity 43
NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 133356
Contig ID 84430_1.R1010
5'-most EST jC-atXLIB327416P4g03a1

Seq. No. 133357
Contig ID 84432_1.R1010
5'-most EST jC-atXLIB327416P4g04a1
Method BLASTN
NCBI GI g3249094
BLAST score 191
E value 1.0e-103
Match length 394
% identity 98
NCBI Description Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133358
Contig ID 84447_1.R1010
5'-most EST jC-atXLIB327416P4g11b1
Method BLASTX
NCBI GI g4583554
BLAST score 748
E value 2.0e-79
Match length 164
% identity 91
NCBI Description (AJ131180) ribosomal protein S14 [Arabidopsis thaliana]

Seq. No. 133359
Contig ID 84453_1.R1010

5'-most EST	jC-atXLIB327416P4h02b1
Method	BLASTN
NCBI GI	g2828183
BLAST score	400
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	133360
Contig ID	84458_1.R1010
5'-most EST	jC-atXLIB327416P4h05a1
Method	BLASTN
NCBI GI	g4056476
BLAST score	85
E value	8.0e-40
Match length	319
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133361
Contig ID	84462_1.R1010
5'-most EST	jC-atXLIB327416P4h07a1
Method	BLASTX
NCBI GI	g3426062
BLAST score	377
E value	4.0e-36
Match length	128
% identity	62
NCBI Description	(AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No.	133362
Contig ID	84464_1.R1010
5'-most EST	jC-atXLIB327416P4h08a1
Method	BLASTN
NCBI GI	g4691223
BLAST score	294
E value	1.0e-164
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	133363
Contig ID	84494_1.R1010
5'-most EST	jC-atXLIB327417P1b03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	9.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133364

Contig ID	84505_1.R1010
5'-most EST	jC-atXLIB327417P1b07a1

Seq. No.	133365
Contig ID	84519_1.R1010
5'-most EST	jC-atXLIB327417P1c03a1
Method	BLASTN
NCBI GI	g3549651
BLAST score	124
E value	6.0e-63
Match length	187
% identity	96
NCBI Description	Arabidopsis thaliana MAP3K epsilon gene

Seq. No.	133366
Contig ID	84522_1.R1010
5'-most EST	jC-atXLIB327417P2c05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133367
Contig ID	84534_1.R1010
5'-most EST	g16653
Method	BLASTN
NCBI GI	g4220468
BLAST score	118
E value	1.0e-59
Match length	300
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133368
Contig ID	84535_1.R1010
5'-most EST	jC-atXLIB327433P2b02a1

Seq. No.	133369
Contig ID	84535_2.R1010
5'-most EST	jC-atXP86CG10A12T7b1

Seq. No.	133370
Contig ID	84537_1.R1010
5'-most EST	jC-atXLIB327417P1d02a1
Method	BLASTX
NCBI GI	g1730502
BLAST score	266
E value	5.0e-23
Match length	89
% identity	53
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	133371
Contig ID	84537_2.R1010
5'-most EST	jC-atXLIB327417P2g10a1
Method	BLASTX
NCBI GI	g1730502
BLAST score	259
E value	3.0e-22
Match length	85
% identity	54
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	133372
Contig ID	84550_1.R1010
5'-most EST	jC-atXLIB327417P1d08a1
Method	BLASTN
NCBI GI	g3108025
BLAST score	277
E value	1.0e-154
Match length	648
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	133373
Contig ID	84552_1.R1010
5'-most EST	jC-atXLIB327417P1d09a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	456
E value	0.0e+00
Match length	537
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	133374
Contig ID	84555_1.R1010
5'-most EST	jC-atXLIB327417P1d11a1

Seq. No.	133375
Contig ID	84564_1.R1010
5'-most EST	jC-atXLIB327417P4e04a1
Method	BLASTX
NCBI GI	g2465923
BLAST score	166
E value	3.0e-11
Match length	137
% identity	35
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	133376
Contig ID	84564_2.R1010
5'-most EST	jC-atXLIB327419P3f06a2

Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	68
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133377
Contig ID	84570_1.R1010
5'-most EST	jC-atXLIB327417P4d07a1
Method	BLASTX
NCBI GI	g2245137
BLAST score	100
E value	2.0e-22
Match length	98
% identity	68
NCBI Description	(Z97344) MYB transcription factor homolog [Arabidopsis thaliana]

Seq. No.	133378
Contig ID	84597_1.R1010
5'-most EST	jC-atXLIB327417P2f10a1
Method	BLASTN
NCBI GI	g3746057
BLAST score	232
E value	1.0e-127
Match length	919
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133379
Contig ID	84617_1.R1010
5'-most EST	jC-atXP46C173I23T7035d1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	2.0e-19
Match length	71
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133380
Contig ID	84619_1.R1010
5'-most EST	jC-atXLIB327417P1g12a1

Seq. No.	133381
Contig ID	84627_1.R1010
5'-most EST	jC-atXLIB327417P1h04a1
Method	BLASTN
NCBI GI	g4376087
BLAST score	109
E value	4.0e-54
Match length	415

% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	133382
Contig ID	84632_1.R1010
5'-most EST	jC-atXLIB327417P1h07a1
Method	BLASTX
NCBI GI	g4538943
BLAST score	144
E value	4.0e-29
Match length	77
% identity	66
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	133383
Contig ID	84643_1.R1010
5'-most EST	jC-atXLIB327417P2a01a1
Method	BLASTX
NCBI GI	g3414809
BLAST score	169
E value	2.0e-11
Match length	197
% identity	3
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	133384
Contig ID	84643_3.R1010
5'-most EST	g2048267
Method	BLASTN
NCBI GI	g4220640
BLAST score	340
E value	0.0e+00
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	133385
Contig ID	84676_1.R1010
5'-most EST	jC-atXLIB327428P1d04a2
Method	BLASTN
NCBI GI	g3985952
BLAST score	279
E value	1.0e-155
Match length	569
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	133386
Contig ID	84690_1.R1010
5'-most EST	jC-atXLIB327417P2c04a1
Method	BLASTX
NCBI GI	g3023956
BLAST score	176

E value	2.0e-12
Match length	102
% identity	4
NCBI Description	VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003 (L28125) beta transducin-like protein [Podospora anserina]

Seq. No.	133387
Contig ID	84700_1.R1010
5'-most EST	jC-atXP119C165C6T7090a1
Method	BLASTX
NCBI GI	g2924777
BLAST score	473
E value	5.0e-47
Match length	217
% identity	45
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	133388
Contig ID	84700_2.R1010
5'-most EST	jC-atXLIB327417P2c09a1
Method	BLASTX
NCBI GI	g2924777
BLAST score	329
E value	3.0e-30
Match length	145
% identity	47
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	133389
Contig ID	84721_1.R1010
5'-most EST	jC-atXLIB327417P2d08a1
Method	BLASTN
NCBI GI	g3241927
BLAST score	38
E value	9.0e-12
Match length	126
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	133390
Contig ID	84744_1.R1010
5'-most EST	jC-atXLIB327417P2e10a1
Method	BLASTN
NCBI GI	g4713943
BLAST score	323
E value	0.0e+00
Match length	461
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	133391
Contig ID	84760_1.R1010
5'-most EST	jC-atXLIB327417P2f06a1

Seq. No.	133392
Contig ID	84766_1.R1010
5'-most EST	jC-atXLIB327417P3e09a1
Method	BLASTN
NCBI GI	g3449330
BLAST score	305
E value	1.0e-171
Match length	462
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	133393
Contig ID	84789_1.R1010
5'-most EST	jC-atXLIB327417P2g09a1
Method	BLASTX
NCBI GI	g1077413
BLAST score	372
E value	2.0e-35
Match length	159
% identity	50
NCBI Description	hypothetical protein YLR186w - yeast (Saccharomyces cerevisiae) >gi_577197 (U17246) Ylr186wp [Saccharomyces cerevisiae]

Seq. No.	133394
Contig ID	84793_1.R1010
5'-most EST	jC-atXLIB327417P3f11a1
Method	BLASTN
NCBI GI	g4309683
BLAST score	263
E value	1.0e-146
Match length	422
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133395
Contig ID	84821_2.R1010
5'-most EST	jC-atXLIB327417P4a02a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	463
E value	0.0e+00
Match length	601
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	133396
Contig ID	84835_1.R1010
5'-most EST	jC-atXLIB327417P4a10a1
Method	BLASTN
NCBI GI	g2494110
BLAST score	326
E value	0.0e+00

Match length	514
% identity	99
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	133397
Contig ID	84837_1.R1010
5'-most EST	jC-atXLIB327417P4a11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133398
Contig ID	84864_2.R1010
5'-most EST	jC-atXLIB327417P4c02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133399
Contig ID	84875_1.R1010
5'-most EST	jC-atXLIB327417P4c09a1
Method	BLASTX
NCBI GI	g2749755
BLAST score	188
E value	6.0e-14
Match length	83
% identity	46
NCBI Description	(AL021086) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /match=(desc:; /motif=(desc:; EST embl_AI387799_AI387799 comes from the 5' UTR [Drosophila melanogaster]

Seq. No.	133400
Contig ID	84877_1.R1010
5'-most EST	jC-atXLIB327417P4c10a1
Method	BLASTX
NCBI GI	g2244860
BLAST score	155
E value	5.0e-10
Match length	83
% identity	42
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	133401
Contig ID	84916_1.R1010
5'-most EST	jC-atXLIB327417P4e07a1
Method	BLASTX
NCBI GI	g4006920

BLAST score	442
E value	1.0e-43
Match length	92
% identity	95
NCBI Description	(Z99708) actin interacting protein [Arabidopsis thaliana]

Seq. No.	133402
Contig ID	84918_1.R1010
5'-most EST	jC-atXLIB327417P4e08a1
Method	BLASTN
NCBI GI	g4376087
BLAST score	322
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	133403
Contig ID	84922_1.R1010
5'-most EST	jC-atXLIB327417P4e10a1
Method	BLASTN
NCBI GI	g2459406
BLAST score	310
E value	1.0e-174
Match length	599
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133404
Contig ID	84923_1.R1010
5'-most EST	jC-atXLIB327417P4e10b1
Method	BLASTX
NCBI GI	g2459441
BLAST score	450
E value	1.0e-44
Match length	120
% identity	72
NCBI Description	(AC002332) putative SWI/SNF complex subunit BAF170 [Arabidopsis thaliana]

Seq. No.	133405
Contig ID	84932_1.R1010
5'-most EST	jC-atXLIB327417P4g07a1
Method	BLASTX
NCBI GI	g4220457
BLAST score	118
E value	2.0e-10
Match length	56
% identity	53
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. EST gb_N96478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	133406

Contig ID	84965_1.R1010
5'-most EST	jC-atXLIB327417P4h12a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	95
E value	8.0e-46
Match length	399
% identity	81
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	133407
Contig ID	84986_2.R1010
5'-most EST	jC-atXLIB327415P3b06a1
Method	BLASTN
NCBI GI	g3108024
BLAST score	45
E value	7.0e-16
Match length	135
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133408
Contig ID	84993_1.R1010
5'-most EST	jC-atXLIB327420P1a04a1
Method	BLASTN
NCBI GI	g4159712
BLAST score	254
E value	1.0e-141
Match length	298
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	133409
Contig ID	85008_1.R1010
5'-most EST	jC-atXLIB327420P1b01a1
Method	BLASTN
NCBI GI	g2828186
BLAST score	65
E value	1.0e-27
Match length	230
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	133410
Contig ID	85081_1.R1010
5'-most EST	jC-atXLIB327420P1e10a1

Seq. No.	133411
Contig ID	85115_1.R1010
5'-most EST	jC-atXLIB327420P1g06a1
Method	BLASTN
NCBI GI	g3702734
BLAST score	72

E value	7.0e-32
Match length	132
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	133412
Contig ID	85152_1.R1010
5'-most EST	jC-atXLIB327421P3a02a1
Method	BLASTN
NCBI GI	g2651294
BLAST score	44
E value	2.0e-15
Match length	80
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133413
Contig ID	85154_1.R1010
5'-most EST	jC-atXLIB327421P3a03a1
Method	BLASTN
NCBI GI	g4691223
BLAST score	222
E value	1.0e-121
Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	133414
Contig ID	85158_1.R1010
5'-most EST	jC-atXLIB327421P3a05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	4.0e-19
Match length	62
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133415
Contig ID	85162_1.R1010
5'-most EST	jC-atXLIB327421P3a07a1
Method	BLASTN
NCBI GI	g540252
BLAST score	36
E value	1.0e-10
Match length	51
% identity	94
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	133416
Contig ID	85172_1.R1010
5'-most EST	jC-atXLIB327421P3b01a1
Method	BLASTX
NCBI GI	g3360289

BLAST score	220
E value	1.0e-17
Match length	70
% identity	64
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	133417
Contig ID	85180_1.R1010
5'-most EST	jC-atXLIB327421P3b06a1
Method	BLASTX
NCBI GI	g1086900
BLAST score	152
E value	9.0e-10
Match length	73
% identity	38
NCBI Description	(U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]

Seq. No.	133418
Contig ID	85182_1.R1010
5'-most EST	jC-atXLIB327421P3b07a1

Seq. No.	133419
Contig ID	85184_1.R1010
5'-most EST	jC-atXLIB327421P3b08a1
Method	BLASTX
NCBI GI	g3522935
BLAST score	565
E value	5.0e-58
Match length	114
% identity	99
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	133420
Contig ID	85198_1.R1010
5'-most EST	jC-atXLIB327421P3c03a1
Method	BLASTN
NCBI GI	g3128142
BLAST score	375
E value	0.0e+00
Match length	419
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	133421
Contig ID	85202_1.R1010
5'-most EST	jC-atXP24C123C22T7043a1
Method	BLASTX
NCBI GI	g4406819
BLAST score	502
E value	1.0e-50
Match length	142
% identity	80

NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.	133422
Contig ID	85218_1.R1010
5'-most EST	jC-atXLIB327421P3d02a1
Method	BLASTX
NCBI GI	g3157945
BLAST score	458
E value	1.0e-45
Match length	87
% identity	99
NCBI Description	(AC002131) Contains similarity to axi 1 gene gb_X80301 from Nicotiana tabacum. [Arabidopsis thaliana]
Seq. No.	133423
Contig ID	85220_1.R1010
5'-most EST	jC-atXLIB327421P3d03a1
Method	BLASTN
NCBI GI	g3184270
BLAST score	303
E value	1.0e-170
Match length	451
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	133424
Contig ID	85229_1.R1010
5'-most EST	jC-atXLIB327427P1e04a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	133425
Contig ID	85238_1.R1010
5'-most EST	jC-atXLIB327421P3e01a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	178
E value	2.0e-95
Match length	375
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence
Seq. No.	133426
Contig ID	85257_1.R1010
5'-most EST	jC-atXLIB327404P4f11a1
Method	BLASTN
NCBI GI	g2342673
BLAST score	249
E value	1.0e-137

Match length	373
% identity	99
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	133427
Contig ID	85257_2.R1010
5'-most EST	jC-atXP116C130C15T7s1
Method	BLASTN
NCBI GI	g2342673
BLAST score	196
E value	1.0e-106
Match length	625
% identity	97
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	133428
Contig ID	85263_1.R1010
5'-most EST	jC-atXLIB327421P3f03a1
Method	BLASTN
NCBI GI	g3869072
BLAST score	229
E value	1.0e-126
Match length	348
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	133429
Contig ID	85273_1.R1010
5'-most EST	g2722956

Seq. No.	133430
Contig ID	85303_1.R1010
5'-most EST	jC-atXLIB327421P3g12a1
Method	BLASTX
NCBI GI	g3080436
BLAST score	443
E value	7.0e-44
Match length	84
% identity	100
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	133431
Contig ID	85313_1.R1010
5'-most EST	jC-atXLIB327421P3h06a1
Method	BLASTN
NCBI GI	g2656030
BLAST score	193
E value	1.0e-104
Match length	413
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	133432

Contig ID	85355_1.R1010
5'-most EST	jC-atXLIB327421P4c02a1
Method	BLASTN
NCBI GI	g2264311
BLAST score	310
E value	1.0e-174
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	133433
Contig ID	85357_1.R1010
5'-most EST	jC-atXLIB327421P1c03a1
Method	BLASTX
NCBI GI	g2499542
BLAST score	73
E value	2.0e-68
Match length	129
% identity	100
NCBI Description	IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP) >gi_1218042 (U48448) secreted purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	133434
Contig ID	85404_1.R1010
5'-most EST	jC-atXLIB327421P4e09a1
Method	BLASTN
NCBI GI	g2264317
BLAST score	287
E value	1.0e-160
Match length	291
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	133435
Contig ID	85408_1.R1010
5'-most EST	jC-atXLIB327427P3e11a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133436
Contig ID	85423_1.R1010
5'-most EST	jC-atXLIB327421P4f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	71
E value	2.0e-31
Match length	75
% identity	99

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	133437
Contig ID	85432_2.R1010
5'-most EST	g510361
Method	BLASTN
NCBI GI	g4191760
BLAST score	33
E value	6.0e-09
Match length	57
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	133438
Contig ID	85467_1.R1010
5'-most EST	jC-atXLIB327422P1a07a1
Method	BLASTX
NCBI GI	g2911049
BLAST score	283
E value	4.0e-25
Match length	65
% identity	86
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	133439
Contig ID	85522_1.R1010
5'-most EST	jC-atXLIB327422P1d09a1
Method	BLASTN
NCBI GI	g2760171
BLAST score	226
E value	1.0e-124
Match length	347
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]

Seq. No.	133440
Contig ID	85524_1.R1010
5'-most EST	jC-atXLIB327422P1d10a1

Seq. No.	133441
Contig ID	85526_1.R1010
5'-most EST	jC-atXP3C81G2T7037a1
Method	BLASTX
NCBI GI	g4455123
BLAST score	284
E value	4.0e-25
Match length	108
% identity	48
NCBI Description	(AF127218) flavonoid 3-O-glucosyltransferase [Forsythia x intermedia]

Seq. No.	133442
Contig ID	85528_1.R1010

5'-most EST	jC-atXLIB327422P1d12a1
Method	BLASTN
NCBI GI	g3128137
BLAST score	319
E value	1.0e-179
Match length	411
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	133443
Contig ID	85537_1.R1010
5'-most EST	jC-atXLIB327422P1e07a1
Method	BLASTX
NCBI GI	g2924781
BLAST score	671
E value	2.0e-70
Match length	156
% identity	78
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	133444
Contig ID	85539_1.R1010
5'-most EST	jC-atXLIB327422P1e08a1
Method	BLASTX
NCBI GI	g4510362
BLAST score	426
E value	7.0e-42
Match length	83
% identity	98
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133445
Contig ID	85547_1.R1010
5'-most EST	jC-atXLIB327422P1h11a1
Method	BLASTX
NCBI GI	g2781363
BLAST score	350
E value	6.0e-33
Match length	76
% identity	84
NCBI Description	(AC003113) F24O1.19 [Arabidopsis thaliana]

Seq. No.	133446
Contig ID	85550_1.R1010
5'-most EST	jC-atXLIB327422P1f02a1
Method	BLASTX
NCBI GI	g1169736
BLAST score	157
E value	3.0e-10
Match length	81
% identity	41
NCBI Description	FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN) >gi_1083778_pir__A54837 rapamycin/FKBP12 target 1 - rat >gi_511229 (U11681) rapamycin and FKBP12 target-1 protein [Rattus norvegicus] >gi_561858 (L37085) rapamycin

target [Rattus norvegicus]

Seq. No.	133447
Contig ID	85554_1.R1010
5'-most EST	jC-atXLIB327422P1f05a1

Seq. No.	133448
Contig ID	85559_1.R1010
5'-most EST	jC-atXLIB327422P1f08a1
Method	BLASTN
NCBI GI	g4544435
BLAST score	393
E value	0.0e+00
Match length	498
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	133449
Contig ID	85569_1.R1010
5'-most EST	jC-atXLIB327422P1g02a1
Method	BLASTX
NCBI GI	g2655098
BLAST score	210
E value	1.0e-16
Match length	65
% identity	63
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	133450
Contig ID	85573_1.R1010
5'-most EST	jC-atXLIB327422P1g04a1
Method	BLASTN
NCBI GI	g4572664
BLAST score	414
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	133451
Contig ID	85579_1.R1010
5'-most EST	jC-atXLIB327422P1g07a1
Method	BLASTN
NCBI GI	g2494110
BLAST score	298
E value	1.0e-167
Match length	451
% identity	100
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	133452
Contig ID	85589_1.R1010
5'-most EST	jC-atXLIB327422P1g12a1
Method	BLASTN

NCBI GI	g2696018
BLAST score	431
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	133453
Contig ID	85595_1.R1010
5'-most EST	jC-atXLIB327422P1h04a1
Method	BLASTN
NCBI GI	g531832
BLAST score	53
E value	1.0e-20
Match length	61
% identity	97
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	133454
Contig ID	85605_1.R1010
5'-most EST	jC-atXLIB327422P1h09a1
Method	BLASTX
NCBI GI	g3582333
BLAST score	261
E value	2.0e-22
Match length	50
% identity	100
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133455
Contig ID	85838_1.R1010
5'-most EST	g807864
Method	BLASTX
NCBI GI	g3123349
BLAST score	209
E value	2.0e-16
Match length	65
% identity	65
NCBI Description	(AJ005788) hypothetical protein [Cicer arietinum]

Seq. No.	133456
Contig ID	85840_1.R1010
5'-most EST	jC-atXLIB327407P3a03a1
Method	BLASTN
NCBI GI	g2564049
BLAST score	363
E value	0.0e+00
Match length	387
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	133457
Contig ID	85906_1.R1010
5'-most EST	jC-atXLIB327407P3d11a1
Method	BLASTN

NCBI GI	g2760173
BLAST score	375
E value	0.0e+00
Match length	419
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	133458
Contig ID	85982_1.R1010
5'-most EST	jC-atXLIB327411P3b01a1
Method	BLASTN
NCBI GI	g4581103
BLAST score	298
E value	1.0e-167
Match length	366
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	133459
Contig ID	85986_1.R1010
5'-most EST	jC-atXLIB327411P3b05a1
Method	BLASTX
NCBI GI	g2618699
BLAST score	198
E value	4.0e-15
Match length	59
% identity	58
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	133460
Contig ID	86003_1.R1010
5'-most EST	jC-atXLIB327411P3d04a1
Method	BLASTX
NCBI GI	g4508074
BLAST score	295
E value	2.0e-26
Match length	69
% identity	87
NCBI Description	(AC005882) 45341 [Arabidopsis thaliana]

Seq. No.	133461
Contig ID	86015_1.R1010
5'-most EST	jC-atXLIB327411P3e07a1
Method	BLASTX
NCBI GI	g3201554
BLAST score	304
E value	2.0e-27
Match length	115
% identity	53
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	133462
Contig ID	86018_1.R1010
5'-most EST	jC-atXLIB327411P3e10a1
Method	BLASTX

NCBI GI	g2459440
BLAST score	206
E value	7.0e-16
Match length	133
% identity	37
NCBI Description	(AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	133463
Contig ID	86025_1.R1010
5'-most EST	g2047818
Method	BLASTN
NCBI GI	g2323343
BLAST score	337
E value	0.0e+00
Match length	437
% identity	95
NCBI Description	Arabidopsis thaliana alpha-glucosidase 1 (Aglu1) gene, complete cds

Seq. No.	133464
Contig ID	86031_1.R1010
5'-most EST	jC-atXLIB327411P3f11a1
Method	BLASTN
NCBI GI	g2760167
BLAST score	216
E value	1.0e-118
Match length	380
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	133465
Contig ID	86068_2.R1010
5'-most EST	g2412830

Seq. No.	133466
Contig ID	86071_1.R1010
5'-most EST	jC-atXLIB327413P1c08a1
Method	BLASTN
NCBI GI	g3510338
BLAST score	49
E value	2.0e-18
Match length	258
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21I16, complete sequence [Arabidopsis thaliana]

Seq. No.	133467
Contig ID	86073_1.R1010
5'-most EST	jC-atXLIB327413P1c10a1
Method	BLASTN
NCBI GI	g2191126
BLAST score	193
E value	1.0e-104
Match length	375
% identity	90
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	133468
Contig ID	86077_1.R1010
5'-most EST	g2747536
Method	BLASTX
NCBI GI	g4406808
BLAST score	235
E value	3.0e-40
Match length	102
% identity	85
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	133469
Contig ID	86082_1.R1010
5'-most EST	jC-atXLIB327413P1e03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	1.0e-16
Match length	46
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133470
Contig ID	86085_1.R1010
5'-most EST	g2749395
Method	BLASTN
NCBI GI	g2326366
BLAST score	373
E value	0.0e+00
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for hypothetical protein SEB2, partial

Seq. No.	133471
Contig ID	86265_1.R1010
5'-most EST	jC-atXLIB327415P3b03a1
Method	BLASTN
NCBI GI	g4220632
BLAST score	41
E value	1.0e-13
Match length	94
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	133472
Contig ID	86271_1.R1010
5'-most EST	jC-atXLIB327427P1g10a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No.	133473
Contig ID	86271_2.R1010
5'-most EST	jC-atXLIB327415P3b09a1

Seq. No.	133474
Contig ID	86278_1.R1010
5'-most EST	jC-atXLIB327415P3c05a1

Seq. No.	133475
Contig ID	86290_1.R1010
5'-most EST	jC-atXLIB327415P3d10a1
Method	BLASTN
NCBI GI	g4741184
BLAST score	391
E value	0.0e+00
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	133476
Contig ID	86300_1.R1010
5'-most EST	jC-atXLIB327415P3e12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	9.0e-16
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133477
Contig ID	86305_1.R1010
5'-most EST	jC-atXP45C171I23T7020a1
Method	BLASTN
NCBI GI	g3395421
BLAST score	184
E value	8.0e-99
Match length	365
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133478
Contig ID	86357_1.R1010
5'-most EST	jC-atXLIB327417P3b08a1
Method	BLASTN
NCBI GI	g2264317
BLAST score	223
E value	1.0e-122
Match length	455
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	133479
Contig ID	86373_1.R1010
5'-most EST	jC-atXLIB327417P3c06a1
Method	BLASTX
NCBI GI	g4056432
BLAST score	276
E value	4.0e-24
Match length	103
% identity	55
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	133480
Contig ID	86437_1.R1010
5'-most EST	jC-atXLIB327417P3f09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	3.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133481
Contig ID	86450_1.R1010
5'-most EST	jC-atXLIB327417P3g06a1
Method	BLASTX
NCBI GI	g4006886
BLAST score	162
E value	9.0e-32
Match length	93
% identity	82
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	133482
Contig ID	86499_1.R1010
5'-most EST	jC-atX25113Q1E1G04a1
Method	BLASTN
NCBI GI	g3150396
BLAST score	220
E value	1.0e-120
Match length	275
% identity	67
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133483
Contig ID	86529_1.R1010
5'-most EST	jC-atXLIB327440P1a08a1
Method	BLASTX
NCBI GI	g4220488
BLAST score	432
E value	2.0e-42
Match length	105
% identity	80

NCBI Description	(AC006069) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	133484
Contig ID	86626_1.R1010
5'-most EST	jC-atXLIB327421P1h11a1
Method	BLASTN
NCBI GI	g4027862
BLAST score	359
E value	0.0e+00
Match length	456
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133485
Contig ID	86703_1.R1010
5'-most EST	jC-atXLIB327422P4e08a1
Method	BLASTN
NCBI GI	g3659491
BLAST score	408
E value	0.0e+00
Match length	472
% identity	97
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	133486
Contig ID	86716_1.R1010
5'-most EST	jC-atXLIB327422P4f05a1
Method	BLASTX
NCBI GI	g4455225
BLAST score	424
E value	1.0e-41
Match length	91
% identity	85
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	133487
Contig ID	86743_1.R1010
5'-most EST	jC-atXLIB327422P4h02a1

Seq. No.	133488
Contig ID	86762_1.R1010
5'-most EST	jC-atXLIB327430P2c11a1
Method	BLASTN
NCBI GI	g2351071
BLAST score	418
E value	0.0e+00
Match length	518
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	133489
Contig ID	86786_1.R1010
5'-most EST	jC-atXLIB327423P1b10a1

Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	8.0e-22
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133490
Contig ID	86791_1.R1010
5'-most EST	jC-atXLIB327423P1c01a1
Method	BLASTN
NCBI GI	g2264314
BLAST score	361
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	133491
Contig ID	86801_1.R1010
5'-most EST	jC-atXP22C121K10T7048a1
Method	BLASTX
NCBI GI	g2244835
BLAST score	289
E value	2.0e-46
Match length	150
% identity	63
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	133492
Contig ID	86801_2.R1010
5'-most EST	jC-atXLIB327423P1c07a1
Method	BLASTX
NCBI GI	g2244835
BLAST score	132
E value	7.0e-39
Match length	109
% identity	75
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	133493
Contig ID	86807_1.R1010
5'-most EST	jC-atXLIB327423P1c11a1
Method	BLASTX
NCBI GI	g3695375
BLAST score	307
E value	9.0e-28
Match length	67
% identity	87
NCBI Description	(AF096370) contains similarity to the major intrinsic protein domain (Pfam: PF00230 MIP, E-value: 5.7e-111) [Arabidopsis thaliana]

Seq. No.	133494

Contig ID	86849_1.R1010
5'-most EST	jC-atXLIB327423P1f01a1
Method	BLASTX
NCBI GI	g4454032
BLAST score	210
E value	2.0e-16
Match length	102
% identity	40
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	133495
Contig ID	86868_1.R1010
5'-most EST	jC-atXLIB327423P1f12a1
Method	BLASTN
NCBI GI	g4585906
BLAST score	490
E value	0.0e+00
Match length	581
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F15A23 genomic sequence, complete sequence

Seq. No.	133496
Contig ID	86887_1.R1010
5'-most EST	jC-atXLIB327423P1g12a1
Method	BLASTX
NCBI GI	g3927825
BLAST score	100
E value	6.0e-17
Match length	86
% identity	58
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	133497
Contig ID	86891_1.R1010
5'-most EST	jC-atXLIB327423P1h02a1
Method	BLASTX
NCBI GI	g2947062
BLAST score	145
E value	9.0e-09
Match length	187
% identity	31
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	133498
Contig ID	86900_1.R1010
5'-most EST	jC-atXLIB327423P1h07a1
Method	BLASTN
NCBI GI	g2924651
BLAST score	133
E value	2.0e-68
Match length	356
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	133499
Contig ID	86921_1.R1010
5'-most EST	jC-atX25021Q1E1G04a1
Method	BLASTN
NCBI GI	g3426033
BLAST score	456
E value	0.0e+00
Match length	548
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133500
Contig ID	86946_1.R1010
5'-most EST	jC-atXLIB327424P4c04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133501
Contig ID	86960_1.R1010
5'-most EST	jC-atXP102CE2H11T7b1

Seq. No.	133502
Contig ID	86979_1.R1010
5'-most EST	jC-atXLIB327424P4d11a1
Method	BLASTN
NCBI GI	g4586241
BLAST score	48
E value	9.0e-18
Match length	563
% identity	77
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	133503
Contig ID	86993_1.R1010
5'-most EST	jC-atXLIB327424P4e08a1
Method	BLASTX
NCBI GI	g2760330
BLAST score	185
E value	1.0e-13
Match length	47
% identity	77
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No.	133504
Contig ID	87000_1.R1010
5'-most EST	jC-atXLIB327424P4e12a1
Method	BLASTN
NCBI GI	g2702261
BLAST score	293
E value	1.0e-164

Match length	355
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133505
Contig ID	87019_1.R1010
5'-most EST	jC-atXLIB327424P4f11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133506
Contig ID	87021_2.R1010
5'-most EST	jC-atXLIB327424P4f12a1
Method	BLASTN
NCBI GI	g4678219
BLAST score	381
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	133507
Contig ID	87029_1.R1010
5'-most EST	jC-atXLIB327424P4g05a1
Method	BLASTN
NCBI GI	g4544461
BLAST score	296
E value	1.0e-166
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F23E6 genomic sequence, complete sequence

Seq. No.	133508
Contig ID	87057_1.R1010
5'-most EST	jC-atXLIB327430P1e07a1

Seq. No.	133509
Contig ID	87097_1.R1010
5'-most EST	jC-atXLIB327425P3b12a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	68
E value	1.0e-29
Match length	122
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No. 133510

Contig ID	87106_1.R1010
5'-most EST	jC-atXLIB327425P3c06a1
Method	BLASTX
NCBI GI	g4099090
BLAST score	150
E value	2.0e-09
Match length	41
% identity	68
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	133511
Contig ID	87114_1.R1010
5'-most EST	jC-atXLIB327425P3c10a1

Seq. No.	133512
Contig ID	87116_1.R1010
5'-most EST	jC-atXP110C119H7T7082a1
Method	BLASTN
NCBI GI	g4235150
BLAST score	307
E value	1.0e-172
Match length	664
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	133513
Contig ID	87118_1.R1010
5'-most EST	jC-atXLIB327425P3c12a1
Method	BLASTX
NCBI GI	g3176874
BLAST score	46
E value	1.0e-12
Match length	114
% identity	41
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	133514
Contig ID	87130_1.R1010
5'-most EST	jC-atXLIB327425P3d07a1

Seq. No.	133515
Contig ID	87132_1.R1010
5'-most EST	jC-atXLIB327425P3d08a1
Method	BLASTN
NCBI GI	g3785968
BLAST score	125
E value	9.0e-64
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133516
Contig ID	87136_1.R1010
5'-most EST	jC-atXLIB327425P3d10a1

Method	BLASTN
NCBI GI	g2264316
BLAST score	250
E value	1.0e-138
Match length	398
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	133517
Contig ID	87138_1.R1010
5'-most EST	jC-atXLIB327425P3d11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	47
E value	4.0e-17
Match length	66
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133518
Contig ID	87143_1.R1010
5'-most EST	jC-atXP40C164A22T7012a1
Method	BLASTN
NCBI GI	g2281081
BLAST score	509
E value	0.0e+00
Match length	577
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133519
Contig ID	87143_2.R1010
5'-most EST	jC-atXLIB327425P3e03a1
Method	BLASTN
NCBI GI	g2281081
BLAST score	319
E value	1.0e-179
Match length	457
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133520
Contig ID	87143_3.R1010
5'-most EST	jC-atXLIB327432P4c04a1
Method	BLASTN
NCBI GI	g2281081
BLAST score	244
E value	1.0e-134
Match length	422
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133521
Contig ID	87152_1.R1010
5'-most EST	jC-atXLIB327425P3e08a1

Seq. No.	133522
Contig ID	87158_1.R1010
5'-most EST	jC-atXLIB327425P3e11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	66
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133523
Contig ID	87178_1.R1010
5'-most EST	jC-atXLIB327425P3f10a1
Method	BLASTX
NCBI GI	g1175426
BLAST score	146
E value	5.0e-09
Match length	80
% identity	45
NCBI Description	PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 >gi_984214_emb_CAA90819_ (Z54140) probable ATP-dependent RNA helicase [Schizosaccharomyces pombe]

Seq. No.	133524
Contig ID	87180_1.R1010
5'-most EST	jC-atXLIB327425P3f11a1
Method	BLASTX
NCBI GI	g1465751
BLAST score	218
E value	2.0e-17
Match length	65
% identity	65
NCBI Description	(U56833) VHL binding protein-1 [Homo sapiens]

Seq. No.	133525
Contig ID	87182_1.R1010
5'-most EST	jC-atXLIB327425P3f12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	6.0e-22
Match length	67
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133526
Contig ID	87185_1.R1010
5'-most EST	jC-atXP15C107O1T7074a1
Method	BLASTX
NCBI GI	g3892054
BLAST score	476

E value	1.0e-47
Match length	125
% identity	63
NCBI Description	(AC002330) putative glycosyltransferase [Arabidopsis thaliana]

Seq. No.	133527
Contig ID	87186_1.R1010
5'-most EST	jC-atXLIB327425P3g03a1
Method	BLASTX
NCBI GI	g4585925
BLAST score	312
E value	6.0e-46
Match length	101
% identity	93
NCBI Description	(AC007211) unknown protein [Arabidopsis thaliana]

Seq. No.	133528
Contig ID	87196_1.R1010
5'-most EST	jC-atXLIB327425P3g08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	62
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133529
Contig ID	87198_1.R1010
5'-most EST	jC-atXLIB327425P3g09a1
Method	BLASTX
NCBI GI	g2462762
BLAST score	597
E value	6.0e-62
Match length	115
% identity	98
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	133530
Contig ID	87221_1.R1010
5'-most EST	jC-atXLIB327425P3h10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133531
Contig ID	87225_1.R1010
5'-most EST	jC-atXLIB327425P3h12a1
Method	BLASTX
NCBI GI	g2982266
BLAST score	208

E value	2.0e-16
Match length	48
% identity	83
NCBI Description	(AF051216) probable fibrillarin [Picea mariana]

Seq. No.	133532
Contig ID	87261_1.R1010
5'-most EST	jC-atXLIB327426P3b09a1
Method	BLASTX
NCBI GI	g3540185
BLAST score	570
E value	1.0e-58
Match length	116
% identity	100
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	133533
Contig ID	87263_1.R1010
5'-most EST	jC-atXLIB327426P2a09a1
Method	BLASTX
NCBI GI	g2191197
BLAST score	295
E value	1.0e-26
Match length	81
% identity	85
NCBI Description	(AF007271) contains similarity to Synechococcus PCC7942 chromosomal region used as basis of neutral siteII recombinational cloning vector (PID:g1174192) [Arabidopsis thaliana]

Seq. No.	133534
Contig ID	87265_1.R1010
5'-most EST	jC-atXP122C159H15T7016a1
Method	BLASTX
NCBI GI	g4584530
BLAST score	511
E value	1.0e-51
Match length	94
% identity	98
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	133535
Contig ID	87265_2.R1010
5'-most EST	jC-atXLIB327426P2a10a1
Method	BLASTX
NCBI GI	g4584530
BLAST score	328
E value	3.0e-30
Match length	168
% identity	36
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	133536
Contig ID	87278_1.R1010
5'-most EST	jC-atXLIB327426P2b07a1
Method	BLASTN

NCBI GI	g4454447
BLAST score	377
E value	0.0e+00
Match length	389
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133537
Contig ID	87281_1.R1010
5'-most EST	jC-atXLIB327426P2b09a1
Method	BLASTN
NCBI GI	g2618601
BLAST score	289
E value	1.0e-161
Match length	317
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	133538
Contig ID	87283_1.R1010
5'-most EST	jC-atXLIB327426P2b10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133539
Contig ID	87285_1.R1010
5'-most EST	jC-atXLIB327426P2b11a1
Method	BLASTX
NCBI GI	g3176678
BLAST score	822
E value	3.0e-88
Match length	152
% identity	100
NCBI Description	(AC003671) Contains similarity to MYB transcription factor isolog T01024.1 from A. thaliana BAC gb_AC002335. [Arabidopsis thaliana]

Seq. No.	133540
Contig ID	87291_1.R1010
5'-most EST	jC-atXLIB327426P2c03a1
Method	BLASTN
NCBI GI	g3150396
BLAST score	210
E value	1.0e-114
Match length	367
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133541

Contig ID	87294_1.R1010
5'-most EST	jC-atXLIB327426P2c05a1
Method	BLASTN
NCBI GI	g4519190
BLAST score	356
E value	0.0e+00
Match length	399
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	133542
Contig ID	87306_1.R1010
5'-most EST	jC-atXLIB327426P2c12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	6.0e-18
Match length	52
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133543
Contig ID	87313_1.R1010
5'-most EST	jC-atXLIB327426P2d04a1
Method	BLASTX
NCBI GI	g4455172
BLAST score	526
E value	1.0e-53
Match length	101
% identity	100
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	133544
Contig ID	87315_1.R1010
5'-most EST	jC-atXLIB327426P2d05a1
Method	BLASTX
NCBI GI	g3414938
BLAST score	202
E value	2.0e-15
Match length	95
% identity	44
NCBI Description	(AF076603) GgtA [Dictyostelium discoideum]

Seq. No.	133545
Contig ID	87317_1.R1010
5'-most EST	jC-atXLIB327426P2d07a1
Method	BLASTN
NCBI GI	g2337888
BLAST score	312
E value	1.0e-175
Match length	482
% identity	75
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	133546

Contig ID	87325_1.R1010
5'-most EST	jC-atXLIB327426P2d11a1
Method	BLASTX
NCBI GI	g2632252
BLAST score	206
E value	3.0e-16
Match length	52
% identity	73
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	133547
Contig ID	87335_1.R1010
5'-most EST	jC-atXLIB327426P2e05a1
Method	BLASTN
NCBI GI	g4218109
BLAST score	221
E value	1.0e-121
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	133548
Contig ID	87358_1.R1010
5'-most EST	jC-atXLIB327426P2f05a1
Method	BLASTX
NCBI GI	g2864610
BLAST score	328
E value	2.0e-30
Match length	68
% identity	62
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	133549
Contig ID	87382_1.R1010
5'-most EST	jC-atXLIB327426P2g06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	7.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133550
Contig ID	87404_1.R1010
5'-most EST	jC-atXLIB327426P2h07a1
Method	BLASTX
NCBI GI	g2981439
BLAST score	46
E value	1.0e-15
Match length	66
% identity	61
NCBI Description	(AF051853) t-SNARE SED5 [Arabidopsis thaliana]

Seq. No.	133551
Contig ID	87414_1.R1010
5'-most EST	jC-atXLIB327426P4a01a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	190
E value	1.0e-102
Match length	273
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	133552
Contig ID	87415_1.R1010
5'-most EST	jC-atXLIB327426P3a02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133553
Contig ID	87416_1.R1010
5'-most EST	jC-atXLIB327426P3a04a1
Method	BLASTN
NCBI GI	g3420042
BLAST score	382
E value	0.0e+00
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133554
Contig ID	87422_1.R1010
5'-most EST	jC-atXLIB327426P4a09a1
Method	BLASTN
NCBI GI	g4335744
BLAST score	162
E value	9.0e-86
Match length	317
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133555
Contig ID	87425_1.R1010
5'-most EST	jC-atXLIB327426P3a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	133556
Contig ID	87430_1.R1010
5'-most EST	jC-atXLIB327426P3b03a1
Method	BLASTN
NCBI GI	g3869067
BLAST score	385
E value	0.0e+00
Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.	133557
Contig ID	87431_1.R1010
5'-most EST	jC-atXLIB327426P3b03b1
Method	BLASTN
NCBI GI	g3869067
BLAST score	182
E value	9.0e-98
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.	133558
Contig ID	87446_1.R1010
5'-most EST	jC-atXLIB327426P3b11a1
Seq. No.	133559
Contig ID	87448_1.R1010
5'-most EST	jC-atXLIB327426P3b12a1
Method	BLASTX
NCBI GI	g4580529
BLAST score	595
E value	1.0e-61
Match length	139
% identity	84
NCBI Description	(AF036308) scarecrow-like 13 [Arabidopsis thaliana]
Seq. No.	133560
Contig ID	87462_1.R1010
5'-most EST	jC-atXLIB327426P4c12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	1.0e-16
Match length	62
% identity	94
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	133561
Contig ID	87474_1.R1010
5'-most EST	g1269552
Seq. No.	133562

Contig ID	87478_1.R1010
5'-most EST	jC-atXLIB327426P4d12a1
Method	BLASTX
NCBI GI	g3600039
BLAST score	258
E value	1.0e-22
Match length	104
% identity	48
NCBI Description	(AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No.	133563
Contig ID	87480_1.R1010
5'-most EST	jC-atXLIB327426P3e01a1
Method	BLASTX
NCBI GI	g4678941
BLAST score	355
E value	1.0e-33
Match length	66
% identity	100
NCBI Description	(AL049711) gamma response I protein [Arabidopsis thaliana]

Seq. No.	133564
Contig ID	87491_1.R1010
5'-most EST	jC-atXLIB327426P3e12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133565
Contig ID	87513_1.R1010
5'-most EST	jC-atXLIB327426P4f12a1
Method	BLASTX
NCBI GI	g2274857
BLAST score	548
E value	4.0e-56
Match length	111
% identity	93
NCBI Description	(AJ000469) glutathione peroxidase [Arabidopsis thaliana] >gi_3482968_emb_CAA20524.1_ (AL031369) glutathione peroxidase precursor [Arabidopsis thaliana]

Seq. No.	133566
Contig ID	87528_1.R1010
5'-most EST	jC-atXLIB327426P3h04a1
Method	BLASTX
NCBI GI	g1256424
BLAST score	159
E value	1.0e-10
Match length	98
% identity	32
NCBI Description	(U51119) cysteine proteinase inhibitor [Brassica campestris]

Seq. No.	133567
Contig ID	87532_1.R1010
5'-most EST	jC-atXP25C125F24T7070a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	5.0e-23
Match length	61
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133568
Contig ID	87609_1.R1010
5'-most EST	jC-atXLIB327411P3f10b1
Method	BLASTN
NCBI GI	g2351067
BLAST score	386
E value	0.0e+00
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	133569
Contig ID	87762_1.R1010
5'-most EST	jC-atXLIB327438P4h03a2
Method	BLASTN
NCBI GI	g3805839
BLAST score	345
E value	0.0e+00
Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	133570
Contig ID	87810_1.R1010
5'-most EST	jC-atXP52C183G15T7s2

Seq. No.	133571
Contig ID	87818_1.R1010
5'-most EST	jC-atXLIB327418P2d07a1
Method	BLASTN
NCBI GI	g3402695
BLAST score	337
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133572
Contig ID	87821_1.R1010
5'-most EST	jC-atXLIB327418P2d10a1
Method	BLASTX
NCBI GI	g2118017

BLAST score	109
E value	6.0e-24
Match length	138
% identity	47
NCBI Description	non-S-RNase (EC 3.1.-.-) - Japanese pear >gi_1526417_dbj_BAA08475_ (D49529) ribonuclease [Pyrus pyrifolia]

Seq. No.	133573
Contig ID	87822_1.R1010
5'-most EST	jC-atXLIB327415P2a03a2
Method	BLASTN
NCBI GI	g2853071
BLAST score	112
E value	5.0e-56
Match length	120
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	133574
Contig ID	87827_1.R1010
5'-most EST	jC-atXLIB327418P2e05a1

Seq. No.	133575
Contig ID	87832_1.R1010
5'-most EST	jC-atXLIB327418P2e11a1
Method	BLASTX
NCBI GI	g2252840
BLAST score	395
E value	3.0e-38
Match length	82
% identity	90
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	133576
Contig ID	87844_1.R1010
5'-most EST	jC-atXP45C172B21T7007a1
Method	BLASTN
NCBI GI	g603055
BLAST score	64
E value	4.0e-27
Match length	272
% identity	81
NCBI Description	Arabidopsis thaliana inner mitochondrial membrane protein mRNA, complete cds

Seq. No.	133577
Contig ID	87903_1.R1010
5'-most EST	jC-atXLIB327418P3f04b1
Method	BLASTX
NCBI GI	g4455322
BLAST score	239
E value	1.0e-19
Match length	138
% identity	50

NCBI Description	(AL035525) putative protein kinase [Arabidopsis thaliana]
Seq. No.	133578
Contig ID	87903_2.R1010
5'-most EST	jC-atXP78C231A2T7b1
Method	BLASTX
NCBI GI	g3688189
BLAST score	577
E value	2.0e-59
Match length	157
% identity	73
NCBI Description	(AL031804) putative protein kinase [Arabidopsis thaliana]
Seq. No.	133579
Contig ID	87949_1.R1010
5'-most EST	g2580758
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	8.0e-10
Match length	43
% identity	95
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	133580
Contig ID	87949_2.R1010
5'-most EST	g2580881
Seq. No.	133581
Contig ID	87954_1.R1010
5'-most EST	jC-atXP22C116K7T7037a1
Method	BLASTX
NCBI GI	g1931638
BLAST score	428
E value	6.0e-42
Match length	106
% identity	77
NCBI Description	(U95973) transcription factor RUSH-1alpha isolog [Arabidopsis thaliana]
Seq. No.	133582
Contig ID	87954_2.R1010
5'-most EST	jC-atXLIB327418P4c09a1
Method	BLASTX
NCBI GI	g1931638
BLAST score	311
E value	3.0e-28
Match length	79
% identity	76
NCBI Description	(U95973) transcription factor RUSH-1alpha isolog [Arabidopsis thaliana]
Seq. No.	133583
Contig ID	87965_1.R1010
5'-most EST	jC-atXLIB327418P4d10a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	45
E value	7.0e-16
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133584
Contig ID	87995_1.R1010
5'-most EST	jC-atXLIB327418P3h12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	46
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133585
Contig ID	88000_1.R1010
5'-most EST	jC-atXLIB327401P2g12a1
Method	BLASTN
NCBI GI	g2980757
BLAST score	202
E value	1.0e-109
Match length	290
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	133586
Contig ID	88007_1.R1010
5'-most EST	jC-atXLIB327404P1g05a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	504
E value	0.0e+00
Match length	523
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	133587
Contig ID	88012_1.R1010
5'-most EST	jC-atXLIB327419P2a09a1
Method	BLASTX
NCBI GI	g4263722
BLAST score	158
E value	1.0e-10
Match length	60
% identity	68
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	133588
Contig ID	88015_1.R1010
5'-most EST	jC-atXLIB327419P2b02a1
Method	BLASTN
NCBI GI	g3785968

BLAST score	305
E value	1.0e-171
Match length	426
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133589
Contig ID	88020_1.R1010
5'-most EST	jC-atXLIB327419P2b08a1
Method	BLASTN
NCBI GI	g3366536
BLAST score	286
E value	1.0e-160
Match length	314
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	133590
Contig ID	88021_1.R1010
5'-most EST	jC-atXP2C78G3T7083a1
Method	BLASTX
NCBI GI	g4581143
BLAST score	291
E value	7.0e-26
Match length	140
% identity	38
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133591
Contig ID	88029_2.R1010
5'-most EST	jC-atXP34C150E12T7a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	7.0e-19
Match length	62
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133592
Contig ID	88041_1.R1010
5'-most EST	jC-atXLIB327419P2d09a1
Method	BLASTN
NCBI GI	g4376087
BLAST score	240
E value	1.0e-132
Match length	396
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	133593
Contig ID	88042_1.R1010
5'-most EST	jC-atXLIB327419P2d10a1
Method	BLASTN

NCBI GI	g2244991
BLAST score	259
E value	1.0e-143
Match length	406
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133594
Contig ID	88043_1.R1010
5'-most EST	jC-atXLIB327419P2d11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133595
Contig ID	88045_1.R1010
5'-most EST	jC-atXP19C111P2T7060a1
Method	BLASTN
NCBI GI	g4589435
BLAST score	410
E value	0.0e+00
Match length	678
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	133596
Contig ID	88045_2.R1010
5'-most EST	g2749679
Method	BLASTN
NCBI GI	g4589435
BLAST score	336
E value	0.0e+00
Match length	389
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	133597
Contig ID	88169_1.R1010
5'-most EST	jC-atXLIB327420P3g04b1
Method	BLASTX
NCBI GI	g2961384
BLAST score	682
E value	9.0e-82
Match length	158
% identity	95
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	133598
Contig ID	88250_1.R1010

5'-most EST	jC-atXLIB327420P4f09b1
Seq. No.	133599
Contig ID	88370_1.R1010
5'-most EST	jC-atXLIB327425P2a02a1
Method	BLASTN
NCBI GI	g4587677
BLAST score	148
E value	2.0e-77
Match length	196
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T22C12 genomic sequence, complete sequence
Seq. No.	133600
Contig ID	88375_1.R1010
5'-most EST	g402991
Method	BLASTN
NCBI GI	g4589421
BLAST score	211
E value	1.0e-115
Match length	447
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence
Seq. No.	133601
Contig ID	88394_1.R1010
5'-most EST	jC-atXLIB327425P2d07a1
Method	BLASTX
NCBI GI	g4335719
BLAST score	152
E value	8.0e-10
Match length	44
% identity	50
NCBI Description	(AC006248) putative RING-H2 finger protein RHG1a [Arabidopsis thaliana]
Seq. No.	133602
Contig ID	88402_1.R1010
5'-most EST	jC-atXLIB327425P2e07a1
Method	BLASTX
NCBI GI	g4204257
BLAST score	408
E value	1.0e-39
Match length	78
% identity	95
NCBI Description	(AC005223) 5493 [Arabidopsis thaliana]
Seq. No.	133603
Contig ID	88409_1.R1010
5'-most EST	jC-atXLIB327425P2f05a1
Method	BLASTN
NCBI GI	g4678705
BLAST score	206
E value	1.0e-112
Match length	315

% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)
Seq. No.	133604
Contig ID	88422_1.R1010
5'-most EST	jC-atXLIB327425P2g08a1
Seq. No.	133605
Contig ID	88593_1.R1010
5'-most EST	jC-atXLIB327427P2a02a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	429
E value	0.0e+00
Match length	437
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]
Seq. No.	133606
Contig ID	88598_1.R1010
5'-most EST	jC-atXLIB327407P1b11a2
Method	BLASTN
NCBI GI	g3399678
BLAST score	371
E value	0.0e+00
Match length	473
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	133607
Contig ID	88616_1.R1010
5'-most EST	jC-atXLIB327427P1b05a2
Method	BLASTX
NCBI GI	g3790581
BLAST score	238
E value	8.0e-20
Match length	56
% identity	64
NCBI Description	(AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]
Seq. No.	133608
Contig ID	88630_1.R1010
5'-most EST	jC-atXLIB327427P2b11a1
Method	BLASTN
NCBI GI	g2564049
BLAST score	276
E value	1.0e-154
Match length	462
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.	133609

Contig ID	88660_1.R1010
5'-most EST	jC-atXLIB327427P2d04a1
Method	BLASTN
NCBI GI	g3150396
BLAST score	217
E value	1.0e-118
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133610
Contig ID	88674_1.R1010
5'-most EST	jC-atXLIB327427P2d12a1
Method	BLASTX
NCBI GI	g417073
BLAST score	572
E value	6.0e-59
Match length	137
% identity	80
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	133611
Contig ID	88702_1.R1010
5'-most EST	jC-atXLIB327427P2f03a1
Method	BLASTX
NCBI GI	g3953482
BLAST score	399
E value	1.0e-38
Match length	113
% identity	72
NCBI Description	(AC002328) F22O2.27 [Arabidopsis thaliana]

Seq. No.	133612
Contig ID	88713_1.R1010
5'-most EST	jC-atXLIB327427P2f10b1

Seq. No.	133613
Contig ID	88718_1.R1010
5'-most EST	jC-atXLIB327427P2f11a1

Seq. No.	133614
Contig ID	88720_1.R1010
5'-most EST	jC-atXP84CG2H7T7b1
Method	BLASTX
NCBI GI	g4455336
BLAST score	319
E value	3.0e-29
Match length	100
% identity	58
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	133615

Contig ID	88724_1.R1010
5'-most EST	jC-atXLIB327427P2g02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133616
Contig ID	88729_1.R1010
5'-most EST	jC-atXLIB327427P2g05a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	238
E value	1.0e-131
Match length	388
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	133617
Contig ID	88731_1.R1010
5'-most EST	jC-atXLIB327427P2g06a1
Method	BLASTX
NCBI GI	g3451074
BLAST score	443
E value	8.0e-44
Match length	103
% identity	74
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	133618
Contig ID	88733_1.R1010
5'-most EST	jC-atXLIB327427P2g07a1
Method	BLASTX
NCBI GI	g3913142
BLAST score	285
E value	2.0e-25
Match length	62
% identity	81
NCBI Description	ALTERNATIVE OXIDASE 1C PRECURSOR >gi_2506049_dbj_BAA22635_ (AB003175) alternative oxidase [Arabidopsis thaliana]

Seq. No.	133619
Contig ID	88763_1.R1010
5'-most EST	jC-atXLIB327427P2h12a1
Method	BLASTX
NCBI GI	g3559811
BLAST score	328
E value	2.0e-30
Match length	63
% identity	100
NCBI Description	(AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No.	133620

Contig ID	88794_1.R1010
5'-most EST	jC-atXLIB327402P1b08a1
Method	BLASTN
NCBI GI	g3510343
BLAST score	326
E value	0.0e+00
Match length	386
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	133621
Contig ID	88797_1.R1010
5'-most EST	jC-atXLIB327402P1b10a1
Method	BLASTX
NCBI GI	g4469020
BLAST score	582
E value	4.0e-60
Match length	114
% identity	100
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	133622
Contig ID	88829_1.R1010
5'-most EST	g2047801
Method	BLASTN
NCBI GI	g2894591
BLAST score	258
E value	1.0e-143
Match length	399
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	133623
Contig ID	88835_1.R1010
5'-most EST	jC-atXLIB327401P2b02a1
Method	BLASTN
NCBI GI	g3449311
BLAST score	315
E value	1.0e-177
Match length	468
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15I22, complete sequence [Arabidopsis thaliana]

Seq. No.	133624
Contig ID	88849_1.R1010
5'-most EST	jC-atXLIB327402P1e08a1
Method	BLASTX
NCBI GI	g3204106
BLAST score	173
E value	3.0e-12
Match length	77
% identity	53
NCBI Description	(AJ006763) putative beta-amilase [Cicer arietinum]

Seq. No.	133625
Contig ID	88853_1.R1010
5'-most EST	jC-atXLIB327402P1e10a1
Method	BLASTX
NCBI GI	g140185
BLAST score	194
E value	1.0e-14
Match length	82
% identity	45
NCBI Description	PROBABLE GYP7 PROTEIN >gi_173243 (M17741) unidentified peptide [Yarrowia lipolytica]

Seq. No.	133626
Contig ID	88855_1.R1010
5'-most EST	jC-atXLIB327402P1e11a1
Method	BLASTX
NCBI GI	g3894158
BLAST score	344
E value	3.0e-32
Match length	104
% identity	71
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	133627
Contig ID	88865_1.R1010
5'-most EST	jC-atXLIB327402P1f04a1
Method	BLASTX
NCBI GI	g1170408
BLAST score	358
E value	6.0e-34
Match length	94
% identity	77
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT14 (HD-ZIP PROTEIN 14) >gi_549885 (U09334) homeobox protein [Arabidopsis thaliana]

Seq. No.	133628
Contig ID	88872_1.R1010
5'-most EST	jC-atXLIB327402P1f08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133629
Contig ID	88877_1.R1010
5'-most EST	jC-atXP12C99M10T7021a1
Method	BLASTX
NCBI GI	g872116
BLAST score	457
E value	3.0e-45
Match length	160
% identity	24

NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	133630
Contig ID	88885_2.R1010
5'-most EST	jC-atXLIB327402P1g03a1
Method	BLASTN
NCBI GI	g2656029
BLAST score	325
E value	0.0e+00
Match length	425
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	133631
Contig ID	88925_1.R1010
5'-most EST	jC-atXLIB327402P2a01a1
Method	BLASTX
NCBI GI	g2194127
BLAST score	521
E value	5.0e-53
Match length	114
% identity	93
NCBI Description	(AC002062) Strong similarity to Arabidopsis receptor-like protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis thaliana]

Seq. No.	133632
Contig ID	88926_1.R1010
5'-most EST	jC-atXLIB327402P2a02a1
Method	BLASTN
NCBI GI	g4733957
BLAST score	355
E value	0.0e+00
Match length	405
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C18 genomic sequence, complete sequence

Seq. No.	133633
Contig ID	88949_1.R1010
5'-most EST	jC-atXLIB327418P3b11a2
Method	BLASTX
NCBI GI	g2982466
BLAST score	496
E value	5.0e-50
Match length	119
% identity	79
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	133634
Contig ID	88953_1.R1010
5'-most EST	jC-atXLIB327402P2c06a1
Method	BLASTX
NCBI GI	g4467156
BLAST score	261
E value	2.0e-22

Match length	77
% identity	64
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	133635
Contig ID	88971_1.R1010
5'-most EST	jC-atXLIB327402P2e04a1
Method	BLASTX
NCBI GI	g3212871
BLAST score	356
E value	1.0e-33
Match length	70
% identity	89
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	133636
Contig ID	88975_1.R1010
5'-most EST	jC-atXLIB327402P2e09a1
Method	BLASTN
NCBI GI	g2351063
BLAST score	211
E value	1.0e-115
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	133637
Contig ID	88976_1.R1010
5'-most EST	jC-atXLIB327402P2e10a1

Seq. No.	133638
Contig ID	88983_1.R1010
5'-most EST	jC-atXLIB327402P2f06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133639
Contig ID	88984_1.R1010
5'-most EST	jC-atXLIB327402P2f07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133640
Contig ID	88998_1.R1010

5'-most EST	jC-atXP125C244D7T7037a1
Method	BLASTX
NCBI GI	g3549679
BLAST score	220
E value	2.0e-17
Match length	107
% identity	46
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	133641
Contig ID	89018_1.R1010
5'-most EST	jC-atXLIB327427P1a02a2
Method	BLASTX
NCBI GI	g3378491
BLAST score	170
E value	7.0e-12
Match length	75
% identity	44
NCBI Description	(AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.	133642
Contig ID	89047_1.R1010
5'-most EST	jC-atXLIB327402P3c08a1
Method	BLASTN
NCBI GI	g3702723
BLAST score	280
E value	1.0e-156
Match length	421
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14B20, complete sequence [Arabidopsis thaliana]

Seq. No.	133643
Contig ID	89072_1.R1010
5'-most EST	jC-atXLIB327402P3e05a1
Method	BLASTX
NCBI GI	g4063741
BLAST score	245
E value	1.0e-20
Match length	76
% identity	61
NCBI Description	(AC005851) putative Na/H antiporter [Arabidopsis thaliana]

Seq. No.	133644
Contig ID	89081_1.R1010
5'-most EST	jC-atXLIB327402P3e10a1
Method	BLASTX
NCBI GI	g2317904
BLAST score	938
E value	1.0e-101
Match length	208
% identity	88
NCBI Description	(U89959) Similar to rice chalcone synthase homolog, gp_U90341_2507617 and anther specific protein, gp_Y14507_2326772 [Arabidopsis thaliana]

Seq. No.	133645

Contig ID	89088_1.R1010
5'-most EST	jC-atXLIB327402P3f03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	133646
Contig ID	89098_1.R1010
5'-most EST	jC-atXLIB327402P3f09a1
Method	BLASTN
NCBI GI	g4512690
BLAST score	382
E value	0.0e+00
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	133647
Contig ID	89110_2.R1010
5'-most EST	g2750093
Method	BLASTN
NCBI GI	g4415928
BLAST score	272
E value	1.0e-151
Match length	324
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133648
Contig ID	89152_1.R1010
5'-most EST	jC-atXLIB327402P4b04a1
Method	BLASTN
NCBI GI	g2288979
BLAST score	305
E value	1.0e-171
Match length	336
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133649
Contig ID	89155_1.R1010
5'-most EST	jC-atXLIB327402P4b08a1
Method	BLASTN
NCBI GI	g4490324
BLAST score	246
E value	1.0e-136
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	133650
Contig ID	89158_1.R1010
5'-most EST	jC-atXLIB327432P4h07a1
Method	BLASTX
NCBI GI	g4567273
BLAST score	65
E value	2.0e-23
Match length	65
% identity	79
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	133651
Contig ID	89169_1.R1010
5'-most EST	jC-atXLIB327402P4c05a1
Method	BLASTX
NCBI GI	g4506125
BLAST score	224
E value	4.0e-18
Match length	107
% identity	48
NCBI Description	UNKNOWN >gi_3024444_sp_Q13523_PR4H_HUMAN SERINE/THREONINE-PROTEIN KINASE PRP4 HOMOLOG >gi_1399462 (U48736) serine/threonine-protein kinase PRP4h [Homo sapiens]

Seq. No.	133652
Contig ID	89204_2.R1010
5'-most EST	jC-atXP19C111J7T7042a1
Method	BLASTN
NCBI GI	g4582428
BLAST score	498
E value	0.0e+00
Match length	820
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	133653
Contig ID	89204_3.R1010
5'-most EST	g3450246
Method	BLASTN
NCBI GI	g4582428
BLAST score	185
E value	1.0e-99
Match length	355
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	133654
Contig ID	89206_1.R1010
5'-most EST	jC-atXLIB327402P4e05a1
Method	BLASTX
NCBI GI	g2335108
BLAST score	161

E value	7.0e-11
Match length	63
% identity	56
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	133655
Contig ID	89243_1.R1010
5'-most EST	jC-atXLIB327402P4g01a1
Method	BLASTN
NCBI GI	g4589439
BLAST score	41
E value	2.0e-13
Match length	109
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	133656
Contig ID	89272_1.R1010
5'-most EST	jC-atXLIB327402P4h08a1
Method	BLASTX
NCBI GI	g3763917
BLAST score	596
E value	1.0e-61
Match length	135
% identity	90
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana] >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133657
Contig ID	89275_1.R1010
5'-most EST	jC-atXLIB327402P4h12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133658
Contig ID	89279_1.R1010
5'-most EST	jC-atXLIB327403P1a03a1
Method	BLASTX
NCBI GI	g4454033
BLAST score	623
E value	8.0e-65
Match length	139
% identity	91
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	133659
Contig ID	89283_1.R1010
5'-most EST	jC-atXLIB327403P1a07a1

Method	BLASTX
NCBI GI	g2558664
BLAST score	348
E value	9.0e-33
Match length	66
% identity	100
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133660
Contig ID	89286_1.R1010
5'-most EST	jC-atXLIB327403P1a11a1
Method	BLASTN
NCBI GI	g4454587
BLAST score	711
E value	0.0e+00
Match length	727
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	133661
Contig ID	89288_1.R1010
5'-most EST	jC-atXLIB327403P1a12a1

Seq. No.	133662
Contig ID	89291_1.R1010
5'-most EST	jC-atXLIB327403P1b02a1
Method	BLASTN
NCBI GI	g2264318
BLAST score	489
E value	0.0e+00
Match length	571
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	133663
Contig ID	89293_1.R1010
5'-most EST	jC-atXLIB327403P1b03a1
Method	BLASTX
NCBI GI	g3355465
BLAST score	443
E value	7.0e-44
Match length	101
% identity	89
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	133664
Contig ID	89302_1.R1010
5'-most EST	jC-atXLIB327403P1b11a1

Seq. No.	133665
Contig ID	89312_1.R1010
5'-most EST	jC-atXLIB327406P3c05a2

Seq. No.	133666

Contig ID	89314_1.R1010
5'-most EST	jC-atXLIB327403P1c07a1
Method	BLASTX
NCBI GI	g3281850
BLAST score	631
E value	7.0e-66
Match length	121
% identity	100
NCBI Description	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]

Seq. No.	133667
Contig ID	89318_1.R1010
5'-most EST	jC-atXLIB327403P1c09a1
Method	BLASTN
NCBI GI	g1353764
BLAST score	184
E value	6.0e-99
Match length	342
% identity	98
NCBI Description	Arabidopsis thaliana profilin 2 and profilin 3 genes, complete cds

Seq. No.	133668
Contig ID	89326_1.R1010
5'-most EST	jC-atXLIB327403P1d01a1

Seq. No.	133669
Contig ID	89327_1.R1010
5'-most EST	jC-atXLIB327403P1d02a1
Method	BLASTN
NCBI GI	g3659491
BLAST score	229
E value	1.0e-125
Match length	453
% identity	97
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	133670
Contig ID	89331_1.R1010
5'-most EST	jC-atXLIB327403P1d04a1
Method	BLASTN
NCBI GI	g2924729
BLAST score	112
E value	6.0e-56
Match length	200
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	133671
Contig ID	89339_1.R1010
5'-most EST	jC-atXLIB327403P1d08a1
Method	BLASTN
NCBI GI	g2618601
BLAST score	328

E value	0.0e+00
Match length	574
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	133672
Contig ID	89345_1.R1010
5'-most EST	jC-atXLIB327403P1d12a1
Method	BLASTX
NCBI GI	g3287962
BLAST score	215
E value	5.0e-17
Match length	92
% identity	49
NCBI Description	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (ENDOPEPTIDASE CLP) (CASEINOLYTIC PROTEASE) (PROTEASE TI) >gi_1945673_emb_CAB08043_ (Z94043) hypothetical protein [Bacillus subtilis] >gi_2635967_emb_CAB15459_ (Z99121) ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein) [Bacillus subtilis] >gi_2668494 (U59754) ClpP [Bacillus subtilis]

Seq. No.	133673
Contig ID	89347_1.R1010
5'-most EST	g2048350

Seq. No.	133674
Contig ID	89351_1.R1010
5'-most EST	jC-atXLIB327403P1e04a1
Method	BLASTX
NCBI GI	g4678333
BLAST score	200
E value	2.0e-15
Match length	62
% identity	68
NCBI Description	(AL049658) H+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	133675
Contig ID	89353_1.R1010
5'-most EST	jC-atXLIB327403P1e05a1
Method	BLASTX
NCBI GI	g2760317
BLAST score	251
E value	2.0e-21
Match length	92
% identity	58
NCBI Description	(AC002130) F1N21.1 [Arabidopsis thaliana]

Seq. No.	133676
Contig ID	89357_1.R1010
5'-most EST	jC-atXLIB327403P1e07a1
Method	BLASTN
NCBI GI	g2264309
BLAST score	436
E value	0.0e+00

Match length	560
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	133677
Contig ID	89373_1.R1010
5'-most EST	jC-atXLIB327403P1f04a1

Seq. No.	133678
Contig ID	89375_1.R1010
5'-most EST	jC-atXLIB327403P1f06a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	292
E value	1.0e-163
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	133679
Contig ID	89378_1.R1010
5'-most EST	jC-atXLIB327403P1f08a1

Seq. No.	133680
Contig ID	89386_1.R1010
5'-most EST	jC-atXP118C144F19T7044a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133681
Contig ID	89389_1.R1010
5'-most EST	jC-atXLIB327403P1g03a1
Method	BLASTX
NCBI GI	g1730560
BLAST score	309
E value	4.0e-28
Match length	64
% identity	91
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]

Seq. No.	133682
Contig ID	89390_1.R1010
5'-most EST	jC-atXLIB327430P2a04a1
Method	BLASTN
NCBI GI	g2828278
BLAST score	158
E value	2.0e-83
Match length	446

% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	133683
Contig ID	89393_1.R1010
5'-most EST	jC-atXLIB327403P1g06a1
Method	BLASTN
NCBI GI	g4220510
BLAST score	426
E value	0.0e+00
Match length	426
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	133684
Contig ID	89397_1.R1010
5'-most EST	jC-atXLIB327403P1g08a1
Method	BLASTN
NCBI GI	g4580386
BLAST score	396
E value	0.0e+00
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	133685
Contig ID	89399_1.R1010
5'-most EST	jC-atXLIB327403P1g09a1
Method	BLASTN
NCBI GI	g3420042
BLAST score	405
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133686
Contig ID	89403_1.R1010
5'-most EST	jC-atXLIB327403P1g11a1
Method	BLASTN
NCBI GI	g3449322
BLAST score	276
E value	1.0e-154
Match length	401
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	133687
Contig ID	89407_1.R1010
5'-most EST	jC-atXP5C89O11T7069a1
Method	BLASTX
NCBI GI	g3540183

BLAST score	691
E value	8.0e-73
Match length	154
% identity	91
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	133688
Contig ID	89413_1.R1010
5'-most EST	jC-atXP123C159O2T7049a1
Method	BLASTX
NCBI GI	g1944319
BLAST score	398
E value	2.0e-38
Match length	142
% identity	56
NCBI Description	(D31700) cysteine proteinase inhibitor [Glycine max] >gi_1944342_dbj_BAA19610_ (D64115) cysteine proteinase inhibitor [Glycine max]

Seq. No.	133689
Contig ID	89422_1.R1010
5'-most EST	jC-atXLIB327403P1h11a1

Seq. No.	133690
Contig ID	89430_1.R1010
5'-most EST	jC-atXLIB327403P3a04a1

Seq. No.	133691
Contig ID	89528_1.R1010
5'-most EST	jC-atXLIB327403P4d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	8.0e-15
Match length	55
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133692
Contig ID	89530_1.R1010
5'-most EST	jC-atXP22C121L4T7088a1
Method	BLASTN
NCBI GI	g2564048
BLAST score	266
E value	1.0e-147
Match length	346
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	133693
Contig ID	89533_1.R1010
5'-most EST	jC-atXLIB327438P4g11b2
Method	BLASTN
NCBI GI	g3702315
BLAST score	321

E value	0.0e+00
Match length	329
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133694
Contig ID	89534_1.R1010
5'-most EST	jC-atXLIB327404P1b02a1

Seq. No.	133695
Contig ID	89553_1.R1010
5'-most EST	jC-atXLIB327404P1c03b1
Method	BLASTX
NCBI GI	g99809
BLAST score	276
E value	3.0e-24
Match length	88
% identity	55
NCBI Description	gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608) Bplo [Brassica napus]

Seq. No.	133696
Contig ID	89573_1.R1010
5'-most EST	jC-atXLIB327404P1d03a1

Seq. No.	133697
Contig ID	89584_1.R1010
5'-most EST	jC-atXLIB327404P1d09a1

Seq. No.	133698
Contig ID	89587_1.R1010
5'-most EST	jC-atXLIB327404P1d11a1
Method	BLASTX
NCBI GI	g4467134
BLAST score	272
E value	8.0e-24
Match length	76
% identity	75
NCBI Description	(AL035540) protein kinase like protein [Arabidopsis thaliana]

Seq. No.	133699
Contig ID	89591_1.R1010
5'-most EST	jC-atXLIB327404P1e01a1
Method	BLASTX
NCBI GI	g3608495
BLAST score	73
E value	2.0e-16
Match length	95
% identity	58
NCBI Description	(AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No.	133700
Contig ID	89613_1.R1010

5'-most EST	jC-atXLIB327404P1f02a1
Method	BLASTN
NCBI GI	g4056476
BLAST score	516
E value	0.0e+00
Match length	516
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133701
Contig ID	89618_1.R1010
5'-most EST	jC-atXLIB327404P1f05a1

Seq. No.	133702
Contig ID	89626_1.R1010
5'-most EST	jC-atXLIB327404P1f09a1
Method	BLASTN
NCBI GI	g3241926
BLAST score	385
E value	0.0e+00
Match length	465
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	133703
Contig ID	89664_1.R1010
5'-most EST	jC-atXLIB327404P2a02b1
Method	BLASTX
NCBI GI	g4056462
BLAST score	391
E value	8.0e-38
Match length	86
% identity	88
NCBI Description	(AC005990) Strong similarity to gb_Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF_00171. ESTs gb_F15117, gb_R83958 and gb_586262 come from this gene. [Arabidopsis thaliana]

Seq. No.	133704
Contig ID	89765_1.R1010
5'-most EST	jC-atXLIB327415P1b09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133705
Contig ID	89774_1.R1010
5'-most EST	jC-atXLIB327415P1c07a1
Method	BLASTN

NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	62
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133706
Contig ID	89776_1.R1010
5'-most EST	jC-atXLIB327415P1c08a1
Method	BLASTN
NCBI GI	g3702722
BLAST score	327
E value	0.0e+00
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No.	133707
Contig ID	89788_1.R1010
5'-most EST	jC-atXLIB327415P1d07a1
Method	BLASTN
NCBI GI	g4757411
BLAST score	317
E value	1.0e-178
Match length	590
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	133708
Contig ID	89791_1.R1010
5'-most EST	jC-atXLIB327430P1a08a1
Method	BLASTN
NCBI GI	g3869073
BLAST score	264
E value	1.0e-146
Match length	432
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	133709
Contig ID	89794_2.R1010
5'-most EST	jC-atXLIB327415P1d11a1
Method	BLASTN
NCBI GI	g2618600
BLAST score	273
E value	1.0e-152
Match length	332
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	133710
Contig ID	89807_1.R1010

5'-most EST	jC-atXLIB327415P1e08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133711
Contig ID	89837_1.R1010
5'-most EST	jC-atXLIB327415P2a08a2
Method	BLASTN
NCBI GI	g3204096
BLAST score	242
E value	1.0e-133
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana tapetum-specific A3 gene >gi_3410243_gb_I90303_I90303 Sequence 7 from patent US

Seq. No.	133712
Contig ID	89847_1.R1010
5'-most EST	jC-atXLIB327415P2c02a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	57
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133713
Contig ID	89853_1.R1010
5'-most EST	jC-atXLIB327415P2d02a2

Seq. No.	133714
Contig ID	89857_1.R1010
5'-most EST	jC-atXLIB327415P2d09a2
Method	BLASTN
NCBI GI	g4455168
BLAST score	313
E value	1.0e-176
Match length	357
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	133715
Contig ID	89862_1.R1010
5'-most EST	jC-atXLIB327415P2e02a2
Method	BLASTN
NCBI GI	g2656026
BLAST score	327
E value	0.0e+00
Match length	429

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	133716
Contig ID	89869_1.R1010
5'-most EST	jC-atXLIB327415P2e10a2
Method	BLASTX
NCBI GI	g4490294
BLAST score	236
E value	1.0e-19
Match length	57
% identity	82
NCBI Description	(AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No.	133717
Contig ID	89870_1.R1010
5'-most EST	jC-atXLIB327415P2e11a2
Method	BLASTN
NCBI GI	g2262155
BLAST score	289
E value	1.0e-161
Match length	351
% identity	99
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	133718
Contig ID	89871_1.R1010
5'-most EST	jC-atXLIB327415P2e12a1
Method	BLASTN
NCBI GI	g4589444
BLAST score	335
E value	0.0e+00
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence

Seq. No.	133719
Contig ID	89872_1.R1010
5'-most EST	jC-atXLIB327415P2f03a2
Method	BLASTN
NCBI GI	g4314374
BLAST score	106
E value	2.0e-52
Match length	222
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133720
Contig ID	89875_1.R1010
5'-most EST	jC-atXLIB327415P2f10a2

Seq. No.	133721

Contig ID 89877_2.R1010
5'-most EST g757601
Method BLASTN
NCBI GI g2244829
BLAST score 201
E value 1.0e-109
Match length 213
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 133722
Contig ID 90065_1.R1010
5'-most EST jC-atXLIB327420P3b07a1

Seq. No. 133723
Contig ID 90120_1.R1010
5'-most EST jC-atXLIB327420P4b03a1

Seq. No. 133724
Contig ID 90131_1.R1010
5'-most EST jC-atXLIB327420P4c06a1
Method BLASTX
NCBI GI g3201554
BLAST score 290
E value 4.0e-26
Match length 91
% identity 59
NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 133725
Contig ID 90135_1.R1010
5'-most EST jC-atXLIB327420P4c10a1
Method BLASTX
NCBI GI g2190553
BLAST score 312
E value 2.0e-28
Match length 113
% identity 65
NCBI Description (AC001229) Strong similarity to Arabidopsis zeta-crystallin-like protein (gb_Z49268). [Arabidopsis thaliana]

Seq. No. 133726
Contig ID 90140_1.R1010
5'-most EST jC-atXLIB327420P4d03a1
Method BLASTN
NCBI GI g2760316
BLAST score 248
E value 1.0e-137
Match length 493
% identity 88
NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 133727
Contig ID 90142_1.R1010

5'-most EST	jC-atXLIB327420P4d05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	6.0e-16
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133728
Contig ID	90147_1.R1010
5'-most EST	jC-atXLIB327420P4d11a1
Method	BLASTX
NCBI GI	g2832696
BLAST score	260
E value	2.0e-22
Match length	109
% identity	45
NCBI Description	(AL021713) putative protein [Arabidopsis thaliana]

Seq. No.	133729
Contig ID	90156_1.R1010
5'-most EST	jC-atXLIB327420P4e11a1
Method	BLASTN
NCBI GI	g4587677
BLAST score	322
E value	0.0e+00
Match length	500
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T22C12 genomic sequence, complete sequence

Seq. No.	133730
Contig ID	90164_1.R1010
5'-most EST	jC-atXLIB327420P4f09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133731
Contig ID	90166_1.R1010
5'-most EST	jC-atXLIB327420P4f11a1
Method	BLASTN
NCBI GI	g3449329
BLAST score	120
E value	1.0e-60
Match length	599
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	133732
Contig ID	90167_1.R1010

5'-most EST	jC-atXLIB327420P4f12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133733
Contig ID	90174_1.R1010
5'-most EST	jC-atXLIB327420P4g07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	49
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133734
Contig ID	90181_1.R1010
5'-most EST	jC-atXLIB327420P4h03a1
Method	BLASTN
NCBI GI	g3108025
BLAST score	383
E value	0.0e+00
Match length	515
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	133735
Contig ID	90184_1.R1010
5'-most EST	jC-atXLIB327420P4h08a1
Method	BLASTX
NCBI GI	g2924512
BLAST score	71
E value	3.0e-11
Match length	68
% identity	55
NCBI Description	(AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No.	133736
Contig ID	90291_1.R1010
5'-most EST	g2062893
Method	BLASTN
NCBI GI	g2618604
BLAST score	94
E value	3.0e-45
Match length	332
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 133737

Contig ID	90291_2.R1010
5'-most EST	jC-atXLIB327423P2b07a1
Method	BLASTN
NCBI GI	g483612
BLAST score	138
E value	2.0e-71
Match length	210
% identity	92
NCBI Description	B.napus (Topas) mRNA for 44kDa chloroplast envelope protein

Seq. No.	133738
Contig ID	90364_1.R1010
5'-most EST	jC-atXLIB327423P2f11a1
Method	BLASTX
NCBI GI	g2979553
BLAST score	268
E value	3.0e-23
Match length	103
% identity	46
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133739
Contig ID	90416_1.R1010
5'-most EST	jC-atXLIB327423P3a12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	3.0e-09
Match length	34
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133740
Contig ID	90470_1.R1010
5'-most EST	g2413921
Method	BLASTX
NCBI GI	g3080425
BLAST score	571
E value	9.0e-59
Match length	113
% identity	100
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	133741
Contig ID	90470_2.R1010
5'-most EST	jC-atXLIB327423P3d08a1
Method	BLASTX
NCBI GI	g3080425
BLAST score	513
E value	1.0e-117
Match length	217
% identity	92
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	133742
Contig ID	90481_1.R1010
5'-most EST	jC-atXLIB327427P3a02a2

Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	133743
Contig ID	90487_1.R1010
5'-most EST	jC-atXLIB327423P3e07a1
Method	BLASTN
NCBI GI	g2337888
BLAST score	455
E value	0.0e+00
Match length	463
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	133744
Contig ID	90524_1.R1010
5'-most EST	jC-atXLIB327423P3g04a1

Seq. No.	133745
Contig ID	90543_1.R1010
5'-most EST	jC-atXP24C123J7T7082a1
Method	BLASTN
NCBI GI	g4585952
BLAST score	221
E value	1.0e-121
Match length	553
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	133746
Contig ID	90593_1.R1010
5'-most EST	jC-atXLIB327423P4c07a1
Method	BLASTN
NCBI GI	g4539432
BLAST score	308
E value	1.0e-173
Match length	452
% identity	53
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4F9 (ESSA project)

Seq. No.	133747
Contig ID	90676_1.R1010
5'-most EST	jC-atXLIB327423P4g09a1
Method	BLASTX
NCBI GI	g2984119
BLAST score	160
E value	9.0e-11
Match length	61
% identity	43

NCBI Description	(AE000758) peptide chain release factor RF-2 [Aquifex aeolicus]

Seq. No.	133748
Contig ID	90719_1.R1010
5'-most EST	jC-atXLIB327424P1b06a1
Method	BLASTX
NCBI GI	g2245120
BLAST score	699
E value	6.0e-74
Match length	151
% identity	91
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133749
Contig ID	90749_1.R1010
5'-most EST	jC-atXLIB327424P1e04a1

Seq. No.	133750
Contig ID	90766_1.R1010
5'-most EST	jC-atXLIB327424P1g01a1
Method	BLASTX
NCBI GI	g3850823
BLAST score	249
E value	3.0e-21
Match length	58
% identity	78
NCBI Description	(Y18351) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]

Seq. No.	133751
Contig ID	90768_1.R1010
5'-most EST	jC-atXLIB327424P1g03a1
Method	BLASTN
NCBI GI	g2642152
BLAST score	155
E value	1.0e-81
Match length	265
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133752
Contig ID	90777_1.R1010
5'-most EST	jC-atXP70C220K16T7005a1
Method	BLASTX
NCBI GI	g3738288
BLAST score	337
E value	2.0e-31
Match length	118
% identity	56
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	133753
Contig ID	90788_1.R1010
5'-most EST	g2048637

Method	BLASTN
NCBI GI	g2564049
BLAST score	356
E value	0.0e+00
Match length	380
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	133754
Contig ID	90868_1.R1010
5'-most EST	jC-atXLIB327424P3e10b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	42
E value	3.0e-14
Match length	46
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	133755
Contig ID	90882_1.R1010
5'-most EST	jC-atXLIB327424P3f10a1

Seq. No.	133756
Contig ID	90888_1.R1010
5'-most EST	jC-atXLIB327424P3g02a1

Seq. No.	133757
Contig ID	90898_1.R1010
5'-most EST	g870901
Method	BLASTN
NCBI GI	g2645198
BLAST score	216
E value	1.0e-118
Match length	317
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133758
Contig ID	90902_1.R1010
5'-most EST	jC-atXP44C170I2T7068a1
Method	BLASTN
NCBI GI	g2760173
BLAST score	731
E value	0.0e+00
Match length	843
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	133759
Contig ID	90902_2.R1010
5'-most EST	jC-atXLIB327424P3g09a1
Method	BLASTN

NCBI GI	g2760173
BLAST score	304
E value	1.0e-170
Match length	428
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	133760
Contig ID	90943_1.R1010
5'-most EST	jC-atXP2C74B9T7015a1
Method	BLASTX
NCBI GI	g3355490
BLAST score	266
E value	2.0e-88
Match length	166
% identity	100
NCBI Description	(AC004218) putative dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	133761
Contig ID	91019_2.R1010
5'-most EST	jC-atXLIB327430P1f10a1
Method	BLASTX
NCBI GI	g3142300
BLAST score	201
E value	2.0e-15
Match length	62
% identity	55
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	133762
Contig ID	91022_2.R1010
5'-most EST	jC-alX25046Q1E1F03a1
Method	BLASTX
NCBI GI	g3548802
BLAST score	148
E value	2.0e-09
Match length	45
% identity	67
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	133763
Contig ID	91030_2.R1010
5'-most EST	jC-alX25053Q1E1A07a1
Method	BLASTN
NCBI GI	g4455168
BLAST score	181
E value	3.0e-97
Match length	461
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10

(ESSAII project)

Seq. No.	133764
Contig ID	91066_1.R1010
5'-most EST	jC-atXLIB327406P4g08a2
Method	BLASTN
NCBI GI	g3193282
BLAST score	413
E value	0.0e+00
Match length	445
% identity	99
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	133765
Contig ID	91066_3.R1010
5'-most EST	jC-atXmonuni25Ah11a1
Method	BLASTN
NCBI GI	g3193282
BLAST score	379
E value	0.0e+00
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	133766
Contig ID	91141_2.R1010
5'-most EST	jC-atXLIB327426P1e04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133767
Contig ID	91182_1.R1010
5'-most EST	jC-atXLIB327426P1g05a1
Method	BLASTN
NCBI GI	g2760169
BLAST score	104
E value	3.0e-51
Match length	333
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	133768
Contig ID	91191_1.R1010
5'-most EST	jC-atXP54C188I8T7046a1
Method	BLASTN
NCBI GI	g2618677
BLAST score	187
E value	1.0e-100
Match length	417
% identity	94
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No.	133769
Contig ID	91309_1.R1010
5'-most EST	jC-atXLIB327427P4c09a2

Seq. No.	133770
Contig ID	91392_1.R1010
5'-most EST	jC-atXP112C129A24T7d2
Method	BLASTX
NCBI GI	g4454026
BLAST score	489
E value	6.0e-49
Match length	109
% identity	83
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	133771
Contig ID	91397_1.R1010
5'-most EST	jC-atXLIB327428P4c07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133772
Contig ID	91429_1.R1010
5'-most EST	jC-atXLIB327428P4f08a2
Method	BLASTN
NCBI GI	g2264311
BLAST score	436
E value	0.0e+00
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	133773
Contig ID	91456_1.R1010
5'-most EST	jC-atXLIB327431P1a03a1
Method	BLASTX
NCBI GI	g4678384
BLAST score	400
E value	7.0e-39
Match length	90
% identity	84
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	133774
Contig ID	91458_1.R1010
5'-most EST	jC-atXLIB327431P1a05a1
Method	BLASTN
NCBI GI	g4538990
BLAST score	317

E value	1.0e-178
Match length	449
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	133775
Contig ID	91460_1.R1010
5'-most EST	jC-atXLIB327431P1a06a1
Method	BLASTN
NCBI GI	g4510323
BLAST score	394
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	133776
Contig ID	91464_1.R1010
5'-most EST	jC-atXLIB327431P1a09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	58
E value	9.0e-24
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133777
Contig ID	91510_1.R1010
5'-most EST	jC-atXLIB327431P1d08b1
Method	BLASTX
NCBI GI	g4510402
BLAST score	204
E value	8.0e-33
Match length	104
% identity	72
NCBI Description	(AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No.	133778
Contig ID	91546_1.R1010
5'-most EST	jC-atXLIB327431P1f08b1
Method	BLASTN
NCBI GI	g3021263
BLAST score	36
E value	2.0e-10
Match length	209
% identity	29
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSAII project)

Seq. No.	133779
Contig ID	91561_1.R1010
5'-most EST	jC-atXLIB327431P1g05b1
Method	BLASTN
NCBI GI	g3327922

BLAST score	288
E value	1.0e-161
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133780
Contig ID	91568_1.R1010
5'-most EST	jC-atXLIB327431P1g11b1
Method	BLASTN
NCBI GI	g4689365
BLAST score	337
E value	0.0e+00
Match length	396
% identity	96
NCBI Description	Arabidopsis thaliana RING finger protein mRNA, complete cds

Seq. No.	133781
Contig ID	91570_1.R1010
5'-most EST	jC-atXLIB327431P1g12b1
Method	BLASTX
NCBI GI	g4835246
BLAST score	505
E value	4.0e-51
Match length	115
% identity	81
NCBI Description	(AL049862) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	133782
Contig ID	91598_1.R1010
5'-most EST	jC-atXLIB327431P2a08a1

Seq. No.	133783
Contig ID	91602_1.R1010
5'-most EST	jC-atXP78CF6G9T7b1
Method	BLASTN
NCBI GI	g4220645
BLAST score	301
E value	1.0e-168
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	133784
Contig ID	91606_1.R1010
5'-most EST	jC-atXLIB327431P2a12a1
Method	BLASTN
NCBI GI	g4589409
BLAST score	413
E value	0.0e+00
Match length	477
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	133785
Contig ID	91651_1.R1010
5'-most EST	jC-atXP122C152P6T7039a1
Method	BLASTX
NCBI GI	g1903347
BLAST score	90
E value	1.0e-15
Match length	251
% identity	30
NCBI Description	(AC000104) EST gb_ATTS5672 comes from this gene. [Arabidopsis thaliana]

Seq. No.	133786
Contig ID	91651_2.R1010
5'-most EST	jC-atXLIB327431P2d06b1
Method	BLASTN
NCBI GI	g2828182
BLAST score	228
E value	1.0e-125
Match length	389
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	133787
Contig ID	91715_1.R1010
5'-most EST	jC-atXLIB327431P2g07b1
Method	BLASTN
NCBI GI	g2191126
BLAST score	366
E value	0.0e+00
Match length	425
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	133788
Contig ID	91731_1.R1010
5'-most EST	jC-atXLIB327431P2h06b1

Seq. No.	133789
Contig ID	91817_1.R1010
5'-most EST	g2748381
Method	BLASTX
NCBI GI	g3608127
BLAST score	241
E value	3.0e-20
Match length	89
% identity	60
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	133790
Contig ID	91831_1.R1010
5'-most EST	jC-atXLIB327431P3f05b1
Method	BLASTX
NCBI GI	g4587997
BLAST score	955

E value	1.0e-103
Match length	187
% identity	100
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133791
Contig ID	91872_1.R1010
5'-most EST	jC-atXLIB327431P3h12b1
Method	BLASTX
NCBI GI	g4539327
BLAST score	263
E value	1.0e-22
Match length	55
% identity	95
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	133792
Contig ID	91872_2.R1010
5'-most EST	jC-atXP51C179O16T7s1
Method	BLASTN
NCBI GI	g4539309
BLAST score	287
E value	1.0e-160
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	133793
Contig ID	91925_1.R1010
5'-most EST	jC-atXLIB327431P4e01b1
Method	BLASTN
NCBI GI	g2827138
BLAST score	370
E value	0.0e+00
Match length	442
% identity	96
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit (RSW1) gene, complete cds

Seq. No.	133794
Contig ID	91940_1.R1010
5'-most EST	jC-atXLIB327431P4e10b1

Seq. No.	133795
Contig ID	91945_2.R1010
5'-most EST	g402949
Method	BLASTN
NCBI GI	g3399678
BLAST score	287
E value	1.0e-160
Match length	302
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133796